**Supplementary Table 3. PSORTb predictions of subcellular localisation of gonococcal proteins identified by mass spectrometry.**

Raw data are provided for each of the bands, number from \_001 to \_018.

**Band\_001**

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01967

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599939: N utilization substance protein A[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01917

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00938

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

**Band\_002**

SeqID: PCKMOKAE\_00616

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 34395980: Prolyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00307

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131370: oligopeptidase A [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01561

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 24212422: Aspartyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00579

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128878: 30S ribosomal subunit protein S1 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00222

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 21263546: Elongation factor G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01908

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01997

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 130758: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 9.44

Cytoplasmic 0.33

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Final Prediction:

Periplasmic 9.44

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00009

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128916: fused predicted transporter subunits of ABC superfamily: ATP-binding components [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00747

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599525: pyruvate kinase II[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00618

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129056: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00619

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159292: Dihydrolipoyl dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02013

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128916: fused predicted transporter subunits of ABC superfamily: ATP-binding components [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00406

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 2507372: Cytoplasmic membrane associated cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01331

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599957: DNA repair protein RecN[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01317

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 66773832: Phenylalanyl-tRNA synthetase beta chain]

SCL-BLASTe- Cytoplasmic [matched 100% 66773832: Phenylalanyl-tRNA synthetase beta chain]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00696

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01196

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00213

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139600: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00611

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.52

Extracellular 0.38

Periplasmic 0.09

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.52

-------------------------------------------------------------------------------

**Band\_003**

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00170

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598964: GMP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00527

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67461599: Glutamyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00621

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01579

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598721: argininosuccinate synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01948

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16129225: component I of anthranilate synthase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168735: Ribonuclease G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01065

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 67461600: Seryl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01771

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595528: threonine dehydratase, biosynthetic[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00656

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81311142: Cysteinyl-tRNA synthetase]

SCL-BLASTe- Cytoplasmic [matched 100% 81311142: Cysteinyl-tRNA synthetase]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01670

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599679: |Glu-tRNA(Gln) amidotransferase subunit A|5013974 - 5015428]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01508

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599890: acetolactate synthase large subunit[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 8.46

Cytoplasmic 1.33

Periplasmic 0.21

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

CytoplasmicMembrane 8.46

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01429

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 13959695: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00243

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130340: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00617

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600208: pyruvate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02015

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 83288413: Peptidyl-prolyl cis-trans isomerase D]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.82

Cytoplasmic 0.15

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Final Prediction:

CytoplasmicMembrane 9.82

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00642

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599836: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01805

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 90111550: ATP-dependent RNA helicase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01838

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 61248979: Trk system potassium uptake protein trkA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01138

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81311251: Peptide chain release factor 3]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02067

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595745: transketolase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01133

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596032: phosphate acetyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02028

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00616

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 34395980: Prolyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01059

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599943: phosphoglucosamine mutase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01968

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81311174: Translation initiation factor IF-2]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.94

Periplasmic 0.04

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.94

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01672

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01986

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599175: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00714

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68565958: Methionyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01879

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 118671: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00591

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01275

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 62297827: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02186

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00579

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128878: 30S ribosomal subunit protein S1 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01024

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00325

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 34395929: Ribonuclease E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01440

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 7404369: Fumarate hydratase class II]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00309

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16130926: DNA topoisomerase IV, subunit B [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01748

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [7 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01561

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 24212422: Aspartyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00424

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168303: Acetate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00619

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159292: Dihydrolipoyl dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00436

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75355970: Arginyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01533

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600047: phosphoribosylaminoimidazolecarboxamide formyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02136

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 121372: Glutamine synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00831

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599215: UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00345

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68056567: (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00675

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597725: hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01168

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [11 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00213

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139600: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02060

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00253

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598533: ADP-L-glycero-D-mannoheptose 6-epimerase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01503

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596984: aconitate hydratase 2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02019

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 3915974: Lipoprotein-releasing system ATP-binding protein lolD]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01924

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596414: probable 2-isopropylmalate synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01702

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 15595963: serine protease MucD precursor[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 9.44

Cytoplasmic 0.33

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Final Prediction:

Periplasmic 9.44

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01034

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597216: probable transcriptional regulator[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02088

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 128512: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 9.44

Cytoplasmic 0.33

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Final Prediction:

Periplasmic 9.44

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01965

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141771: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

**Band\_004**

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00222

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 21263546: Elongation factor G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01405

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1708408: Isocitrate dehydrogenase [NADP]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00569

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596353: NrdA, catalytic component of class Ia ribonucleotide reductase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00309

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16130926: DNA topoisomerase IV, subunit B [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01256

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 62297831: NADH-quinone oxidoreductase subunit 3 (NADH dehydrogenase I chain 3)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01147

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172701: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00617

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600208: pyruvate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00737

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128878: 30S ribosomal subunit protein S1 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01067

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16130926: DNA topoisomerase IV, subunit B [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01503

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596984: aconitate hydratase 2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01317

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 66773832: Phenylalanyl-tRNA synthetase beta chain]

SCL-BLASTe- Cytoplasmic [matched 100% 66773832: Phenylalanyl-tRNA synthetase beta chain]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00404

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133466: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00215

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139601: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02199

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600406: glycine cleavage system protein P1[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00170

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598964: GMP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 1766042: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01567

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Extracellular [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Extracellular 6.26

OuterMembrane 3.73

Periplasmic 0.02

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01858

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 12230400: Proline iminopeptidase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00808

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141685: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01531

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75432448: Alanyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01989

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595752: fructose-1,6-bisphosphate aldolase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01878

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01491

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 109894963: Glutaminyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01748

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [7 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01460

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 16130915: DNA topoisomerase IV, subunit A [Escherichia coli str. K-12 substr. MG1655]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01088

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2507434: Isoleucyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01217

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01910

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00739

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00307

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131370: oligopeptidase A [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01308

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 73919809: Threonyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01261

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 2499323: NADH-quinone oxidoreductase subunit 5 (NADH dehydrogenase I chain 5) (NDH-1 subunit 5)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00619

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159292: Dihydrolipoyl dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01283

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00984

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596389: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00213

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139600: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

**Band\_005**

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01818

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16129636: selenocysteine lyase, PLP-dependent [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 37538304: NAD-specific glutamate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 4.74

Cytoplasmic 4.28

Periplasmic 0.37

Extracellular 0.37

CytoplasmicMembrane 0.24

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00519

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599646: UDP-N-acetylglucosamine 1-carboxyvinyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01984

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599283: probable aminotransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01128

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600456: argininosuccinate lyase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00424

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168303: Acetate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00298

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 6093519: Nodulation protein E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00652

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01035

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 1709008: Multidrug resistance protein mexA precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00834

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599604: cell division protein FtsA[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01286

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595234: tryptophan synthase beta chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00461

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168262: Aspartate aminotransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01752

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 75507409: Histidyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00044

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598931: homoserine dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01278

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598307: folylpolyglutamate synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00835

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 17380383: Cytoplasmic membrane associated cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00520

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1730514: Phosphoglycerate kinase, plasmid]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02175

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 8134631: P-protein]

SCL-BLASTe- Cytoplasmic [matched 100% 8134631: P-protein]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01037

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- OuterMembrane [matched 3 rules (Rule64, Rule116, Rule137)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 11353796: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01153

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 118129: Sulfate/thiosulfate import ATP-binding protein cysA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.82

Cytoplasmic 0.15

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Final Prediction:

CytoplasmicMembrane 9.82

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02068

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 120601: Fumarate hydratase class II]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00152

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159297: DNA polymerase III subunit beta]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01926

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2507237: Gamma-glutamyl phosphate reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01644

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598930: threonine synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00549

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 84028839: Tyrosyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00760

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00445

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00564

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 66774125: Enolase]

SCL-BLASTe- Cytoplasmic [matched 100% 66774125: Enolase]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01854

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01487

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 8039808: tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01258

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 2499313: NADH-quinone oxidoreductase subunit 1 (NADH dehydrogenase I chain 1) (NDH-1 subunit 1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00021

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141520: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00258

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67471590: Adenylosuccinate synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00303

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 6647446: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00170

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598964: GMP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00270

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600436: delta-aminolevulinic acid dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01221

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597825: adenylosuccinate lyase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 5.96

Cytoplasmic 4.03

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01150

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597972: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01065

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 67461600: Seryl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00539

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600048: phosphoribosylamine--glycine ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01112

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 33518621: Oxygen-independent coproporphyrinogen III oxidase 1]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00436

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75355970: Arginyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00215

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139601: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00569

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596353: NrdA, catalytic component of class Ia ribonucleotide reductase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00812

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01696

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599177: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00642

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599836: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00828

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 127537: UDP-N-acetylmuramoylalanine--D-glutamate ligase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01275

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 62297827: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00794

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599952: carbamoyl-phosphate synthase small chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01206

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01503

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596984: aconitate hydratase 2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01731

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 109892642: S-adenosylmethionine synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00729

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 120576: Cytoplasmic membrane associated cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01748

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [7 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01879

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 118671: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02183

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 48474290: Guanylate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00617

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600208: pyruvate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01773

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [5 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 118165: Cytoplasmic membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00222

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 21263546: Elongation factor G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01397

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598024: probable aminotransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00252

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00630

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599242: GTP cyclohydrolase II[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00110

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00153

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399394: Chromosomal replication initiator protein dnaA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01405

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1708408: Isocitrate dehydrogenase [NADP]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00556

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 15599196: |soluble lytic transglycosylase B|sltB1|PA4001[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.99

Periplasmic 0.01

Extracellular 0.01

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.99

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01329

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

**Band\_006**

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01818

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16129636: selenocysteine lyase, PLP-dependent [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01633

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597809: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 37538304: NAD-specific glutamate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 4.74

Cytoplasmic 4.28

Periplasmic 0.37

Extracellular 0.37

CytoplasmicMembrane 0.24

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02068

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 120601: Fumarate hydratase class II]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01984

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599283: probable aminotransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00258

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67471590: Adenylosuccinate synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01128

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600456: argininosuccinate lyase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00298

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 6093519: Nodulation protein E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00519

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599646: UDP-N-acetylglucosamine 1-carboxyvinyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01286

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595234: tryptophan synthase beta chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01942

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 61224538: Serine hydroxymethyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00424

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168303: Acetate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00461

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168262: Aspartate aminotransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01752

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 75507409: Histidyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00834

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599604: cell division protein FtsA[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01150

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597972: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01037

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- OuterMembrane [matched 3 rules (Rule64, Rule116, Rule137)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 11353796: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01035

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 1709008: Multidrug resistance protein mexA precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00520

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1730514: Phosphoglycerate kinase, plasmid]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00445

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00152

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159297: DNA polymerase III subunit beta]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00044

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598931: homoserine dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01221

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597825: adenylosuccinate lyase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 5.96

Cytoplasmic 4.03

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00652

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00021

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141520: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01879

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 118671: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00549

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 84028839: Tyrosyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00835

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 17380383: Cytoplasmic membrane associated cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02175

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 8134631: P-protein]

SCL-BLASTe- Cytoplasmic [matched 100% 8134631: P-protein]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01278

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598307: folylpolyglutamate synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01258

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 2499313: NADH-quinone oxidoreductase subunit 1 (NADH dehydrogenase I chain 1) (NDH-1 subunit 1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00360

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133395: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01667

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595944: probable aldehyde dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01895

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599215: UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01644

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598930: threonine synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00564

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 66774125: Enolase]

SCL-BLASTe- Cytoplasmic [matched 100% 66774125: Enolase]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01153

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 118129: Sulfate/thiosulfate import ATP-binding protein cysA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.82

Cytoplasmic 0.15

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Final Prediction:

CytoplasmicMembrane 9.82

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00539

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600048: phosphoribosylamine--glycine ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00303

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 6647446: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01787

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598855: probable aminotransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01608

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131851: glucosephosphate isomerase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00808

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141685: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01926

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2507237: Gamma-glutamyl phosphate reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01487

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 8039808: tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01731

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 109892642: S-adenosylmethionine synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01854

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01106

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600239: malic enzyme[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01885

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3123196: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00270

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600436: delta-aminolevulinic acid dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00642

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599836: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02186

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00715

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3915705: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00436

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75355970: Arginyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01361

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 13959695: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01533

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600047: phosphoribosylaminoimidazolecarboxamide formyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01147

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172701: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01148

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 732261: Probable ATP synthase yscN]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00325

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 34395929: Ribonuclease E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00794

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599952: carbamoyl-phosphate synthase small chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00569

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596353: NrdA, catalytic component of class Ia ribonucleotide reductase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01892

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595550: dihydroxy-acid dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01500

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 113724: Cytosol aminopeptidase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00617

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600208: pyruvate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02206

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598087: geranyl-CoA carboxylase, alpha-subunit (biotin-containing)[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00822

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01275

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 62297827: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00914

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600470: diaminopimelate decarboxylase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01484

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129041: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01065

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 67461600: Seryl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00828

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 127537: UDP-N-acetylmuramoylalanine--D-glutamate ligase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01206

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01483

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 124106279: Dihydrolipoyl dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02067

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595745: transketolase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00855

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 13959695: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00759

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 417166: Transcriptional regulatory protein zraR]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00170

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598964: GMP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00760

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 119391048: Phosphoribosylformylglycinamidine synthase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01055

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595451: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00714

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68565958: Methionyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01809

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 62288339: ATP-dependent hsl protease ATP-binding subunit hslU]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00667

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 115015: Bifunctional protein birA [Includes: Biotin operon repressor; Biotin--[acetyl-CoA-carboxylase] synthetase (Biotin--protein ligase)]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01112

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 33518621: Oxygen-independent coproporphyrinogen III oxidase 1]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01308

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 73919809: Threonyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00831

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599215: UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00260

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [12 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 2507511: Multidrug resistance protein mdtK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01613

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598390: phosphogluconate dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01471

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01485

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598833: CTP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00729

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 120576: Cytoplasmic membrane associated cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01297

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600528: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01643

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00611

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.52

Extracellular 0.38

Periplasmic 0.09

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.52

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01968

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81311174: Translation initiation factor IF-2]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.94

Periplasmic 0.04

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.94

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596129: cysteine synthase B[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00514

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00340

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00213

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139600: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01063

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75432438: Peptide chain release factor 1]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01227

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 15600682: thiol:disulfide interchange protein DsbA[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 1766042: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01652

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

**Band\_007**

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598441: |cell division topological specificity factor MinE|3632430 - 3632684]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00598

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133030: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 37538304: NAD-specific glutamate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 4.74

Cytoplasmic 4.28

Periplasmic 0.37

Extracellular 0.37

CytoplasmicMembrane 0.24

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00321

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 8134599: Outer membrane lipoprotein omlA precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.93

Periplasmic 0.03

Extracellular 0.03

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.93

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00438

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00372

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 132813: 50S ribosomal protein L24]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00781

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00879

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595776: |30S ribosomal protein S21|639115 - 638900]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00373

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599449: |50S ribosomal protein L14|4762635 - 4762267]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

**Band\_008**

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01769

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599866: probable ribosomal protein L25[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598441: |cell division topological specificity factor MinE|3632430 - 3632684]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01154

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599935: |30S ribosomal protein S15|5325922 - 5325653]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00384

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599460: |30S ribosomal protein S10|4767654 - 4767343]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00081

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00471

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 729371: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 9.44

Cytoplasmic 0.33

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Final Prediction:

Periplasmic 9.44

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00848

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00321

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 8134599: Outer membrane lipoprotein omlA precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.93

Periplasmic 0.03

Extracellular 0.03

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.93

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00373

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599449: |50S ribosomal protein L14|4762635 - 4762267]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00438

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01363

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00689

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599628: |30S ribosomal protein S9|4965501 - 4965109]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00875

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 128372: Lipoprotein 28 precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00381

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599457: |50S ribosomal protein L23|4766012 - 4765713]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00379

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599455: |30S ribosomal protein S19|4764863 - 4764588]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00672

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01437

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600609: |50S ribosomal protein L28|5986119 - 5985883]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00879

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595776: |30S ribosomal protein S21|639115 - 638900]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00253

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598533: ADP-L-glycero-D-mannoheptose 6-epimerase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 37538304: NAD-specific glutamate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 4.74

Cytoplasmic 4.28

Periplasmic 0.37

Extracellular 0.37

CytoplasmicMembrane 0.24

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00882

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599624: stringent starvation protein A[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01284

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128045: S-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

**-------------------------------------------------------------------------------**

**Band\_009**

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00081

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598441: |cell division topological specificity factor MinE|3632430 - 3632684]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01266

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01154

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599935: |30S ribosomal protein S15|5325922 - 5325653]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00689

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599628: |30S ribosomal protein S9|4965501 - 4965109]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00438

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00384

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599460: |30S ribosomal protein S10|4767654 - 4767343]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02172

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00672

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00321

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 8134599: Outer membrane lipoprotein omlA precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.93

Periplasmic 0.03

Extracellular 0.03

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.93

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01466

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01650

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01966

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599940: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00732

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [18 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00113

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

**Band\_010**

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01769

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599866: probable ribosomal protein L25[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01511

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123136: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01614

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 584746: KHG/KDPG aldolase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01336

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600256: ubiquinone biosynthesis methyltransferase UbiE[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01095

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01459

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01994

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600524: orotate phosphoribosyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01729

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596401: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00934

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599201: nicotinic acid mononucleotide adenylyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00882

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599624: stringent starvation protein A[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00754

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595217: polypeptide deformylase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00078

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00361

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599435: 30S ribosomal protein S4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01219

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01736

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 12230895: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00337

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 31076875: Ribosome recycling factor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01368

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599841: uracil phosphoribosyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01169

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 83287787: Transcriptional regulatory protein cpxR]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02143

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599654: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00208

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599471: transcription antitermination protein NusG[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00797

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01655

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598316: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00857

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595591: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01179

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 2506102: Ferrichrome transport ATP-binding protein fhuC]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00471

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 729371: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 9.44

Cytoplasmic 0.33

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Final Prediction:

Periplasmic 9.44

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00865

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 81175157: NADH-quinone oxidoreductase subunit 9]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 6.29

Cytoplasmic 3.70

Periplasmic 0.01

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00115

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 137035: Uracil-DNA glycosylase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00267

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01674

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599412: probable pyridoxamine 5'-phosphate oxidase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02019

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 3915974: Lipoprotein-releasing system ATP-binding protein lolD]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01411

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00262

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595564: probable transcriptional regulator[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00693

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 1717955: Ubiquinol-cytochrome c reductase iron-sulfur subunit]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.82

Cytoplasmic 0.15

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Final Prediction:

CytoplasmicMembrane 9.82

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00429

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598829: 4-diphosphocytidyl-2-C-methylerythritol synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00331

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01741

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 15600235: type 4 fimbrial biogenesis protein PilO[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

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SeqID: PCKMOKAE\_02009

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595804: ribulose-phosphate 3-epimerase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00925

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00855

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 13959695: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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SeqID: PCKMOKAE\_02183

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 48474290: Guanylate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00578

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 62288348: Cytidylate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02184

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 22653651: Adenine phosphoribosyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01126

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595584: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00408

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 122116: H.8 outer membrane protein precursor]

SCL-BLASTe- OuterMembrane [matched 100% 122116: H.8 outer membrane protein precursor]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01241

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596163: |Holliday junction resolvase RuvC|1051132 - 1051656]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01124

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3913939: Inorganic pyrophosphatase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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SeqID: PCKMOKAE\_00672

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00330

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 20455199: Cytoplasmic membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00699

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599840: probable purine/pyrimidine phosphoribosyl transferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01027

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00856

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598299: general secretion pathway protein E [Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00250

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00638

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128162: 30S ribosomal subunit protein S2 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01758

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00280

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2507227: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00630

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599242: GTP cyclohydrolase II[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01227

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 15600682: thiol:disulfide interchange protein DsbA[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00272

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599946: cell division protein FtsJ[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00159

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598168: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02003

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 118438: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01097

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595233: tryptophan synthase alpha chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00908

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00590

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 116523: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01281

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 121397: Glutamine transport ATP-binding protein glnQ]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.99

Cytoplasmic 0.01

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 9.99

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00989

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02061

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 118793: DNA polymerase III polC-type]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01991

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00377

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131193: 30S ribosomal subunit protein S3 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01710

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01109

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 113730: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01166

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599674: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01497

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596141: phosphoribosylaminoimidazole synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00573

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00368

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599444: 50S ribosomal protein L6[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02192

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01203

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595794: probable nucleotidyl transferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00684

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01963

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01611

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01360

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01646

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598593: ferredoxin--NADP+ reductase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 16078059: molecular chaperone [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00487

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599956: heat shock protein GrpE[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00635

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598850: uridylate kinase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01806

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02006

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16079384: riboflavin synthase subunit alpha [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01748

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [7 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00360

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133395: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01965

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141771: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02133

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01740

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 15600236: type 4 fimbrial biogenesis protein PilN[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.82

Cytoplasmic 0.15

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Final Prediction:

CytoplasmicMembrane 9.82

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00319

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67467385: Leucyl/phenylalanyl-tRNA--protein transferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01422

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 84028072: Enoyl-[acyl-carrier-protein] reductase [NADH]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00618

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129056: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01034

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597216: probable transcriptional regulator[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01136

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20455028: Imidazole glycerol phosphate synthase subunit hisF]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00905

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 19862632: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00608

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00325

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 34395929: Ribonuclease E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00219

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

**Band\_011**

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02172

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01266

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00586

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Extracellular [matched 15599002: nucleoside diphosphate kinase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Extracellular 9.45

Cytoplasmic 0.34

Periplasmic 0.19

CytoplasmicMembrane 0.02

OuterMembrane 0.00

Final Prediction:

Extracellular 9.45

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00598

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133030: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00373

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599449: |50S ribosomal protein L14|4762635 - 4762267]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00376

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599452: |50S ribosomal protein L16|4763532 - 4763119]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01708

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597862: probable 6-pyruvoyl tetrahydrobiopterin synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00689

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599628: |30S ribosomal protein S9|4965501 - 4965109]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01769

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599866: probable ribosomal protein L25[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01409

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01326

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 141380: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02099

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599704: probable transcriptional regulator[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01966

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599940: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01344

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01095

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

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SeqID: PCKMOKAE\_01511

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123136: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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SeqID: PCKMOKAE\_00220

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131221: 30S ribosomal subunit protein S12 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01495

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00274

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00863

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 67462174: ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 6.29

Cytoplasmic 3.70

Periplasmic 0.01

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00211

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599468: |50S ribosomal protein L10|4781786 - 4781286]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159412: ATP-dependent protease La]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01405

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1708408: Isocitrate dehydrogenase [NADP]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00345

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68056567: (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00384

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599460: |30S ribosomal protein S10|4767654 - 4767343]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01154

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599935: |30S ribosomal protein S15|5325922 - 5325653]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01343

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 15596066: |D-alanyl-D-alanine-endopeptidase|950648 - 949716]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01729

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596401: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01808

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 39932236: Taurine--pyruvate aminotransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01835

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01039: SBP\_BACTERIAL\_3 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 3183509: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00889

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01994

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600524: orotate phosphoribosyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00766

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00078

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

**Band\_012**

SeqID: PCKMOKAE\_01355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596129: cysteine synthase B[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01515

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123158: Histidine biosynthesis bifunctional protein hisB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00296

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 67471945: Dihydroorotate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01181

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 14195456: Putative periplasmic iron-binding protein HI0362 precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01768

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67466690: Ribose-phosphate pyrophosphokinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01901

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 78099211: Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 16078059: molecular chaperone [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01490

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595604: glutathione synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01297

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600528: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00819

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140164: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01377

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600227: uroporphyrinogen decarboxylase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00251

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01127

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597219: UTP--glucose-1-phosphate uridylyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00006

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS01068: OMPA Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129131: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129131: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01762

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599924: pantoate--beta-alanine ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00354

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 150421534: HTH-type transcriptional regulator cynR]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01812

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131058: tRNA pseudouridine synthase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01512

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00636

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75507282: Elongation factor Ts]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 2507359: Thiamine-binding periplasmic protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00392

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3023329: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01519

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 84028736: Probable protease sohB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00166

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68566320: 3-oxoacyl-[acyl-carrier-protein] synthase 3]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01610

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183526: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01860

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 66774113: Dihydrodipicolinate synthase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596786: succinyl-CoA synthetase alpha chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01949

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01442

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01865

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600138: delta 2-isopentenylpyrophosphate transferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00335

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00536

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00117

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00662

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596993: 5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 5.96

Cytoplasmic 4.03

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01801

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600113: NH3-dependent NAD synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00601

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71164789: Thioredoxin reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 4.99

CytoplasmicMembrane 4.90

Extracellular 0.10

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01663

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599012: probable methyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00865

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 81175157: NADH-quinone oxidoreductase subunit 9]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 6.29

Cytoplasmic 3.70

Periplasmic 0.01

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01246

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1170589: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00650

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00755

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131167: 10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00469

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 15596632: probable Resistance-Nodulation-Cell Division (RND) efflux membrane fusion protein precursor[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01266

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01804

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598244: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00951

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128089: UDP-3-O-acyl N-acetylglucosamine deacetylase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00575

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16130121: 16S rRNA pseudouridylate 516 synthase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00922

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 33112656: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01769

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599866: probable ribosomal protein L25[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01096

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598308: acetyl-CoA carboxylase beta subunit[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01101

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128885: 3-deoxy-manno-octulosonate cytidylyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00635

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598850: uridylate kinase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01565

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 15595498: polyamine transport protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2507438: Valyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

**-------------------------------------------------------------------------------**

**Band\_013**

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596129: cysteine synthase B[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00296

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 67471945: Dihydroorotate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 16078059: molecular chaperone [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 2507359: Thiamine-binding periplasmic protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00373

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599449: |50S ribosomal protein L14|4762635 - 4762267]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01515

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123158: Histidine biosynthesis bifunctional protein hisB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00251

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00636

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75507282: Elongation factor Ts]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01490

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595604: glutathione synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01512

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01297

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600528: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01442

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01610

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183526: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01181

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 14195456: Putative periplasmic iron-binding protein HI0362 precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01768

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67466690: Ribose-phosphate pyrophosphokinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00392

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3023329: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01901

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 78099211: Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00819

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140164: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00372

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 132813: 50S ribosomal protein L24]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00384

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599460: |30S ribosomal protein S10|4767654 - 4767343]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02172

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00166

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68566320: 3-oxoacyl-[acyl-carrier-protein] synthase 3]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00381

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599457: |50S ribosomal protein L23|4766012 - 4765713]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00369

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599445: |30S ribosomal protein S8|4760872 - 4760480]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596786: succinyl-CoA synthetase alpha chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01812

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131058: tRNA pseudouridine synthase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01329

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01519

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 84028736: Probable protease sohB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00006

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS01068: OMPA Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129131: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129131: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00354

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 150421534: HTH-type transcriptional regulator cynR]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01762

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599924: pantoate--beta-alanine ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01998

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01377

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600227: uroporphyrinogen decarboxylase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00736

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598533: ADP-L-glycero-D-mannoheptose 6-epimerase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01769

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599866: probable ribosomal protein L25[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01266

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01127

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597219: UTP--glucose-1-phosphate uridylyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01949

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00288

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00755

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131167: 10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00750

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183104: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00221

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599463: 30S ribosomal protein S7[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00689

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599628: |30S ribosomal protein S9|4965501 - 4965109]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00536

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598441: |cell division topological specificity factor MinE|3632430 - 3632684]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00209

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599470: |50S ribosomal protein L11|4783111 - 4782680]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01695

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600453: porphobilinogen deaminase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00889

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01207

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [10 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 81174960: O-acetyltransferase oatA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Periplasmic 0.00

Extracellular 0.00

Cytoplasmic 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01270

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 462020: GTP-binding protein era]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01663

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599012: probable methyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01865

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600138: delta 2-isopentenylpyrophosphate transferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01566

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 417861: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01801

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600113: NH3-dependent NAD synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00638

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128162: 30S ribosomal subunit protein S2 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00335

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00523

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 3915974: Lipoprotein-releasing system ATP-binding protein lolD]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02014

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00856

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598299: general secretion pathway protein E [Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01101

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128885: 3-deoxy-manno-octulosonate cytidylyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00601

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71164789: Thioredoxin reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 4.99

CytoplasmicMembrane 4.90

Extracellular 0.10

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01264

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02179

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01349

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

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SeqID: PCKMOKAE\_01696

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599177: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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SeqID: PCKMOKAE\_01463

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [2 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 9.49

Extracellular 0.38

Periplasmic 0.09

Cytoplasmic 0.03

CytoplasmicMembrane 0.01

Final Prediction:

OuterMembrane 9.49

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SeqID: PCKMOKAE\_01725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1168735: Ribonuclease G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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SeqID: PCKMOKAE\_00983

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00033

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01569

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595771: hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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SeqID: PCKMOKAE\_00321

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 8134599: Outer membrane lipoprotein omlA precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.93

Periplasmic 0.03

Extracellular 0.03

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.93

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**Band\_014**

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

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SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596129: cysteine synthase B[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 16078059: molecular chaperone [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

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SeqID: PCKMOKAE\_00296

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 67471945: Dihydroorotate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

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SeqID: PCKMOKAE\_00373

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599449: |50S ribosomal protein L14|4762635 - 4762267]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 2507359: Thiamine-binding periplasmic protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01297

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600528: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00251

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01490

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595604: glutathione synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01768

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67466690: Ribose-phosphate pyrophosphokinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01901

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 78099211: Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01610

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183526: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01515

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123158: Histidine biosynthesis bifunctional protein hisB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01181

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 14195456: Putative periplasmic iron-binding protein HI0362 precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01442

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01512

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00166

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68566320: 3-oxoacyl-[acyl-carrier-protein] synthase 3]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00636

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75507282: Elongation factor Ts]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00372

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 132813: 50S ribosomal protein L24]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00392

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3023329: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00288

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00384

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599460: |30S ribosomal protein S10|4767654 - 4767343]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596786: succinyl-CoA synthetase alpha chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01329

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00819

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140164: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00381

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599457: |50S ribosomal protein L23|4766012 - 4765713]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01812

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131058: tRNA pseudouridine synthase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01566

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 417861: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01266

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01763

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01762

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599924: pantoate--beta-alanine ligase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01127

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597219: UTP--glucose-1-phosphate uridylyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00369

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599445: |30S ribosomal protein S8|4760872 - 4760480]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00354

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 150421534: HTH-type transcriptional regulator cynR]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01663

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599012: probable methyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01377

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600227: uroporphyrinogen decarboxylase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01519

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 84028736: Probable protease sohB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00755

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131167: 10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01804

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598244: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00689

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599628: |30S ribosomal protein S9|4965501 - 4965109]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01949

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00117

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00006

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS01068: OMPA Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129131: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129131: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00736

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598533: ADP-L-glycero-D-mannoheptose 6-epimerase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02172

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00221

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599463: 30S ribosomal protein S7[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00601

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71164789: Thioredoxin reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 4.99

CytoplasmicMembrane 4.90

Extracellular 0.10

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01695

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600453: porphobilinogen deaminase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01270

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 462020: GTP-binding protein era]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00750

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183104: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01096

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598308: acetyl-CoA carboxylase beta subunit[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00889

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00983

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01246

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1170589: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00022

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00536

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01865

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600138: delta 2-isopentenylpyrophosphate transferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00922

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 33112656: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01860

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 66774113: Dihydrodipicolinate synthase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00335

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00653

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01998

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598441: |cell division topological specificity factor MinE|3632430 - 3632684]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00005

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71152743: HTH-type transcriptional regulator cysB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00753

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02019

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 3915974: Lipoprotein-releasing system ATP-binding protein lolD]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00874

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599214: probable aromatic acid decarboxylase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00643

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00638

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128162: 30S ribosomal subunit protein S2 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01272

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 19862632: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01044

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [11 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 1176075: Hypothetical sodium-dependent transporter HI1690]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00209

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599470: |50S ribosomal protein L11|4783111 - 4782680]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

**Band\_015**

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00373

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599449: |50S ribosomal protein L14|4762635 - 4762267]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00919

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 399238: 10 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01178

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598937: |50S ribosomal protein L19|4195358 - 4195008]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00369

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599445: |30S ribosomal protein S8|4760872 - 4760480]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01023

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02172

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01810

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140742: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00209

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599470: |50S ribosomal protein L11|4783111 - 4782680]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00372

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 132813: 50S ribosomal protein L24]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00384

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599460: |30S ribosomal protein S10|4767654 - 4767343]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01266

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01433

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599764: 50S ribosomal protein L21[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00381

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599457: |50S ribosomal protein L23|4766012 - 4765713]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00600

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 133976: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00210

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599469: 50S ribosomal protein L1[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00362

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599437: |30S ribosomal protein S13|4756848 - 4756492]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00889

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02008

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00689

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599628: |30S ribosomal protein S9|4965501 - 4965109]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598441: |cell division topological specificity factor MinE|3632430 - 3632684]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02052

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01311

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597937: |50S ribosomal protein L20|3103999 - 3103643]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00383

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599459: |50S ribosomal protein L3|4767260 - 4766625]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00288

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01817

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00370

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599446: |30S ribosomal protein S14|4761367 - 4761062]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00367

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599442: |30S ribosomal protein S5|4759570 - 4759070]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00221

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599463: 30S ribosomal protein S7[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599433: |50S ribosomal protein L17|4754379 - 4753990]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00438

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00371

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599447: 50S ribosomal protein L5[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02014

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00643

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00586

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Extracellular [matched 15599002: nucleoside diphosphate kinase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Extracellular 9.45

Cytoplasmic 0.34

Periplasmic 0.19

CytoplasmicMembrane 0.02

OuterMembrane 0.00

Final Prediction:

Extracellular 9.45

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00751

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 2507359: Thiamine-binding periplasmic protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00523

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 3915974: Lipoprotein-releasing system ATP-binding protein lolD]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00407

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01966

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599940: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02089

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 128512: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00638

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128162: 30S ribosomal subunit protein S2 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01891

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01825

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3914271: DNA topoisomerase 4 subunit A]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01740

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 15600236: type 4 fimbrial biogenesis protein PilN[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.82

Cytoplasmic 0.15

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Final Prediction:

CytoplasmicMembrane 9.82

**-------------------------------------------------------------------------------**

**Band\_016**

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 1766042: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00574

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00328

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600758: glucose-inhibited division protein A[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00861

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 25009341: Glycyl-tRNA synthetase beta chain]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00325

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 34395929: Ribonuclease E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00246

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128850: ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00151

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 67470831: Polyphosphate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00273

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [2 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 120570: Cytoplasmic membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01561

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 24212422: Aspartyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02067

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595745: transketolase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00619

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159292: Dihydrolipoyl dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00579

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128878: 30S ribosomal subunit protein S1 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00618

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129056: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00307

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131370: oligopeptidase A [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01613

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598390: phosphogluconate dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00617

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600208: pyruvate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00616

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 34395980: Prolyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00215

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139601: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01745

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 153933103: ATP-dependent DNA helicase PcrA [Clostridium botulinum A str. ATCC 19397]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01586

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 7520765: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159412: ATP-dependent protease La]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00782

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 153933103: ATP-dependent DNA helicase PcrA [Clostridium botulinum A str. ATCC 19397]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00611

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.52

Extracellular 0.38

Periplasmic 0.09

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.52

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00569

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596353: NrdA, catalytic component of class Ia ribonucleotide reductase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01308

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 73919809: Threonyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00715

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3915705: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01722

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 153931726: ATP-dependent DNA helicase RecG [Clostridium botulinum A str. ATCC 19397]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00714

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68565958: Methionyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00222

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 21263546: Elongation factor G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00380

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599456: 50S ribosomal protein L2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00472

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16077123: transcription-repair coupling factor [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02181

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01968

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81311174: Translation initiation factor IF-2]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.94

Periplasmic 0.04

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.94

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00046

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128916: fused predicted transporter subunits of ABC superfamily: ATP-binding components [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01566

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 417861: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01121

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 4.90

Periplasmic 2.50

Extracellular 2.50

OuterMembrane 0.10

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01908

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01225

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 134034978: LPS-assembly protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01886

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129037: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01405

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1708408: Isocitrate dehydrogenase [NADP]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00808

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141685: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01567

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Extracellular [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Extracellular 6.26

OuterMembrane 3.73

Periplasmic 0.02

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01946

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128916: fused predicted transporter subunits of ABC superfamily: ATP-binding components [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01359

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01485

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598833: CTP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00684

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01559

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 34395944: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 5.41

Periplasmic 4.48

CytoplasmicMembrane 0.06

Extracellular 0.05

OuterMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01892

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595550: dihydroxy-acid dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01882

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 122425298: Succinate dehydrogenase flavoprotein subunit]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01017

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00793

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00992

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00213

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139600: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00371

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599447: 50S ribosomal protein L5[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00667

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 115015: Bifunctional protein birA [Includes: Biotin operon repressor; Biotin--[acetyl-CoA-carboxylase] synthetase (Biotin--protein ligase)]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00006

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS01068: OMPA Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129131: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129131: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01491

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 109894963: Glutaminyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01272

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 19862632: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00777

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600139: DNA mismatch repair protein MutL[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00210

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599469: 50S ribosomal protein L1[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01147

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172701: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01486

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 2506182: Cytoplasmic membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00688

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599629: 50S ribosomal protein L13 [Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00990

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599430: excinuclease ABC subunit A[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01223

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00009

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128916: fused predicted transporter subunits of ABC superfamily: ATP-binding components [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2507438: Valyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01498

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 400262: Outer membrane protein MIP precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.93

Periplasmic 0.03

Extracellular 0.03

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.93

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00345

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68056567: (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01287

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Extracellular [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane, Extracellular [matched 124244: Outer membrane (Autotransporter)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 5.87

Extracellular 4.13

Periplasmic 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00610

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 1172610: Tail-specific protease precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00609

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598334: excinuclease ABC subunit B[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01218

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596242: hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 8.46

Cytoplasmic 1.33

Periplasmic 0.21

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

CytoplasmicMembrane 8.46

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01067

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16130926: DNA topoisomerase IV, subunit B [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01056

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00603

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67474772: UvrABC system protein C]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00209

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599470: |50S ribosomal protein L11|4783111 - 4782680]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00173

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599013: extragenic suppressor protein SuhB[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00762

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15610782: DNA topoisomerase I [Mycobacterium tuberculosis H37Rv]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01503

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596984: aconitate hydratase 2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00799

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599950: carbamoyl phosphate synthase large subunit [Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 4.99

CytoplasmicMembrane 4.90

Extracellular 0.10

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01406

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01070

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599914: tRNA (uracil-5-)-methyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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**Band\_017**

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 1766042: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00574

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00273

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [2 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 120570: Cytoplasmic membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00222

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 21263546: Elongation factor G]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00861

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 25009341: Glycyl-tRNA synthetase beta chain]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01613

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598390: phosphogluconate dehydratase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00618

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129056: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00617

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600208: pyruvate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00619

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159292: Dihydrolipoyl dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01398

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54036848: Chaperone clpB (Heat-shock protein F84.1)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00325

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 34395929: Ribonuclease E]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00215

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139601: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00610

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 1172610: Tail-specific protease precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00616

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 34395980: Prolyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01405

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1708408: Isocitrate dehydrogenase [NADP]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00246

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128850: ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02067

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595745: transketolase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00684

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00579

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16128878: 30S ribosomal subunit protein S1 [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 46397475: GTP-binding protein lepA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00328

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600758: glucose-inhibited division protein A[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00715

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3915705: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00041

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 71159412: ATP-dependent protease La]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01561

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Cytoplasmic [matched PS50862: AA\_TRNA\_LIGASE\_II Profile - Cytoplasmic ]

SCL-BLAST- Cytoplasmic [matched 24212422: Aspartyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 10.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01586

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 7520765: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01485

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598833: CTP synthase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00307

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131370: oligopeptidase A [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01878

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01566

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 417861: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

Cytoplasmic 0.00

CytoplasmicMembrane 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00611

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 9.52

Extracellular 0.38

Periplasmic 0.09

CytoplasmicMembrane 0.01

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 9.52

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00151

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 67470831: Polyphosphate kinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00808

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20141685: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01460

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 16130915: DNA topoisomerase IV, subunit A [Escherichia coli str. K-12 substr. MG1655]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01565

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 15595498: polyamine transport protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00569

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596353: NrdA, catalytic component of class Ia ribonucleotide reductase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01886

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129037: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00210

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599469: 50S ribosomal protein L1[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00213

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 20139600: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01272

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 19862632: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01882

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 122425298: Succinate dehydrogenase flavoprotein subunit]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

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SeqID: PCKMOKAE\_01225

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 134034978: LPS-assembly protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01877

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01908

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01968

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81311174: Translation initiation factor IF-2]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.94

Periplasmic 0.04

CytoplasmicMembrane 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.94

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00371

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599447: 50S ribosomal protein L5[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00992

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00472

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16077123: transcription-repair coupling factor [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00714

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68565958: Methionyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00284

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Periplasmic [matched PS01039: SBP\_BACTERIAL\_3 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 84028140: Cystine-binding periplasmic protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Periplasmic 10.00

Cytoplasmic 0.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01017

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01503

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596984: aconitate hydratase 2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01957

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [14 internal helices found]

Motif- CytoplasmicMembrane [matched PS00077: COX1 Pattern - Cytoplasmic Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 2493822: Cytoplasmic membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00258

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67471590: Adenylosuccinate synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01722

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 153931726: ATP-dependent DNA helicase RecG [Clostridium botulinum A str. ATCC 19397]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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**Band\_018**

SeqID: PCKMOKAE\_01130

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Periplasmic [matched PS01037: SBP\_BACTERIAL\_1 Pattern - Periplasmic]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Periplasmic [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 60416398: Major ferric iron-binding protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 10.00

Extracellular 0.00

CytoplasmicMembrane 0.00

OuterMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

Periplasmic 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00353

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- OuterMembrane [matched PS00576: GRAM\_NEG\_PORIN Pattern - Outer Membrane]

OMPMotif- Unknown [No motifs found]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 129119: Outer membrane integral membrane protein]

SCL-BLASTe- OuterMembrane [matched 100% 129119: Outer membrane integral membrane protein]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00725

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 2507359: Thiamine-binding periplasmic protein precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 16078059: molecular chaperone [Bacillus subtilis subsp. subtilis str. 168]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 9.97

OuterMembrane 0.01

Periplasmic 0.01

Extracellular 0.01

Cytoplasmic 0.00

Final Prediction:

CytoplasmicMembrane 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01743

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- OuterMembrane [matched PS00875: T2SP\_D Pattern - Outer Membrane]

OMPMotif- OuterMembrane [matched 5 rules (Rule114, Rule143, Rule187, Rule264, Rule267)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 62900657: Type IV pilus biogenesis and competence protein pilQ precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00856

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598299: general secretion pathway protein E [Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01355

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596129: cysteine synthase B[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00296

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 67471945: Dihydroorotate dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00636

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 75507282: Elongation factor Ts]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01515

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123158: Histidine biosynthesis bifunctional protein hisB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01490

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595604: glutathione synthetase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01610

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183526: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01768

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67466690: Ribose-phosphate pyrophosphokinase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00251

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00922

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 33112656: Periplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15596786: succinyl-CoA synthetase alpha chain[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01512

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00117

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01037

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- OuterMembrane [matched 3 rules (Rule64, Rule116, Rule137)]

OMSVM- OuterMembrane [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- OuterMembrane [matched 11353796: Outer membrane integral membrane protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

OuterMembrane 10.00

Extracellular 0.00

Periplasmic 0.00

CytoplasmicMembrane 0.00

Cytoplasmic 0.00

Final Prediction:

OuterMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00618

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 129056: Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01329

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00210

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599469: 50S ribosomal protein L1[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00386

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 54040965: Elongation factor Tu]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00371

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599447: 50S ribosomal protein L5[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01901

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 78099211: Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00209

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599470: |50S ribosomal protein L11|4783111 - 4782680]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01442

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.50

OuterMembrane 2.50

Periplasmic 2.50

Extracellular 2.50

Cytoplasmic 0.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00392

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3023329: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01342

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131994: HF-I, host factor for RNA phage Q beta replication [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01297

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600528: conserved hypothetical protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01064

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 27461218: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00866

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 81175143: ATP synthase subunit alpha (ATPase subunit alpha) (ATP synthase F1 sector subunit alpha)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00378

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599454: |50S ribosomal protein L22|4764575 - 4764243]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00819

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 140164: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00536

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01514

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599643: histidinol-phosphate aminotransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01519

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 84028736: Probable protease sohB]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00994

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595847: anthranilate phosphoribosyltransferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00166

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 68566320: 3-oxoacyl-[acyl-carrier-protein] synthase 3]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01350

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1172546: Polyribonucleotide nucleotidyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00368

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599444: 50S ribosomal protein L6[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00755

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 16131167: 10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase [Escherichia coli K12]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00171

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 130017: Acetoacetyl-CoA reductase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 6.49

CytoplasmicMembrane 3.24

OuterMembrane 0.14

Extracellular 0.14

Cytoplasmic 0.00

Final Prediction:

Unknown (This protein may have multiple localization sites.)

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00531

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2494644: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00958

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599753: LytB protein[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01160

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 135560: L-threonine 3-dehydrogenase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00918

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 1705797: 60 kDa chaperonin]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00750

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 3183104: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01181

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Periplasmic [matched 14195456: Putative periplasmic iron-binding protein HI0362 precursor]

SCL-BLASTe- Unknown [No matches against database]

Signal- Non-Cytoplasmic [Signal peptide detected]

Localization Scores:

Periplasmic 9.76

Extracellular 0.11

CytoplasmicMembrane 0.06

OuterMembrane 0.06

Cytoplasmic 0.00

Final Prediction:

Periplasmic 9.76

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00042

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15597001: |DNA-binding protein HU|1958759 - 1959031]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00224

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [1 internal helix found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 2.00

Cytoplasmic 2.00

OuterMembrane 2.00

Periplasmic 2.00

Extracellular 2.00

Final Prediction:

Unknown

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00382

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599458: 50S ribosomal protein L4[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00480

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 67462334: Chaperone protein dnaK]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00965

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 118794: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00864

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic, CytoplasmicMembrane[matched 81175147: ATP synthase subunit beta (ATPase subunit beta) (ATP synthase F1 sector subunit beta)]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.12

CytoplasmicMembrane 0.88

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic (This protein may have multiple localization sites.) 9.12

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SeqID: PCKMOKAE\_00571

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 3914395: 1-acyl-sn-glycerol-3-phosphate acyltransferase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

OuterMembrane 0.00

Extracellular 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01949

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Unknown [No matches against database]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 8.96

CytoplasmicMembrane 0.51

Periplasmic 0.26

Extracellular 0.26

OuterMembrane 0.01

Final Prediction:

Cytoplasmic 8.96

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01305

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 2506401: Ferrochelatase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01511

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 123136: Cytoplasmic protein]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01060

Analysis Report:

CMSVM- CytoplasmicMembrane [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- CytoplasmicMembrane [4 internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 81175262: Protein dedA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 10.00

Cytoplasmic 0.00

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 10.00

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00380

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599456: 50S ribosomal protein L2[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_02137

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15595223: shikimate dehydrogenase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_00736

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Unknown [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15598533: ADP-L-glycero-D-mannoheptose 6-epimerase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.26

Periplasmic 0.48

CytoplasmicMembrane 0.24

OuterMembrane 0.01

Extracellular 0.01

Final Prediction:

Cytoplasmic 9.26

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01421

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15600206: branched-chain amino acid transferase[Pseudomonas aeruginosa PAO1]]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01132

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- CytoplasmicMembrane [matched 118129: Sulfate/thiosulfate import ATP-binding protein cysA]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

CytoplasmicMembrane 7.88

Cytoplasmic 2.11

Periplasmic 0.00

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

CytoplasmicMembrane 7.88

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SeqID: PCKMOKAE\_00367

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 15599442: |30S ribosomal protein S5|4759570 - 4759070]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

-------------------------------------------------------------------------------

SeqID: PCKMOKAE\_01399

Analysis Report:

CMSVM- Unknown [No details]

CytoSVM- Cytoplasmic [No details]

ECSVM- Unknown [No details]

ModHMM- Unknown [No internal helices found]

Motif- Unknown [No motifs found]

OMPMotif- Unknown [No motifs found]

OMSVM- Unknown [No details]

PPSVM- Unknown [No details]

Profile- Unknown [No matches to profiles found]

SCL-BLAST- Cytoplasmic [matched 25009447: Tryptophanyl-tRNA synthetase]

SCL-BLASTe- Unknown [No matches against database]

Signal- Unknown [No signal peptide detected]

Localization Scores:

Cytoplasmic 9.97

Periplasmic 0.01

CytoplasmicMembrane 0.01

Extracellular 0.00

OuterMembrane 0.00

Final Prediction:

Cytoplasmic 9.97

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