

## Supplement

*Oligonucleotides used for the generation of the variants PfPdx1, PfPdx1<sub>Δ270-301</sub>, PfPdx1<sub>Δ273-301</sub>, PfPdx1<sub>Δ279-301</sub> and PfPdx1<sub>Δ287-301</sub>*

For the generation of *PfPdx1*, *PfPdx1<sub>Δ270-301</sub>*, *PfPdx1<sub>Δ273-301</sub>*, *PfPdx1<sub>Δ279-301</sub>* and *PfPdx1<sub>Δ287-301</sub>*

the following primer pairs were used: *PfPdx1* (*PfPdx1.fwd* (5'-GAAGAAGGATCCATATGGAAAATCATAAAGATGATGCAG-3')/

*PfPdx1\_stop\_XhoI.rev* (5'-

CGGCGGCTCGAGTTATTGTGGTGTAAAAATTTGGTGTGTTCTTC-3')), *PfPdx1<sub>Δ270-</sub>*

*301* (*PfPdx1<sub>Δ270-301</sub>.fwd* (5'-CTAAAATACTTTTAGATGTTTGATAGCTCGAG-3')/

*PfPdx1<sub>Δ270-301</sub>.rev* (5'-TTTCTCGAGCTATCAAACATCTAAAAGTATTTTAG-3')),

*PfPdx1<sub>Δ273-301</sub>* (*PfPdx1.fwd* (5'-

GAAGAAGGATCCATATGGAAAATCATAAAGATGATGCAG-3')/ *PfPdx1<sub>Δ273-301</sub>.rev* (5'-

TAATAACTCGAGTTAATTCATACTAACATCTAAAAGTATTTTAGG-3')), *PfPdx1<sub>Δ279-</sub>*

*301* (*PfPdx1<sub>Δ279-301</sub>.fwd* (5'-GGAAAAGCCATGTGTTGATAGCTCGAGAAAA-3')/

*PfPdx1<sub>Δ279-301</sub>.rev* (5'-TTTTCTCGAGCTATCACACATGGCTTTTTCC-3')) and

*PfPdx1<sub>Δ287-301</sub>* (*PfPdx1.fwd* (5'-

GAAGAAGGATCCATATGGAAAATCATAAAGATGATGCAG-3')/ *PfPdx1<sub>Δ287-301</sub>.rev* (5'-

TAATAACTCGAGTTATTTATCCGAAACGCGTGTGC-3')).

*Generation of the variants PfPdx1<sub>Δ293-301</sub>, PfPdx1<sub>Δ295-301</sub> and PfPdx1<sub>S270AΔ273-301</sub>*

The variants *PfPdx1<sub>Δ293-301</sub>*, *PfPdx1<sub>Δ295-301</sub>* and *PfPdx1<sub>S270AΔ273-301</sub>* have been generated in the same way as the variants described in the main publication using the following primers pairs:

*PfPdx1<sub>Δ293-301</sub>* (*PfPdx1<sub>Δ293-301</sub>.fwd* (5'-

AAAAACTCGAGCTATTATTCATTTTTATTTTTCC-3')/ *PfPdx1<sub>Δ293-301</sub>.rev* (5'-

GGAAAATAAAAATGAATAATAGCTCGAGTTTTT-3')), *PfPdx1<sub>Δ295-301</sub>* (*PfPdx1.fwd*

Derrer et al.

(5'-GAAGAAGGATCCATATGGAAAATCATAAAGATGATGCAG-3'/ *PfPdx1*<sub>Δ295-301</sub>.rev

(5'-TAATAACTCGAGTTAGTGTTCTTCATTTTTATTTTTCCATTTATCC-3'),

*PfPdx1*<sub>S270AΔ273-301</sub>

(*PfPdx1*.fwd (5'-GAAGAAGGATCCATATGGAAAATCATAAAGATGATGCAG-3'/

*PfPdx1*<sub>S270AΔ273-301</sub>.rev

(5'-

TAATAACTCGAGTTAATTCATTGCAACATCTAAAAGTATTTTAGGGTTATTAAAAT

TGC-3').

**Table S1**

protein	R5P binding <sup>a</sup>	I <sub>320</sub> -specific activity		PLP-specific activity		Oligomeric state <sup>b</sup>
		nmol min <sup>-1</sup> mg <sup>-1</sup>	%	pmol min <sup>-1</sup> mg <sup>-1</sup>	%	
<i>PfPdx1</i>	+	1.22 ± 0.04	100	695 ± 71	100	dodecamer
<i>PfPdx1</i> <sub>Δ270-301</sub>	-	n.d.	0	n.d.	0	mainly monomer
<i>PfPdx1</i> <sub>Δ273-301</sub>	-	n.d.	0	n.d.	0	dodecamer
<i>PfPdx1</i> <sub>Δ279-301</sub>	+	1.3 ± 0.4	107	351 ± 77	51	dodecamer
<i>PfPdx1</i> <sub>Δ287-301</sub>	+	1.9 ± 0.2	155	- <sup>c</sup>	- <sup>c</sup>	dodecamer
<i>PfPdx1</i> <sub>Δ295-301</sub>	+	1.75 ± 0.1	143	-	-	dodecamer
<i>PfPdx1</i> <sub>S270AΔ273-301</sub>	-	n.d.	0	n.d.	0	dodecamer

Biochemical characterization of *PfPdx1* and its C-terminal truncation variants using NH<sub>4</sub>Cl as ammonium donor. Assays were performed with 20 μM protein, 1 mM R5P, 1 mM G3P, 10 mM NH<sub>4</sub>Cl in 20 mM Tris-HCl pH 8.0, 10 mM NaCl, 0.5 mM EDTA. The activity of *PfPdx1* was set as 100 %. Experimental results are means of at least three different measurements. n.d.: not detected; <sup>a</sup> compare Table 4; <sup>b</sup> compare Table 3; <sup>c</sup> protein precipitated upon addition of G3P.

**Table S2**

Protein + <i>PfPdx2</i>	I <sub>320</sub> -specific activity		PLP-specific activity		Glutaminase-specific activity	
	nmol min <sup>-1</sup> mg <sup>-1</sup>	%	pmol min <sup>-1</sup> mg <sup>-1</sup>	%	nmol min <sup>-1</sup> mg <sup>-1</sup>	%
<i>PfPdx1</i>	2.76 ± 0.2	100	779 ± 130	100	193.9 ± 14	100
<i>PfPdx1</i> <sub>Δ270-301</sub>	n.d.	0	n.d.	0	190.60 ± 3	99
<i>PfPdx1</i> <sub>Δ273-301</sub>	n.d.	0	n.d.	0	202.77 ± 16	105
<i>PfPdx1</i> <sub>Δ279-301</sub>	4.62 ± 0.4	167	250 ± 32	32	271.62 ± 8	140
<i>PfPdx1</i> <sub>Δ287-301</sub>	2.25 ± 0.1	83	- <sup>a</sup>	- <sup>a</sup>	182.76 ± 9	94
<i>PfPdx1</i> <sub>Δ295-301</sub>	1.75 ± 0.1	63	- <sup>a</sup>	- <sup>a</sup>	200.75 ± 11	103
<i>PfPdx1</i> <sub>S270AΔ273-301</sub>	n.d.	0	n.d.	0	160.8 ± 4	87

Biochemical characterization of *PfPdx1* and its C-terminal truncation variants in presence of *PfPdx2*. Assays were performed with 20 μM protein, 1 mM R5P, 1 mM G3P, 10 mM L-glutamine in 20 mM Tris-HCl pH 8.0, 10 mM NaCl, 0.5 mM EDTA. The activity of *PfPdx1/PfPdx2* was set as 100 %. Experimental results are means of at least three different measurements. n.d. - none detected. <sup>a</sup> - protein precipitated on addition of G3P.

**Table S3**

Analysis of Pdx1 and the C-terminal truncation variants by analytical ultracentrifugation (velocity sedimentation)

Protein	$s_{\text{exp}}$ (S) <sup>a</sup>	$M_{\text{exp}}$ (kDa) <sup>b</sup>	$M_{\text{cal}}$ (kDa) <sup>c</sup>
<i>PfPdx1</i>	14.0	363	420
<i>PfPdx1</i> $_{\Delta 270-301}$ <sup>d</sup>	Peak 1: $3.0 \pm 0.1$ Peak 2: $4.8 \pm 0.5$ Peak 3: $6.9 \pm 1.1$	$29 \pm 3$ $60 \pm 12$ $110 \pm 26$	31 - -
<i>PfPdx1</i> $_{\Delta 273-301}$	12.9	324	380
<i>PfPdx1</i> $_{\Delta 279-301}$	13.0	330	387
<i>PfPdx1</i> $_{\Delta 287-301}$	13.8	354	400
<i>PfPdx1</i> $_{\Delta 295-301}$	13.6	340	412
<i>PfPdx1</i> $_{S270A\Delta 273-301}$	13.0	319	382

<sup>a</sup> The  $c(S)$  distribution of sedimentation coefficients was determined with SEDFIT [21] and corrected to standard conditions (20 °C, H<sub>2</sub>O). Calculated  $s$ -values using HYDROPRO and 3.1-Å bead size [22] are 2.7 S for the monomeric and 15.4 S for the dodecameric species.

<sup>b</sup> Molecular mass derived from molar mass distributions  $c(M)$  calculated by SEDFIT. For all dodecameric variants the frictional ratio was fixed to 1.25 (average of all experiments).

<sup>c</sup> Molecular mass calculated from the amino acid composition.

<sup>d</sup> Three different species were detected. The monomeric form fitted to  $3.0 \pm 0.1$  S and comprised about two thirds of the total protein. The standard deviation is given on the basis of three independent experiments. Higher oligomeric forms are probably in fast equilibrium giving rise to larger errors as discussed in the text (no theoretical  $s$  and  $M$  values calculated).

**Table 4**

Molecular mass of *PfPdx1* and the C-terminal truncation variants in the absence or presence of ribose 5-phosphate as determined by ESI-MS

Protein	- R5P (Da)	+ R5P (Da)
<i>PfPdx1</i>	35,320.7	35,532.6
<i>PfPdx1</i> $_{\Delta 270-301}$	31,506.8	31,506.8
<i>PfPdx1</i> $_{\Delta 273-301}$	31,722.6	31,722.6