Supplementary Table 3. Conserved active site residues of StPGM with proposed functional roles

Residue	Putative Role	% conservation
R48	General acid/base	99
T44	Domain 1-4 latch	99
T511		98
S146	Phosphoserine involved in phosphoryl transfer (i)	99
D304	Metal binding ligands (ii)	100
D306		99
D308		100
E390	Sugar binding loop (iii)	99
S392		74 (A=24%)
R507	Phosphate binding site (iv)	99
S509		99
G510		99
K516		73 (R=26%)

Percentage conservation is calculated from a multiple sequence alignment of 416 PGM sequences derived from the PIR database (ref). The four conserved active site regions discussed in the text are indicated by (i-iv).