

Figure S1. Sequence comparison between CpPGM1A and CpPGM1B proteins and annotation of active site residues

CpPGM1B	MM KILNILFSLVLVSQYVNANESVGNLRYLQKINLIEPTDGQAKVVTSD	50
CpPGM1B	VQINQGRALIKKKVSVVTRNVIETETTETYYYSDDKGLDAWSPNENDNLLD	100
CpPGM1A	MEQ VQ VT PYLDQKPGT S GLRKKTRVFMEGTYLANFIESYFQSFPPENF	48
CpPGM1B	MLVQE VQ IS PYLDQKPGT S GLRKKTRVFMEGTYLANFIESYFQSFPPENF	150
CpPGM1A	EGATLLVAGDGRFFLPEAIQIIISEIAAAHKKVKRIWTGVNGLCSTPAGSAI	98
CpPGM1B	EGATLLVAGDGRFFLPEAIQIIISEIAAAHKKVKRIWTGVNGLCSTPAGSAI	200
CpPGM1A	IREREGGIAVGGILLTA S HNPGGIDEDFGVKFN G KNGGPAQDSVTN T IFE	148
CpPGM1B	IREREGGIAVGGILLTA S HNPGGIDEDFGVKFN E KNGGPAQDSVTN A IFE	250
CpPGM1A	ITKKLTSSYKKISLPKIDLSKIGVQELIPNQFTVEVIDTSEDWLKLMKKIF	198
CpPGM1B	ITKKLTSSYKKISLPKIDLSKIGVQELIPNQFTVEVIDTSEDWLKLMKKIF	300
CpPGM1A	DFQKIQNLLNRKDFK M AFDSMHGVAGPYARKL F VDEFGLPESSLLHLESK	248
CpPGM1B	DFQKIQNLLNRKDFK M VFDSMHGVAGPYARKL I DEFGLPESSLLHLESK	350
CpPGM1A	PDFGGLHDPNLTAKDLVELMKVKSPKVDK S TPDFGAAG D G D C D R NMI	298
CpPGM1B	PDFGGLHDPNLTAKDLVELMKVKSPKVDK N TPDFGAAG D G D C D R NMI	400
CpPGM1A	LKGFFVTPSDSVAIIASYAKEAIPYFSKGLAGVSRSM P TSTSLNNVAEK	348
CpPGM1B	LKGFFVTPSDSVAIIASYAKEAIPYFSKGLAGVSRSM P TSTSLNNVAEK	450
CpPGM1A	LGIPCYEVP T G W KYFGNLMDAKMIDIC G E E S F G TGSDHIRE K DGLWAVLA	398
CpPGM1B	LGIPCYEVP T G W KYFGNLMDAKMIDIC G E E S F G TGSDHIRE K DGLWAVLA	500
CpPGM1A	WLSILAH H KNPDPTK P LVSVEDITREFWKTYGRNYYTRFDYES I ETEKADQ	448
CpPGM1B	WLSILAY Y KNPDPTK S LVSVEDITREFWKTYGRNYYTRFDYES V ETEKADQ	550
CpPGM1A	FFKHLNSLMED H QKLREIIKPY G IDIKLTDNFTYNDPVD K SVAKNQGLRF	498
CpPGM1B	FFKHLNSLMED S QKLRLNSLRSS G LKVK F MDNFTYNDPVD G SVTKNQGVRI	600
CpPGM1A	IFQ D NSRVV F R L S G T GSVGAT I R I Y IEKTVSDQTKVNST S NEIL G DLIEI	548
CpPGM1B	IF T D GSRI I F R I S G T GSVGAT I R V Y MEKTVKNPQEFKTT Q QAL N HLEI	650
CpPGM1A	VEKKIKLKE S TGRDRPTVIT	568
CpPGM1B	VEKKIKLKE I TGR S KPTVIT	670

Note: **X** = Conserved active site residue based on structure 1KFI_A (*Paramecium tetraurelia* parafusin)
X = Conserved metal (Mg^{2+}) binding site residues based on structure 3PMG_A (*Oryctolagus cuniculus* Phosphoglucomutase)
X = Conserved substrate binding site residue based on the structures of *Candida albicans* AGM1 (N-Acetylglucosamine-phosphate mutase) and *Pseudomonas aeruginosa* PMM/PGM bound to their substrates.
X = Mismatched residues between CpPGM1A and CpPGM1B