



STRUCTURAL  
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**Supporting information for article:**

**Structural and functional insights into phosphomannose  
isomerase: role of zinc and catalytic residues**

**Mamata Bangera, Giri Gowda K., S. R. Sagurthi and M. R. N. Murthy**

**S1. Primers used for site directed mutagenesis**

**E35A** : CAGCAGCCAATGGCTGCACTCTGGATGGGAGCTCAT

**K86A** : GAGCTCCCGTTTCTGTTTGCAGTACTGTGCGCCGCA

**S95A** :GCCGCACAACCGCTAGCTATTCAGGTGCACCCG

**Q97A**: CAACCGCTCTCGATCGCGGTGCCCGAATAAACGC

**H99A\_sense primer** :CCGCTCTCTATTCAGGTGGCACCGAATAAACGCAACTCC

**H99A\_antisense primer** :GGAGTTGCGTTTATTCGGTGCCACCTGAATAGAGAGCGG

**H99Q** :TCTATTCAGGTGCAACCGAATAAACGGAATTCCGAA

**K132A** :TATAAAGATCCTAACCATGCACCAGAGCTCGTT

**E134A** :CATAAACCAGCGCTGGTTTTTTGCGTTAACGCCT

**E134H** :AACCATAAACCACATCTGGTTTTTTGCGTTAACGCCT

**H255A** :CTGTTTGCTGAAACGCCAGCTGCTTATCTGCAGGGC

**H255E** : TTTGCTGAAACGCCTGAAGCTTATCTGCAGGGC

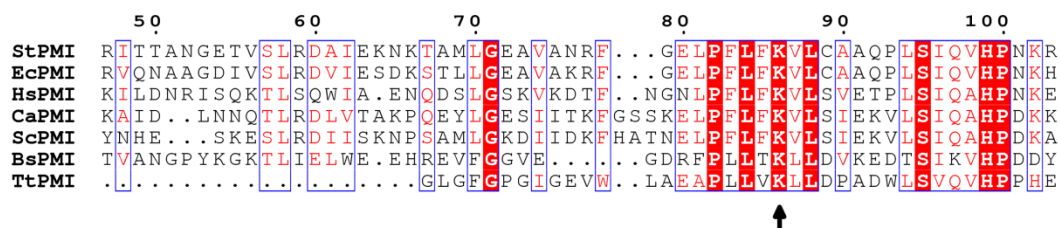
**Y257A** : GAAACGCCTCATGCTGCTCTCCAGGGCGTTGCG

**E264A** :CAGGGCGTTGCGCTAGCAGTCATGGCGAAC

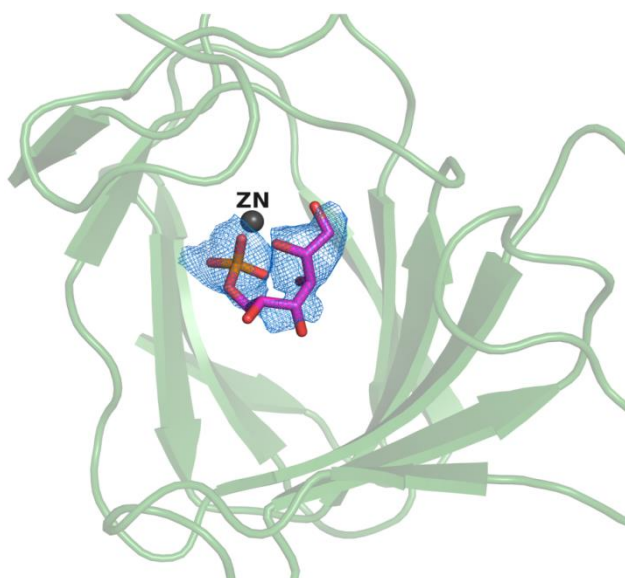
**E264Q** : CAGGGCGTTGCGCTGCAAGTCATGGCGAATTCC

**D270A** :GTCATGGCGAATTCCGCTAACGTTCTGCGCGCT

**R274A** :TCCGATAACGTGCTAGCCGCTGGCCTTACGCCA



**Figure S1** Multiple sequence alignment of phosphomannose isomerases from various organisms. St, *Salmonella typhimurium*; Ec, *Escherichia coli*; Hs, *Homo sapiens*; Ca, *Candida albicans*; Sc, *Saccharomyces cerevisiae*; Bs, *Bacillus subtilis*; Tt, *Thermus thermophilus*. The black arrow marks the position of the conserved lysine (Lys86 in StPMI). The alignment was generated using Clustal Omega server and drawn in ESPript 3.0.



**Figure S2** Location of additional density (map in blue) observed at centre of the catalytic cupin domain close to zinc (shown as grey sphere) binding site. Open chain form of F6P (shown as stick model) has been fitted into the Fo-Fc electron density map contoured at  $2.8 \sigma$