

Fig. S1

A **WT PGM3**
MDLGAITKYSALHAKPNGLIILQYGTAGFRTKAEHLDHVMFRMGLLAVLRSKQT **KSTIGVM**
VTASHNPEEDNGVKLVDPLGEMLAPSWEEHATCLANAEEQDMQRVLIDI SEKEA **VNLQDA**
AFVVIGRDTRPSSEKLSQSVIDGVTVLGGQFHDYGLLTPQLHYMVYCR **NTGGRYGKATI**
EGYYQKLSKAFVELTKQASCSGDEYRSLKVDCANGIGALKLREMEHYFSQGLSVQLFNDG
SKGKLNHLGADDFVKSHQKPPQGMEIKSNERCCSFDGDADRIVYYYHDADGHFHLIDGDK
IATLISSFLKELLVEIGESLNIGVVQTAYANGSSSTRYLEEVMKVPVYCTKTGVKHLHKA
QEFDIGVYFEANGHTALFSTAVEMKIKQSAEQLEDKRRKAAKMLENI IDLFNQAAAGDAI
SDMLVIEAILALKGLTVQQWDALYTDLPNRQLKVQVADRRVISTTDAERQAVTTPGLQEA
INDLVKKYKLSRAFVRPSGTEDVVRVYAEADSQESADHLAHEVSLAVFQLAGGIGERPQP
GF

Rearranged PGM3 (Grouped Segments)
MDLGAITKYSALHAKPNGLIILQYGTAGFRTKAEHLDHVMFRMGLLAVLRSKQT **VNLQDA**
FVVIGRDTRPSSEKLSQSVIDGVTVLGGQFHDYGLLTPQLHYMVYCR **KSTIGVMVTASH**
NPEEDNGVKLVDPLGEMLAPSWEEHATCLANAEEQDMQRVLIDI SEKEA **NTGGRYGKATI**
EGYYQKLSKAFVELTKQASCSGDEYRSLKVDCANGIGALKLREMEHYFSQGLSVQLFNDG
SKGKLNHLGADDFVKSHQKPPQGMEIKSNERCCSFDGDADRIVYYYHDADGHFHLIDGDK
IATLISSFLKELLVEIGESLNIGVVQTAYANGSSSTRYLEEVMKVPVYCTKTGVKHLHKA
QEFDIGVYFEANGHTALFSTAVEMKIKQSAEQLEDKRRKAAKMLENI IDLFNQAAAGDAI
SDMLVIEAILALKGLTVQQWDALYTDLPNRQLKVQVADRRVISTTDAERQAVTTPGLQEA
INDLVKKYKLSRAFVRPSGTEDVVRVYAEADSQESADHLAHEVSLAVFQLAGGIGERPQP
GF

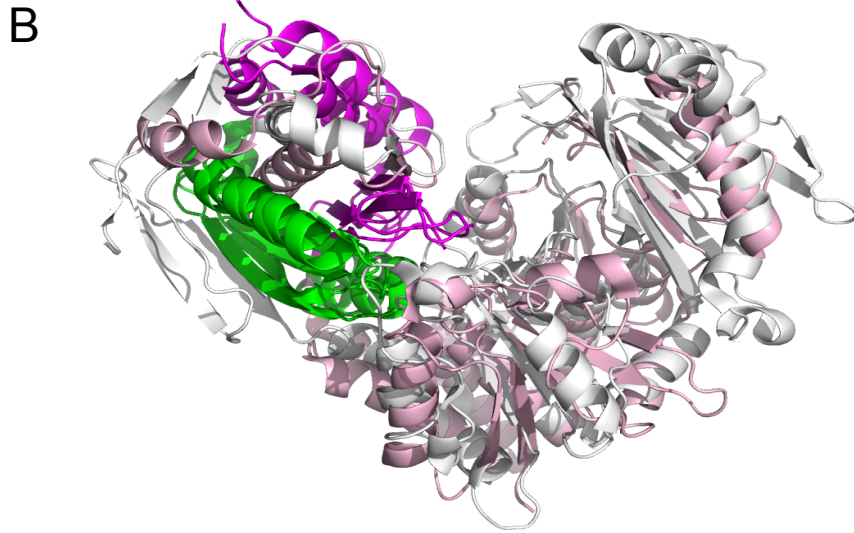


Fig. S1. Details of the sequence modification made to human PGM3.

(A) Sequences of wild-type and human PGM3 and the modified version used for sequence alignments, showing the transposed regions (see text). Residues highlighted in magenta were swapped with those in green. **(B)** Superposition of human PGM1 (white) and the PGM3 homolog from *C. albicans* (PDB ID 2DKA) (pink). Green/magenta highlight the regions affected by circular permutation (and swapped in the amino acid sequence), showing how they are structurally conserved despite the different sequence connectivity in PGM3.