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Supporting information for article:

Effects of the T337M and G391V disease-related variants on human phosphoglucomutase 1: structural disruptions large and small

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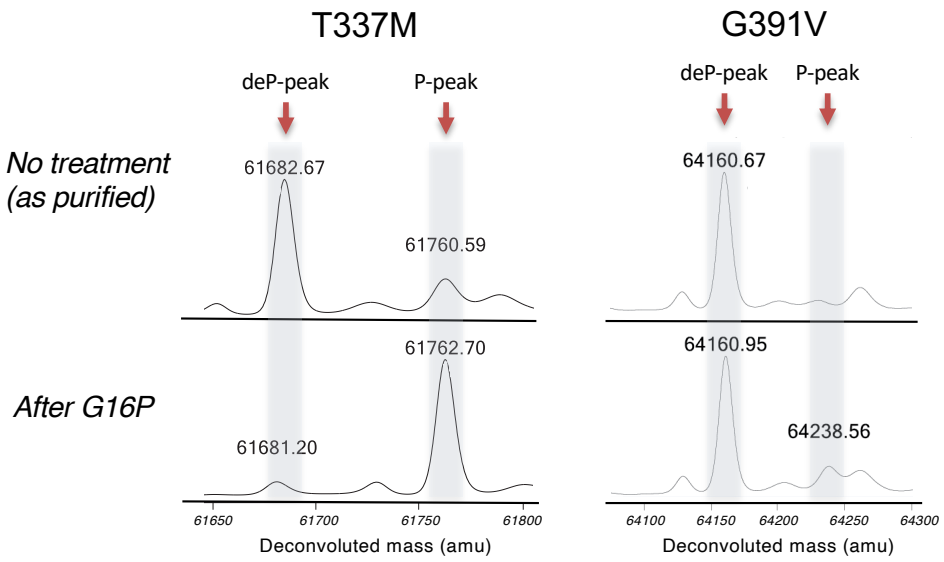

Fig. S1. Electrospray ionization mass spectra for the T337M (left) and G391V (right) missense variants. The two major peaks (gray shading) are for phospho-enzyme (P) and dephospho-enzyme (deP). Spectra are shown for the protein as purified (top panel) and after treatment with glucose 1,6-bisphosphate (bottom panels). The mass of the two major peaks is shown and agrees with the expected value for each species based on amino acid sequence. (The relative difference between T337M and G391V is due to cleavage of the N-ter His_6-affinity tag for the T337M sample.) The percentage of phosphoenzyme was calculated by normalizing the sum of the P and deP peak heights to 1.0.

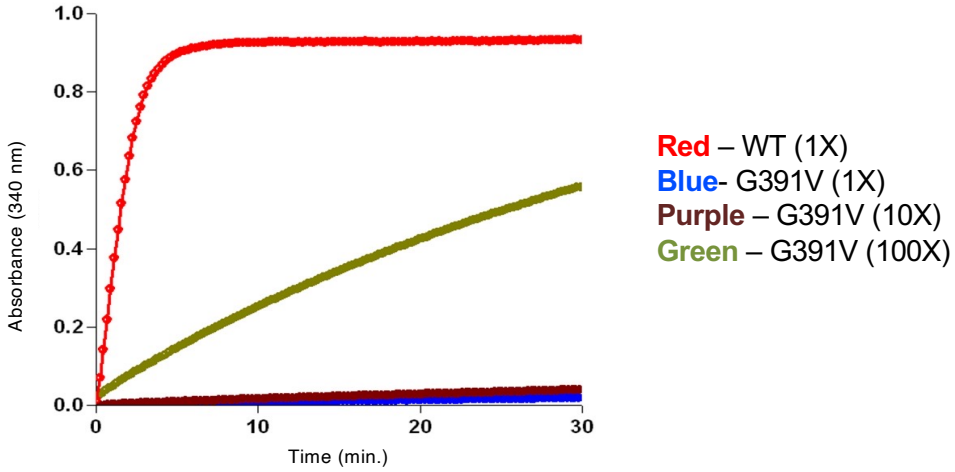

Fig. S2. Time course of PGM activity comparing WT PGM1 with the G391V variant. Enzyme concentration for WT was 4.5 nM (1X). G391V was assayed at 1X, 10X, and 100X that of WT. Note how the green curve fails to reach a plateau, even after 30 minutes.

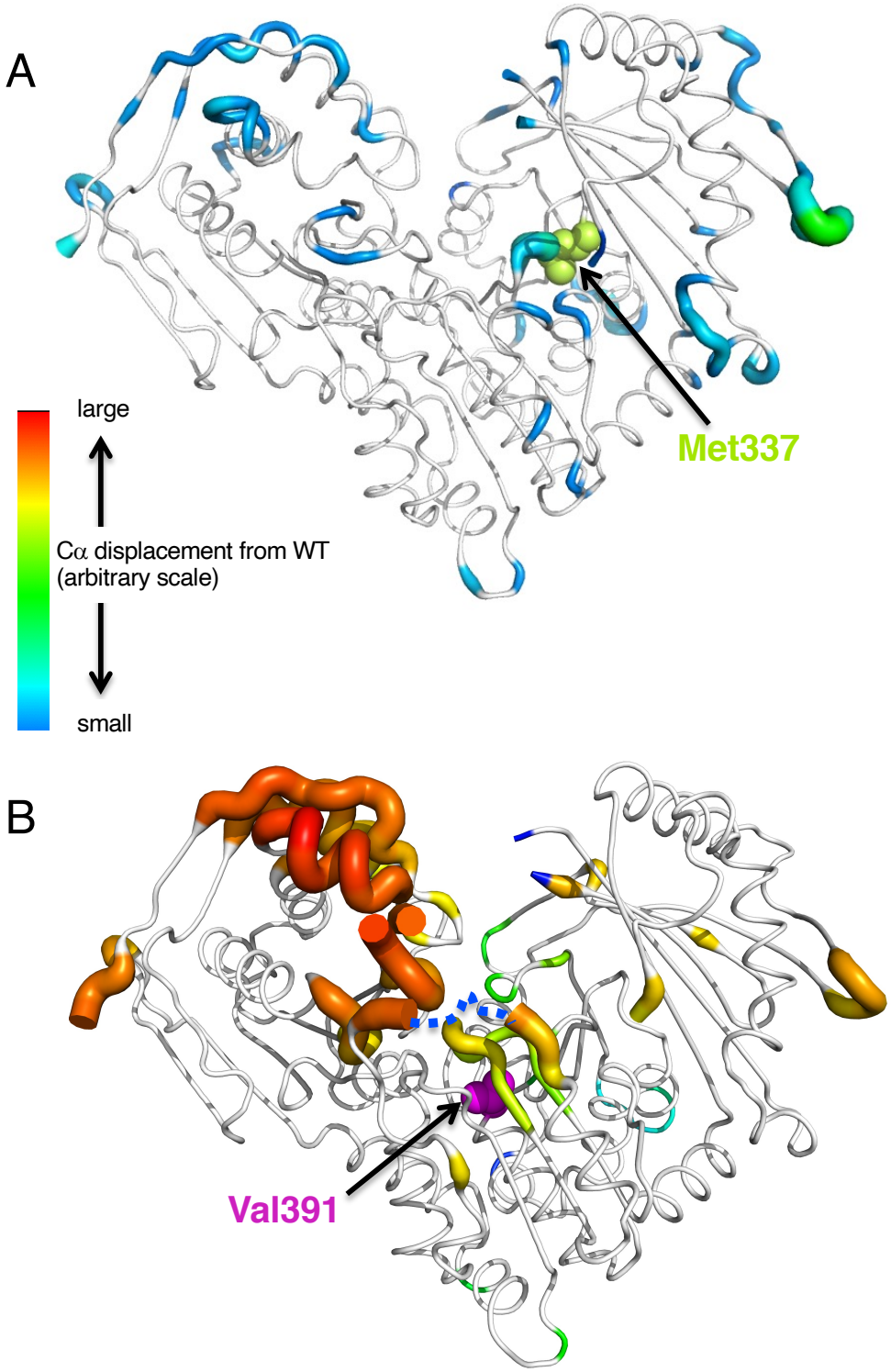

Fig. S3. Ribbon representations of the T337M (A) and G391V (B) variants of PGM1 created in PyMol [44]. Displacement between the C_a atoms of the variant and WT structures was calculated using the Colorbydisplacement script available on PyMolWiki (https://pymolwiki.org/index.php/Colorbydisplacement). Displacement is shown by both color, from small (blue) to large (red), and also the width of the ribbon. A region of missing residues in G391V (B) is indicated by a blue dashed line.

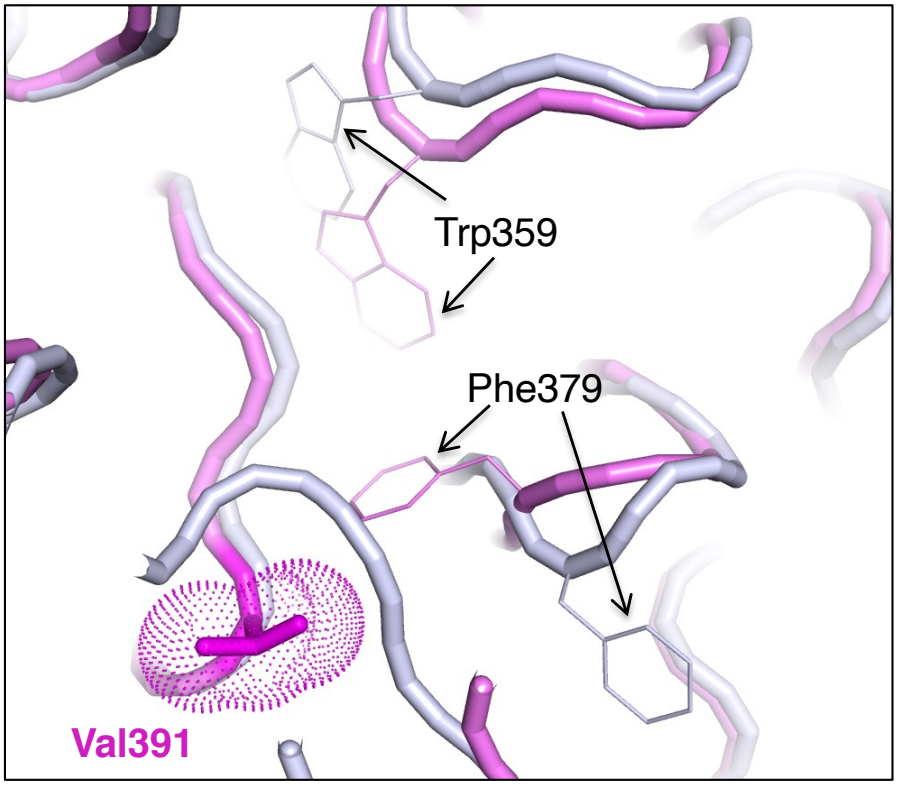

Fig. S4. A closeup view of the re-packing of aromatic residues in the hydrophobic core of the G391V variant of PGM1. A superposition of WT PGM1 (gray) and the G391V variant (magenta) are shown in the vicinity of the mutation. Side chains of Trp359 and Phe379 are shown to highlight their altered arrangement in the interior of the protein.