**Supplementary Table 2.** Residues that form hydrogen bonds/salt bridges in the StPGM dimer interface

| Chain A Residue [atom] | Chain B Residue [atom] | Distance (Å) |
|---|---|---|
| Gln13 [NE2] | Val262 [O] | 3.17 |
| Asn18 [ND2] | Glu92 [OE2] | 3.06 |
| [OD1] | Gln264 [NE2] | 2.83 |
| Val19 [N] | Gln264 [OE1] | 3.36 |
| Ala20 [N] | Gln264 [OE1] | 2.92 |
| Glu92 [OE2] | Asn18 [ND2] | 2.99 |
| Gln261 [OE1] | Arg267 [NH1] | 2.84 |
| Val262 [O] | Arg267 [NH1] | 3.14 |
| [O] | Arg267 [NH2] | 3.03 |
| [O] | Gln13 [NE2] | 3.11 |
| Asp263 [OD2] | Arg267 [ NE ] | 3.31* |
| [OD1] | Arg267 [NH2] | 3.84* |
| [OD2] | Arg267 [NH2] | 3.53* |
| Gln264 [NE2] | Asn18 [OD1] | 2.91 |
| [OE1] | Val19 [N] | 3.38 |
| [OE1] | Ala20 [N] | 2.90 |
| Arg267 [NH1] | Gln261 [OE1] | 2.84 |
| [NH1] | Val262 [O] | 3.21 |
| [NH2] | Val262 [O] | 3.10 |
| [ NE ] | Asp263 [OD2] | 3.32* |
| [NH2] | Asp263 [OD1] | 3.80* |
| [NH2] | Asp263 [OD2] | 3.57* |

Contacts calculated by PISA [60]. Only contacts found between corresponding residues in both chain A and chain B were included. Asterisks indicate salt bridges, others contacts are hydrogen bonds.