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| **Table S1| Q5 Site-directed mutagenesis oligonucleotides.**  |
| SyTPI Tyr102Val | Up |  ACGACGGCAAgttTTTGGGGAAACG |
| Lower |  TCACTGTGGCCGATAACC |
| SyTPI Thr106Ser | Up | TTTTGGGGAAtcgGACGAAACTG |
| Lower | TATTGCCGTCGTTCACTG |
| SyTPI Thr109Leu | Up |  AACGGACGAActtGCCAATTTGAGAGTATTG |
| Lower | TCCCCAAAATATTGCCGTC |
| SyTPI Thr106ser/Thr109Leu | Up | GGGGAAtCGGACGAActTGCCAATTTGA |
| SyTPI-Triple |

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| Lower |
| Up |

 | AAAATATTGCCGTCGTTCACTGTGGCCGACGACGGCAAgttTTTGGGGAAtCGGACGAActTGCCAATTTGA |
|  |

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| Lower |
|  |

 | TCACTGTGGCCGATAACCACATAATGAATACCGATTTCCGTC |
| HsTPI Val101TyrHsTPI Ser105Thr | UpLowerUpLower | GAGAAGGCATtacTTTGGGGAGTCAGTCTGAGTGCCCCAGGACCCTTTGGGGAGacaGATGAGCTGAACATGCCTTCTCTCTGAG |
| HsTPI Leu108ThrHsTPI Ser105Thr/Leu108ThrHsTPI-Triple | UpLowerUpLowerUpLower | GTCAGATGAGacgATTGGGCAGAAAGTCCCCAAAGACATGCCTTTTTGGGGAGacaGATGAGacgATTGGGCAGAAAGGACATGCCTTCTCTCTGAGTGCCCCAGGACCACCGAGAAGGCATtacTTTGGGGAGacaGATGAGacgATTGGGCAGAAAGTCTGAGTGCCCCAGGACCACCCACGTGGCTCCGCAGTCTTTGATCATG |
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| **Table S2|** **Data collection and refinement statistics of Triosephosphate isomerase from *Synechocystis* in complex with 2-Phosphoglycolic acid.** |
| **Identification** | **SyTPI** |
| **PDB code** | **6BVE** |
| **Wavelength** | 1.542 |
| **Resolution range** | 55.38 - 1.78 (1.844 - 1.78) |
| **Space group** | P 21 21 21 |
| **Unit cell** | 72.8799 73.0988 85.1753 90 90 90 |
| **Total reflections** | 358881 (27447) |
| **Unique reflections** | 44255 (4330) |
| **Multiplicity** | 8.1 (6.3) |
| **Completeness (%)** | 99.98 (99.98) |
| **Mean I/sigma(I)** | 16.93 (4.65) |
| **Wilson B-factor** | 15.54 |
| **R-merge** | 0.07286 (0.3655) |
| **Reflections used in refinement** | 44255 (4330) |
| **Reflections used for R-free** | 2006 (200) |
| **R-work** | 0.1543 (0.1888) |
| **R-free** | 0.1902 (0.2310) |
| **Number of non-hydrogen atoms** | 4091 |
|  **Macromolecules** | 3723 |
|  **Ligands** | 20 |
|  **Solvent** | 348 |
| **Protein residues** | 484 |
| **RMS(bonds)** | 0.008 |
| **RMS(angles)** | 0.85 |
| **Ramachandran favored (%)** | 96.88 |
| **Ramachandran allowed (%)** | 2.71 |
| **Ramachandran outliers (%)** | 0.42 |
| **Rotamer outliers (%)** | 0.00 |
| **Clashscore** | 1.22 |
| **Average B-factor** | 17.26 |
|  **Macromolecules** | 16.73 |
|  **Ligands** | 17.29 |
|  **Solvent** | 22.88 |

Statistics for the highest-resolution shell are shown in parentheses.

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| **Table S3** Access coded for the amino acid sequences used to build the Multiple amino acid sequence alignment  |
| **Organism** | **Uniprot accession number** | **Alignment ID** |
| *Synechocystis sp* PCC 6803 | Q59994 | SyTPI |
| *Nostoc punctiforme* | B2JA20 | NoTPI |
| *Arabidopsis thaliana* cytosolic | P48491 | AtcTPI |
| *Arabidopsis thaliana* plastid | Q9SKP6 | AtpdTPI |
| *Chlamydomonas reinhardtii* | Q5S7Y5 | CrTPI |
| *Saccharomyces cerevisiae* | POO942 | ScTPI |
| *Trichomonas vaginalis* | A2EGX9 | TvTPI |
| *Homo sapiens* | P60174 | HsTPI |

**Table S4.** Access code for the TPI sequences used to build the phylogenetic tree

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| **Organism** | **Identification code** |
| *Synechocystis sp* PCC 6803 | Q59994\* |
| *Nostoc punctiforme* | B2JA20\* |
| *Cyanobacterium aponinum* | K9Z135\* |
| *Cyanothece sp* PCC 7822 | E0U7I7\* |
| *Volvox carteri* | Vocar.0001s0851.1+ |
| *Chlamydomonas reinhardtii* | Q5S7Y5\* |
| *Chlorella variabilis* cytosolic | E1ZKB3\* |
| *Chlorela variabilis* plastid | E1ZJ95\* |
| *Oryza sativa* cytosolic | P48494\* |
| *Oryza sativa* plastid | LOC\_Os09g36450.1+ |
| *Zea mays* cytosolic | P12863\* |
| *Zea mays* plastid | PWZ12483.1\* |
| *Secale cereale* cytosolic | P46226\* |
| *Secale cereale* plastid | P46225\* |
| *Nicotiana sylvestris* cytosolic | A0A1U7WBV5\* |
| *Nicotiana sylvestris* plastid | A0A1U7XMB3\* |
| *Arabidopsis thaliana* cytosolic | P48491\* |
| *Arabidopsis thaliana* plastid | Q9SKP6\* |
| *Sellaginella moellendorffii* cytosolic | XP\_002960386- |
| *Sellaginella moellendorfii* plastid | D8SSS6\* |
| *Marchantia polymorpha* cytosolic | Mapoly0042s0045+ |
| *Marchantia polymorpha* plastid | A0A176WT02\* |
| *Physcomitrella patens* cytosolic | XP\_024402314.1- |
| *Physcomitrella patens* plastid | XP\_024398301.1- |
| *Klebsormidium flaccidum* cytosolic | GAQ81916.1- |
| *Klebsormidium flaccidum* plastid | A0A1Y1HSX2\* |

\*Uniprot accession number
+Gene ID Phytozome 12
-NCBI accession number