

Table S3. Superposition of the *TaTT* subunit with the closest homologs.

| Protein (PDB code) | Aligned residues, % | RMSD, Å | Sequence identity, % |
|--|----------------------------|----------------|-----------------------------|
| 1 Amino acid aminotransferase from <i>Burkholderia pseudomallei</i> (4WHX) | 96 | 1.46 | 37 |
| 2 Branched-chain amino acid aminotransferase from <i>Thermus thermophiles</i> (2EJ3) | 96 | 1.39 | 40 |
| 3 Branched-chain amino acid aminotransferase from <i>Thermoproteus uzoniensis</i> (5CE8) | 95 | 1.33 | 43 |
| 4 Branched-chain amino acid aminotransferase from <i>E. coli</i> (1I1K) | 94 | 1.33 | 37 |
| 5 Branched-chain amino acid aminotransferase from <i>Geoglobus acetivorans</i> (5E25) | 98 | 1.43 | 31 |
| 6 (<i>R</i>)-selective amine transferase from <i>Aspergillus fumigatus</i> (4CHI) | 98 | 1.64 | 24 |
| 7 D-amino acid aminotransferase from <i>Bacillus</i> sp. YM-1 (1DAA) | 93 | 1.69 | 30 |
| 8 (<i>R</i>)-amine transaminase from <i>Arthrobacter</i> SP. KNK168 (3WWH) | 82 | 1.65 | 26 |