**Supplementary table 1.** Top 10 structural analogs of *Clonorchis* DNMT2 in PDB identified by I-TASSER.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Ranka | PDB Hit | TM-score | RMSDb | % Identityc | Coveraged | Donor organism | Reference |
| 1 | 4h0nA | 0.855 | 0.90 | 0.392 | 0.866 | *Spodoptera frugiperda* DNMT2 | Li et al., 2013 |
| 2 | 1g55A | 0.765 | 1.88 | 0.428 | 0.805 | *Homo sapiens* DNMT2 | Dong et al., 2001 |
| 3 | 3qv2A | 0.741 | 2.66 | 0.274 | 0.808 | *Entamoeba histolytica* DNMT2 | Schulz et al., 2012 |
| 4 | 3lx6A | 0.704 | 2.96 | 0.214 | 0.800 | *Shigella flexneri* DNA cytosine methylase |  |
| 5 | 3ptaA | 0.700 | 3.79 | 0.196 | 0.826 | *H. sapiens* DNMT1 | Song et al., 2011 |
| 6 | 3av4A | 0.700 | 4.07 | 0.198 | 0.834 | *Mus musculus* DNMT1 | Takeshita et al., 2011 |
| 7 | 3pt6A2 | 0.691 | 4.07 | 0.198 | 0.824 | *M. musculus* DNMT1 | Song et al., 2011 |
| 8 | 3pt9A | 0.687 | 3.99 | 0.191 | 0.816 | *M. musculus* DNMT1 | Song et al., 2011 |
| 9 | 3me5A | 0.675 | 3.14 | 0.197 | 0.779 | *S. flexneri* DNA cytosine methylase |  |
| 10 | 4dkjA | 0.674 | 3.25 | 0.178 | 0.468 | *Mycoplasma penetrans* DNA cytosine methylase | Wojciechowski et al., 2013 |

aRanking of proteins is based on the template modeling-score (TM-score) of the structural alignment between the query structure and known structures in the PDB library.

bRMSD is the root mean square deviation between residues that are structurally aligned by TM-align.

c% identity is the percentage sequence identity in the structurally aligned region.

dCoverage represents the coverage of the alignment by TM-align and is equal to the number of structurally aligned residues divided by length of the query protein.