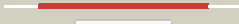



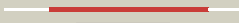



















# Phyre2

|               |                                   |
|---------------|-----------------------------------|
| Email         | mdejesus@rockefeller.edu          |
| Description   | RVBD2267c (-)<br>_2541654_2542820 |
| Date          | Mon Aug 5 13:25:40 BST<br>2019    |
| Unique Job ID | 18995dbf69a98306                  |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c2z6vA_</a> |  Alignment   |    | 100.0      | 20     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of sulfotransferase stf9 from2 mycobacterium avium                                       |
| 2  | <a href="#">c2zq5A_</a> |  Alignment   |    | 100.0      | 22     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)                  |
| 3  | <a href="#">c3ap3A_</a> |  Alignment   |    | 100.0      | 20     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine sulfotransferase 2;<br><b>PDBTitle:</b> crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap                             |
| 4  | <a href="#">c4gbmA_</a> |  Alignment   |    | 100.0      | 17     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> curm sulfotransferase;<br><b>PDBTitle:</b> sulfotransferase domain from the curacin biosynthetic pathway  |
| 5  | <a href="#">c4goxA_</a> |  Alignment |  | 100.0      | 21     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase;<br><b>PDBTitle:</b> sulfotransferase domain from the synechococcus pcc 7002 olefin2 synthase   |
| 6  | <a href="#">c2gwhA_</a> |  Alignment |  | 100.0      | 17     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase 1c2;<br><b>PDBTitle:</b> human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol  |
| 7  | <a href="#">c1vkjA_</a> |  Alignment |  | 100.0      | 14     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate (glucosamine) 3-o-sulfotransferase 1;<br><b>PDBTitle:</b> crystal structure of heparan sulfate 3-o-sulfotransferase isoform 1 in2 the presence of pap |
| 8  | <a href="#">d1vkja_</a> |  Alignment |  | 100.0      | 14     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 9  | <a href="#">d1teta_</a> |  Alignment |  | 100.0      | 15     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 10 | <a href="#">d1j99a_</a> |  Alignment |  | 100.0      | 20     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 11 | <a href="#">d1t8ta_</a> |  Alignment |  | 100.0      | 20     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | <a href="#">c3bd9A_</a> | Alignment |              | 100.0 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate glucosamine 3-o-sulfotransferase<br><b>PDBTitle:</b> human 3-o-sulfotransferase isoform 5 with bound pap  |
| 13 | <a href="#">d1ls6a_</a> | Alignment |              | 100.0 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 14 | <a href="#">c3u3oA_</a> | Alignment |              | 100.0 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase 1a1;<br><b>PDBTitle:</b> crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin   |
| 15 | <a href="#">d1xv1a_</a> | Alignment |              | 100.0 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 16 | <a href="#">d1fmja_</a> | Alignment |              | 100.0 | 17 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 17 | <a href="#">c3rnlA_</a> | Alignment |              | 100.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase;<br><b>PDBTitle:</b> crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius   |
| 18 | <a href="#">c1nstA_</a> | Alignment |              | 99.9  | 16 | <b>PDB header:</b> sulfotransferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate n-deacetylase/n-sulfotransferase;<br><b>PDBTitle:</b> the sulfotransferase domain of human haparin sulfate n-deacetylase/n-2 sulfotransferase          |
| 19 | <a href="#">d1nsta_</a> | Alignment |              | 99.9  | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 20 | <a href="#">d3bfxa1</a> | Alignment |              | 99.9  | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 21 | <a href="#">d2a3ra1</a> | Alignment | not modelled | 99.9  | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 22 | <a href="#">c1q1qA_</a> | Alignment | not modelled | 99.9  | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase family, cytosolic, 2b, member 1 isoform a;<br><b>PDBTitle:</b> crystal structure of human pregnenolone sulfotransferase (sult2b1a) in2 the presence of pap |
| 23 | <a href="#">d1q20a_</a> | Alignment | not modelled | 99.9  | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 24 | <a href="#">d1aqua_</a> | Alignment | not modelled | 99.9  | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 25 | <a href="#">c5x2bK_</a> | Alignment | not modelled | 99.9  | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> K: <b>PDB Molecule:</b> sulfotransferase;<br><b>PDBTitle:</b> crystal structure of mouse sulfotransferase sult7a1 complexed with pap  |
| 26 | <a href="#">c2zvpX_</a> | Alignment | not modelled | 99.9  | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> X: <b>PDB Molecule:</b> tyrosine-ester sulfotransferase;<br><b>PDBTitle:</b> crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol                     |
| 27 | <a href="#">d1g3ma_</a> | Alignment | not modelled | 99.9  | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 28 | <a href="#">c2ovfA_</a> | Alignment | not modelled | 99.9  | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> stal;<br><b>PDBTitle:</b> crystal structure of stal-pap complex   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">c1zd1B_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sulfotransferase 4a1;<br><b>PDBTitle:</b> human sulfotransferase sult4a1  |
| 30 | <a href="#">c3mg9A_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> teg12;<br><b>PDBTitle:</b> teg 12 binary structure complexed with the teicoplanin aglycone   |
| 31 | <a href="#">c3mgbA_</a> | Alignment | not modelled | 99.9 | 21 | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> teg12;<br><b>PDBTitle:</b> teg 12 ternary structure complexed with pap and the teicoplanin2 aglycone   |
| 32 | <a href="#">c2h8kA_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sult1c3 splice variant d;<br><b>PDBTitle:</b> human sulfotransferase sult1c3 in complex with pap  |
| 33 | <a href="#">c5mekA_</a> | Alignment | not modelled | 99.9 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic sulfotransferase 18;<br><b>PDBTitle:</b> sulphotransferase-18 from arabidopsis thaliana in complex with 3'-2 phosphoadenosine 5'-phosphate (pap)  |
| 34 | <a href="#">d1q44a_</a> | Alignment | not modelled | 99.9 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> PAPS sulfotransferase   |
| 35 | <a href="#">c5tizA_</a> | Alignment | not modelled | 99.5 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase;<br><b>PDBTitle:</b> schistosoma japonicum (blood fluke) sulfotransferase  |
| 36 | <a href="#">c4mubA_</a> | Alignment | not modelled | 99.4 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase;<br><b>PDBTitle:</b> schistosoma mansoni (blood fluke) sulfotransferase/oxamniquine complex  |
| 37 | <a href="#">d2bcgy1</a> | Alignment | not modelled | 75.8 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins  |
| 38 | <a href="#">c5t0aB_</a> | Alignment | not modelled | 73.7 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein - heparan sulfate 6-o-<br><b>PDBTitle:</b> crystal structure of heparan sulfate 6-o-sulfotransferase with bound2 pap and heptasaccharide substrate                                    |
| 39 | <a href="#">c4nclB_</a> | Alignment | not modelled | 72.1 | 42 | <b>PDB header:</b> translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein;<br><b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp |
| 40 | <a href="#">d1nija1</a> | Alignment | not modelled | 69.4 | 33 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like   |
| 41 | <a href="#">c1nija_</a> | Alignment | not modelled | 67.1 | 29 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia;<br><b>PDBTitle:</b> yjia protein   |
| 42 | <a href="#">d1p3ja1</a> | Alignment | not modelled | 63.1 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 43 | <a href="#">d1yzna1</a> | Alignment | not modelled | 62.0 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins  |
| 44 | <a href="#">c2oiIA_</a> | Alignment | not modelled | 61.5 | 24 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein rab-25;<br><b>PDBTitle:</b> crystal structure of human rab25 in complex with gdp  |
| 45 | <a href="#">c2qorA_</a> | Alignment | not modelled | 60.5 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase;<br><b>PDBTitle:</b> crystal structure of plasmodium vivax guanylate kinase  |
| 46 | <a href="#">c2gedB_</a> | Alignment | not modelled | 58.1 | 31 | <b>PDB header:</b> protein transport, signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor beta subunit;<br><b>PDBTitle:</b> signal recognition particle receptor beta-subunit in nucleotide-free2 dimerized form                          |
| 47 | <a href="#">c4nu0B_</a> | Alignment | not modelled | 57.5 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of adenylate kinase from streptococcus pneumoniae2 with ap5a  |
| 48 | <a href="#">d1g7sa4</a> | Alignment | not modelled | 57.3 | 41 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins  |
| 49 | <a href="#">c3neyC_</a> | Alignment | not modelled | 57.3 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> 55 kda erythrocyte membrane protein;<br><b>PDBTitle:</b> crystal structure of the kinase domain of mpp1/p55  |
| 50 | <a href="#">d2bmea1</a> | Alignment | not modelled | 56.8 | 32 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins  |
| 51 | <a href="#">d1ak2a1</a> | Alignment | not modelled | 55.5 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 52 | <a href="#">c2if2C_</a> | Alignment | not modelled | 53.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dephospho-coa kinase;<br><b>PDBTitle:</b> crystal structure of the putative dephospho-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.   |
| 53 | <a href="#">d1s3ga1</a> | Alignment | not modelled | 52.8 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 54 | <a href="#">c4nh0A_</a> | Alignment | not modelled | 52.7 | 26 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell divisionfts/spoiii;<br><b>PDBTitle:</b> cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 55 | <a href="#">c3co5B_</a> | Alignment | not modelled | 50.5 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component system<br><b>transcriptional response</b><br><b>PDBTitle:</b> crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae |
| 56 | <a href="#">d1m8pa3</a> | Alignment | not modelled | 50.0 | 26 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ATP sulfurylase C-terminal domain  |
| 57 | <a href="#">c6bbqA_</a> | Alignment | not modelled | 49.9 | 36 | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3,adp-ribosylation factor 6;<br><b>PDBTitle:</b> model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein                                 |
| 58 | <a href="#">d1lw7a2</a> | Alignment | not modelled | 49.9 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 59 | <a href="#">d1kjwa2</a> | Alignment | not modelled | 49.7 | 30 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 60 | <a href="#">d1qf9a_</a> | Alignment | not modelled | 49.5 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 61 | <a href="#">c3bbpA_</a> | Alignment | not modelled | 49.3 | 19 | <b>PDB header:</b> protein transport/splicing<br><b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein rab-6a;<br><b>PDBTitle:</b> rab6-gtp:gcc185 rab binding domain complex  |
| 62 | <a href="#">c4bzpB_</a> | Alignment | not modelled | 49.3 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ras-related protein cysn/cytc;<br><b>PDBTitle:</b> structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp  |
| 63 | <a href="#">c4ag5A_</a> | Alignment | not modelled | 49.0 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> type iv secretory pathway virb4 components-like protein;<br><b>PDBTitle:</b> structure of virb4 of thermoanaerobacter pseudethanolicus   |
| 64 | <a href="#">d2cdna1</a> | Alignment | not modelled | 48.7 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 65 | <a href="#">d1akya1</a> | Alignment | not modelled | 48.2 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 66 | <a href="#">c2bovA_</a> | Alignment | not modelled | 48.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein ral-a;<br><b>PDBTitle:</b> molecular recognition of an adp-ribosylating clostridium2 botulinum c3 exoenzyme by rala gtpase   |
| 67 | <a href="#">c4nkrB_</a> | Alignment | not modelled | 47.9 | 38 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis protein b;<br><b>PDBTitle:</b> the crystal structure of bacillus subtilis mobb  |
| 68 | <a href="#">d1m7gb_</a> | Alignment | not modelled | 47.4 | 26 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Adenosine-5'phosphosulfate kinase (APS kinase)   |
| 69 | <a href="#">c1g7tA_</a> | Alignment | not modelled | 46.4 | 41 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if2/eif5b;<br><b>PDBTitle:</b> x-ray structure of translation initiation factor if2/eif5b2 complexed with gdnpp  |
| 70 | <a href="#">d1zaka1</a> | Alignment | not modelled | 46.2 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 71 | <a href="#">d1e4va1</a> | Alignment | not modelled | 46.0 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 72 | <a href="#">c2ar7A_</a> | Alignment | not modelled | 45.6 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 4;<br><b>PDBTitle:</b> crystal structure of human adenylate kinase 4, ak4   |
| 73 | <a href="#">c4lpsA_</a> | Alignment | not modelled | 45.6 | 27 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein hybp;<br><b>PDBTitle:</b> crystal structure of hybp from helicobacter pylori in complex with2 nickel   |
| 74 | <a href="#">c3cm0A_</a> | Alignment | not modelled | 44.8 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of adenylate kinase from thermus2 thermophilus hb8   |
| 75 | <a href="#">c3vaaC_</a> | Alignment | not modelled | 44.4 | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> shikimate kinase;<br><b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of shikimate kinase from2 bacteroides thetaiotaomicron   |
| 76 | <a href="#">d1rkba_</a> | Alignment | not modelled | 44.3 | 33 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 77 | <a href="#">c1zuiA_</a> | Alignment | not modelled | 44.2 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase;<br><b>PDBTitle:</b> structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase  |
| 78 | <a href="#">c3tlxA_</a> | Alignment | not modelled | 44.1 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 2;<br><b>PDBTitle:</b> crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum   |
| 79 | <a href="#">d1zina1</a> | Alignment | not modelled | 44.0 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
|    |                         |           |              |      |    | <b>PDB header:</b> transferase   |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 80  | <a href="#">c4cw7A_</a> | Alignment | not modelled | 43.9 | 35 | <b>Chain:</b> A: <b>PDB Molecule:</b> putative adenylate kinase;<br><b>PDBTitle:</b> structure of the fap7-rps14 complex in complex with atp   |
| 81  | <a href="#">d2ak3a1</a> | Alignment | not modelled | 43.5 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 82  | <a href="#">c1ankA_</a> | Alignment | not modelled | 43.3 | 12 | <b>PDB header:</b> transferase(phosphotransferase)<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> the closed conformation of a highly flexible protein: the structure of 2 e. coli adenylate kinase with bound amp and amppnp      |
| 83  | <a href="#">c3akyA_</a> | Alignment | not modelled | 43.3 | 15 | <b>PDB header:</b> adenylate kinase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> stability, activity and structure of adenylate kinase2 mutants  |
| 84  | <a href="#">d1yzga1</a> | Alignment | not modelled | 43.0 | 41 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 85  | <a href="#">d1jiva_</a> | Alignment | not modelled | 43.0 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 86  | <a href="#">c3c4bA_</a> | Alignment | not modelled | 42.4 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> poly(adp-ribose) polymerase 3;<br><b>PDBTitle:</b> human poly(adp-ribose) polymerase 3, catalytic fragment in complex2 with an inhibitor dr2313  |
| 87  | <a href="#">d1yzqa1</a> | Alignment | not modelled | 42.4 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 88  | <a href="#">c5g3yA_</a> | Alignment | not modelled | 42.3 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of adenylate kinase ancestor 1 with zn and adp bound   |
| 89  | <a href="#">d1bifa1</a> | Alignment | not modelled | 41.9 | 25 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain                                |
| 90  | <a href="#">c2ak2A_</a> | Alignment | not modelled | 40.3 | 14 | <b>PDB header:</b> phosphotransferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase isoenzyme-2;<br><b>PDBTitle:</b> adenylate kinase isoenzyme-2  |
| 91  | <a href="#">c3a1vB_</a> | Alignment | not modelled | 40.2 | 20 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> iron(ii) transport protein b;<br><b>PDBTitle:</b> crystal structure of the cytosolic domain of t. maritima feob2 iron transporter in apo form  |
| 92  | <a href="#">d1m7ga_</a> | Alignment | not modelled | 40.0 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Adenosine-5'phosphosulfate kinase (APS kinase)   |
| 93  | <a href="#">c2c99A_</a> | Alignment | not modelled | 40.0 | 29 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator;<br><b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf |
| 94  | <a href="#">c4y0aA_</a> | Alignment | not modelled | 39.5 | 32 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase;<br><b>PDBTitle:</b> shikimate kinase from acinetobacter baumannii in complex with2 shikimate   |
| 95  | <a href="#">d1e6ca_</a> | Alignment | not modelled | 39.5 | 36 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Shikimate kinase (AroK)  |
| 96  | <a href="#">d1kgda_</a> | Alignment | not modelled | 39.4 | 9  | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 97  | <a href="#">d1zd9a1</a> | Alignment | not modelled | 38.8 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 98  | <a href="#">c4mitB_</a> | Alignment | not modelled | 38.2 | 32 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> rho family gtpase;<br><b>PDBTitle:</b> crystal structure of e. histolytica racc bound to the ehpk4 pbd   |
| 99  | <a href="#">c1gs0B_</a> | Alignment | not modelled | 38.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> poly (adp-ribose) polymerase-2;<br><b>PDBTitle:</b> crystal structure of the catalytic fragment of murine poly2 (adp-ribose) polymerase-2  |
| 100 | <a href="#">c3bwdD_</a> | Alignment | not modelled | 38.0 | 32 | <b>PDB header:</b> plant protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> rac-like gtp-binding protein arac6;<br><b>PDBTitle:</b> crystal structure of the plant rho protein rop5  |
| 101 | <a href="#">c4ku4B_</a> | Alignment | not modelled | 37.9 | 29 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ras-3 from cryphonectria parasitica;<br><b>PDBTitle:</b> crystal structure of a ras-like protein from cryphonectria parasitica2 in complex with gdp                                  |
| 102 | <a href="#">c5fg3A_</a> | Alignment | not modelled | 37.7 | 41 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor if-2;<br><b>PDBTitle:</b> crystal structure of gdp-bound aif5b from aeropyrum pernix  |
| 103 | <a href="#">c2i1vB_</a> | Alignment | not modelled | 37.0 | 28 | <b>PDB header:</b> transferase, hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-<br><b>PDBTitle:</b> crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate                                       |
| 104 | <a href="#">c6f1yj_</a> | Alignment | not modelled | 36.9 | 19 | <b>PDB header:</b> motor protein<br><b>Chain:</b> J: <b>PDB Molecule:</b><br><b>PDBTitle:</b> dynein light intermediate chain region of the dynein2 tail/dynactin/bicdr1 complex   |
| 105 | <a href="#">c1zakB_</a> | Alignment | not modelled | 36.7 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> adenylate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5')pentaphosphate (ap5a)  |
| 106 | <a href="#">d1viaa_</a> | Alignment | not modelled | 36.7 | 25 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Shikimate kinase (AroK)  |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 107 | <a href="#">d1z0ja1</a> | Alignment | not modelled | 36.2 | 10 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 108 | <a href="#">c2ak3B_</a> | Alignment | not modelled | 36.2 | 12 | <b>PDB header:</b> transferase (phosphotransferase)<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase isoenzyme-3;<br><b>PDBTitle:</b> the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution |
| 109 | <a href="#">c1ys4A_</a> | Alignment | not modelled | 35.8 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase;<br><b>PDBTitle:</b> structure of aspartate-semialdehyde dehydrogenase from methanococcus2 jannaschii  |
| 110 | <a href="#">d1zj6a1</a> | Alignment | not modelled | 35.4 | 33 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 111 | <a href="#">d1z07a1</a> | Alignment | not modelled | 35.3 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 112 | <a href="#">c1f5nA_</a> | Alignment | not modelled | 35.3 | 29 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced guanylate-binding protein 1;<br><b>PDBTitle:</b> human guanylate binding protein-1 in complex with the gtp analogue,2 gmppnp.   |
| 113 | <a href="#">d1jnva3</a> | Alignment | not modelled | 34.8 | 29 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 114 | <a href="#">c2yvua_</a> | Alignment | not modelled | 34.4 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable adenyllyl-sulfate kinase;<br><b>PDBTitle:</b> crystal structure of ape1195  |
| 115 | <a href="#">d2gj8a1</a> | Alignment | not modelled | 34.1 | 29 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |
| 116 | <a href="#">c6gyeB_</a> | Alignment | not modelled | 34.1 | 23 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> nicotinamide-nucleotide adenyllyltransferase nadr family /<br><b>PDBTitle:</b> crystal structure of nadr protein in complex with nr  |
| 117 | <a href="#">c2eu8B_</a> | Alignment | not modelled | 33.8 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of a thermostable mutant of bacillus2 subtilis adenylate kinase (q199r)  |
| 118 | <a href="#">c2vliB_</a> | Alignment | not modelled | 33.4 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> antibiotic resistance protein;<br><b>PDBTitle:</b> structure of deinococcus radiodurans tunicamycin resistance protein   |
| 119 | <a href="#">d1k6ma1</a> | Alignment | not modelled | 33.3 | 27 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain  |
| 120 | <a href="#">d2erxa1</a> | Alignment | not modelled | 33.2 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> G proteins   |