

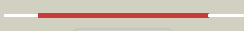








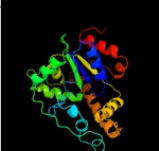

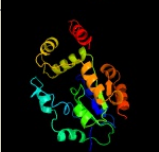



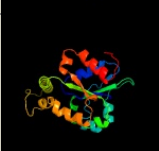






# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD3529c_(-)_3966063_3967217 |
| Date          | Fri Aug 9 18:20:20 BST 2019   |
| Unique Job ID | 9817b939c0bd6bdd              |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">c2zq5A_</a> | <br>Alignment   |    | 100.0      | 99     | <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)                  |
| 2  | <a href="#">c2z6vA_</a> | <br>Alignment   |    | 100.0      | 27     | <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                                       |
| 3  | <a href="#">c4gbmA_</a> | <br>Alignment   |    | 100.0      | 13     | <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  |
| 4  | <a href="#">c3ap3A_</a> | <br>Alignment   |   | 100.0      | 21     | <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                             |
| 5  | <a href="#">c4goxA_</a> | <br>Alignment |  | 100.0      | 17     | <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="#">d1texa_</a> | <br>Alignment |  | 99.9       | 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   |
| 7  | <a href="#">c3rnlA_</a> | <br>Alignment |  | 99.9       | 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   |
| 8  | <a href="#">c1vkjA_</a> | <br>Alignment |  | 99.9       | 15     | <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 |
| 9  | <a href="#">d1vkja_</a> | <br>Alignment |  | 99.9       | 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="#">d1t8ta_</a> | <br>Alignment |  | 99.9       | 22     | <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="#">c1nstA_</a> | <br>Alignment |  | 99.9       | 18     | <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    |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">d1nsta_</a> | Alignment |              | 99.9 | 18 | <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   |
| 13 | <a href="#">c3bd9A_</a> | Alignment |              | 99.9 | 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  |
| 14 | <a href="#">d1ls6a_</a> | Alignment |              | 99.9 | 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   |
| 15 | <a href="#">c2gwhA_</a> | Alignment |              | 99.9 | 16 | <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  |
| 16 | <a href="#">c3u3oA_</a> | Alignment |              | 99.9 | 15 | <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   |
| 17 | <a href="#">d1fmja_</a> | Alignment |              | 99.9 | 18 | <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   |
| 18 | <a href="#">d1xv1a_</a> | Alignment |              | 99.9 | 11 | <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   |
| 19 | <a href="#">d1j99a_</a> | Alignment |              | 99.9 | 13 | <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="#">d2a3ra1</a> | Alignment |              | 99.9 | 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   |
| 21 | <a href="#">c5x2bK_</a> | Alignment | not modelled | 99.9 | 17 | <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  |
| 22 | <a href="#">c3mg9A_</a> | Alignment | not modelled | 99.9 | 13 | <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   |
| 23 | <a href="#">c2zvpX_</a> | Alignment | not modelled | 99.9 | 14 | <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                     |
| 24 | <a href="#">c2ovfA_</a> | Alignment | not modelled | 99.9 | 20 | <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   |
| 25 | <a href="#">c1q1qA_</a> | Alignment | not modelled | 99.9 | 14 | <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 |
| 26 | <a href="#">d1g3ma_</a> | Alignment | not modelled | 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   |
| 27 | <a href="#">d1aqua_</a> | Alignment | not modelled | 99.9 | 11 | <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="#">d3bfxa1</a> | Alignment | not modelled | 99.9 | 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   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">d1q20a_</a> | Alignment | not modelled | 99.9 | 18 | <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   |
| 30 | <a href="#">c3mgbA_</a> | Alignment | not modelled | 99.9 | 14 | <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   |
| 31 | <a href="#">c1zd1B_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sulfotransferase 4a1;<br><b>PDBTitle:</b> human sulfotransferase sult4a1  |
| 32 | <a href="#">c5mekA_</a> | Alignment | not modelled | 99.8 | 16 | <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)          |
| 33 | <a href="#">c2h8kA_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sult1c3 splice variant d;<br><b>PDBTitle:</b> human sulfotranferase sult1c3 in complex with pap   |
| 34 | <a href="#">d1q44a_</a> | Alignment | not modelled | 99.8 | 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   |
| 35 | <a href="#">c5tizA_</a> | Alignment | not modelled | 99.5 | 21 | <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 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase;<br><b>PDBTitle:</b> schistosoma mansoni (blood fluke) sulfotransferase/oxamniquinone complex  |
| 37 | <a href="#">c3neyC_</a> | Alignment | not modelled | 79.8 | 16 | <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  |
| 38 | <a href="#">c3gmtB_</a> | Alignment | not modelled | 79.4 | 12 | <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 burkholderia pseudomallei  |
| 39 | <a href="#">d1kwa2</a>  | Alignment | not modelled | 75.4 | 35 | <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   |
| 40 | <a href="#">d2bcgy1</a> | Alignment | not modelled | 74.2 | 20 | <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  |
| 41 | <a href="#">d1p3ja1</a> | Alignment | not modelled | 74.0 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 42 | <a href="#">c1lw7A_</a> | Alignment | not modelled | 70.6 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator nadr;<br><b>PDBTitle:</b> nadr protein from haemophilus influenzae  |
| 43 | <a href="#">c4xrpA_</a> | Alignment | not modelled | 70.1 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> pnkp1;<br><b>PDBTitle:</b> structure of the pnkp1/rnl/hen1 rna repair complex   |
| 44 | <a href="#">d1kgda_</a> | Alignment | not modelled | 69.7 | 13 | <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   |
| 45 | <a href="#">c2if2C_</a> | Alignment | not modelled | 68.9 | 17 | <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. |
| 46 | <a href="#">c2qorA_</a> | Alignment | not modelled | 68.2 | 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  |
| 47 | <a href="#">d1ak2a1</a> | Alignment | not modelled | 67.0 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 48 | <a href="#">c3lh5A_</a> | Alignment | not modelled | 67.0 | 18 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-1;<br><b>PDBTitle:</b> crystal structure of the sh3-guanylate kinase core domain of zo-1  |
| 49 | <a href="#">c1zuiA_</a> | Alignment | not modelled | 66.7 | 22 | <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                                   |
| 50 | <a href="#">c4nu0B_</a> | Alignment | not modelled | 66.1 | 14 | <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  |
| 51 | <a href="#">d1s3ga1</a> | Alignment | not modelled | 65.4 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 52 | <a href="#">c1m8pB_</a> | Alignment | not modelled | 64.4 | 32 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenyllyltransferase;<br><b>PDBTitle:</b> crystal structure of p. chrysogenum atp sulfurylase in the t-state  |
| 53 | <a href="#">d1lw7a2</a> | Alignment | not modelled | 63.7 | 17 | <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="#">c1nijA_</a> | Alignment | not modelled | 63.5 | 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   |
| 55 | <a href="#">d1yzna1</a> | Alignment | not modelled | 63.3 | 20 | <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  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 56 | <a href="#">d1lvga_</a> | Alignment | not modelled | 62.9 | 26 | <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   |
| 57 | <a href="#">c3tlxA_</a> | Alignment | not modelled | 62.7 | 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  |
| 58 | <a href="#">c2oiIA_</a> | Alignment | not modelled | 62.5 | 25 | <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  |
| 59 | <a href="#">c1kjaA_</a> | Alignment | not modelled | 62.1 | 32 | <b>PDB header:</b> neuropeptide<br><b>Chain:</b> A: <b>PDB Molecule:</b> postsynaptic density protein 95;<br><b>PDBTitle:</b> sh3-guanylate kinase module from psd-95   |
| 60 | <a href="#">c3uatA_</a> | Alignment | not modelled | 61.7 | 21 | <b>PDB header:</b> peptide binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> disks large homolog 1;<br><b>PDBTitle:</b> guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules  |
| 61 | <a href="#">d1jva_</a>  | Alignment | not modelled | 61.7 | 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   |
| 62 | <a href="#">d1viaa_</a> | Alignment | not modelled | 61.5 | 27 | <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)   |
| 63 | <a href="#">d1akya1</a> | Alignment | not modelled | 60.6 | 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   |
| 64 | <a href="#">d2cdna1</a> | Alignment | not modelled | 59.9 | 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="#">d1m8pa3</a> | Alignment | not modelled | 58.9 | 40 | <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   |
| 66 | <a href="#">c1f5nA_</a> | Alignment | not modelled | 58.8 | 34 | <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 gmpnp.   |
| 67 | <a href="#">c6gyeB_</a> | Alignment | not modelled | 58.6 | 27 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> nicotinamide-nucleotide adenyltransferase nadr family /<br><b>PDBTitle:</b> crystal structure of nadr protein in complex with nr  |
| 68 | <a href="#">c4ncIB_</a> | Alignment | not modelled | 58.5 | 33 | <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 |
| 69 | <a href="#">d1m7gb_</a> | Alignment | not modelled | 58.0 | 37 | <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)  |
| 70 | <a href="#">d1rkba_</a> | Alignment | not modelled | 57.5 | 27 | <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="#">c3vaaC_</a> | Alignment | not modelled | 56.8 | 35 | <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  |
| 72 | <a href="#">c2bwjC_</a> | Alignment | not modelled | 56.8 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> adenylate kinase 5;<br><b>PDBTitle:</b> structure of adenylate kinase 5   |
| 73 | <a href="#">d1bifa1</a> | Alignment | not modelled | 56.7 | 29 | <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   |
| 74 | <a href="#">d1zina1</a> | Alignment | not modelled | 56.6 | 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   |
| 75 | <a href="#">c2ar7A_</a> | Alignment | not modelled | 56.5 | 15 | <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  |
| 76 | <a href="#">c1ankA_</a> | Alignment | not modelled | 56.4 | 9  | <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 of2 e. coli adenylate kinase with bound amp and amppnp                          |
| 77 | <a href="#">d2bmea1</a> | Alignment | not modelled | 56.3 | 30 | <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  |
| 78 | <a href="#">c3akyA_</a> | Alignment | not modelled | 55.8 | 14 | <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   |
| 79 | <a href="#">c4y0aA_</a> | Alignment | not modelled | 55.6 | 30 | <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  |
| 80 | <a href="#">c3umfA_</a> | Alignment | not modelled | 55.2 | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> schistosoma mansonii adenylate kinase   |
| 81 | <a href="#">d1e4va1</a> | Alignment | not modelled | 54.8 | 11 | <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  |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 82  | <a href="#">c5g3yA_</a> | Alignment | not modelled | 54.7 | 10 | <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of adenylyate kinase ancestor 1 with zn and adp bound   |
| 83  | <a href="#">d1teva_</a> | Alignment | not modelled | 54.2 | 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   |
| 84  | <a href="#">d1njja1</a> | Alignment | not modelled | 54.0 | 35 | <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   |
| 85  | <a href="#">c3cm0A_</a> | Alignment | not modelled | 53.7 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of adenylyate kinase from thermus2 thermophilus hb8   |
| 86  | <a href="#">c4cw7A_</a> | Alignment | not modelled | 53.7 | 35 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative adenylyate kinase;<br><b>PDBTitle:</b> structure of the fap7-rps14 complex in complex with atp   |
| 87  | <a href="#">d1zaka1</a> | Alignment | not modelled | 53.5 | 11 | <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   |
| 88  | <a href="#">d2ak3a1</a> | Alignment | not modelled | 53.4 | 11 | <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   |
| 89  | <a href="#">c1z6gA_</a> | Alignment | not modelled | 53.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase;<br><b>PDBTitle:</b> crystal structure of guanylate kinase from plasmodium falciparum  |
| 90  | <a href="#">c2grjH_</a> | Alignment | not modelled | 52.7 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> H: <b>PDB Molecule:</b> dephospho-coa kinase;<br><b>PDBTitle:</b> crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution |
| 91  | <a href="#">c1s3gA_</a> | Alignment | not modelled | 52.6 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of adenylyate kinase from bacillus2 globisporus   |
| 92  | <a href="#">d1m7ga_</a> | Alignment | not modelled | 52.2 | 35 | <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="#">c4eunA_</a> | Alignment | not modelled | 52.1 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thermoreistant glucokinase;<br><b>PDBTitle:</b> crystal structure of a sugar kinase (target efi-502144 from janibacter2 sp. htcc2649), unliganded structure                             |
| 94  | <a href="#">c2yvua_</a> | Alignment | not modelled | 51.7 | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable adenylyl-sulfate kinase;<br><b>PDBTitle:</b> crystal structure of ape1195  |
| 95  | <a href="#">d3adka_</a> | Alignment | not modelled | 51.1 | 17 | <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   |
| 96  | <a href="#">c1znyA_</a> | Alignment | not modelled | 50.8 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp   |
| 97  | <a href="#">c2ak2A_</a> | Alignment | not modelled | 50.7 | 12 | <b>PDB header:</b> phosphotransferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase isoenzyme-2;<br><b>PDBTitle:</b> adenylyate kinase isoenzyme-2  |
| 98  | <a href="#">c4i1vB_</a> | Alignment | not modelled | 50.5 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dephospho-coa kinase;<br><b>PDBTitle:</b> crystal structure of a dephospho-coa kinase from burkholderia2 vietnamiensis bound to adp   |
| 99  | <a href="#">c3trfB_</a> | Alignment | not modelled | 49.9 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> shikimate kinase;<br><b>PDBTitle:</b> structure of a shikimate kinase (arok) from coxiella burnetii   |
| 100 | <a href="#">c1zakB_</a> | Alignment | not modelled | 49.7 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> adenylyate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5'-)pentaphosphate (ap5a)   |
| 101 | <a href="#">d1qf9a_</a> | Alignment | not modelled | 48.7 | 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   |
| 102 | <a href="#">d1khta_</a> | Alignment | not modelled | 48.3 | 27 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases   |
| 103 | <a href="#">c2eu8B_</a> | Alignment | not modelled | 48.3 | 19 | <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 adenylyate kinase (q199r)  |
| 104 | <a href="#">c2bovA_</a> | Alignment | not modelled | 48.2 | 10 | <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 ral a gtpase   |
| 105 | <a href="#">c2rhmD_</a> | Alignment | not modelled | 48.1 | 45 | <b>PDB header:</b> unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase;<br><b>PDBTitle:</b> crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution                                |
| 106 | <a href="#">d1kaga_</a> | Alignment | not modelled | 47.6 | 27 | <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="#">c3bbpA_</a> | Alignment | not modelled | 46.8 | 20 | <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   |
| 108 | <a href="#">d1pbya1</a> | Alignment | not modelled | 46.3 | 24 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains   |

|     |                         |           |              |      |   |
|-----|-------------------------|-----------|--------------|------|---|
|     |                         |           |              |      | 1 and 2   |
| 109 | <a href="#">c3be4A_</a> | Alignment | not modelled | 46.2 | 10<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360  |
| 110 | <a href="#">d2bdta1</a> | Alignment | not modelled | 45.9 | 25<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Atu3015-like  |
| 111 | <a href="#">c2xb4A_</a> | Alignment | not modelled | 45.9 | 15<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structures of zinc containing adenylate kinase from2 desulfovibrio gigas  |
| 112 | <a href="#">c3kfvA_</a> | Alignment | not modelled | 45.8 | 23<br><b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-3;<br><b>PDBTitle:</b> crystal structure of the sh3-kinase fragment of tight junction protein2 3 (tjp3) in apo-form   |
| 113 | <a href="#">d1k6ma1</a> | Alignment | not modelled | 45.8 | 25<br><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   |
| 114 | <a href="#">c6bbqA_</a> | Alignment | not modelled | 45.7 | 36<br><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          |
| 115 | <a href="#">d1p3da1</a> | Alignment | not modelled | 45.5 | 20<br><b>Fold:</b> MurCD N-terminal domain<br><b>Superfamily:</b> MurCD N-terminal domain<br><b>Family:</b> MurCD N-terminal domain   |
| 116 | <a href="#">c3uieB_</a> | Alignment | not modelled | 45.3 | 38<br><b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylyl-sulfate kinase 1, chloroplastic;<br><b>PDBTitle:</b> crystal structure of adenosine 5'-phosphosulfate kinase from2 arabidopsis thaliana in complex with amppnp and aps |
| 117 | <a href="#">c6qp0A_</a> | Alignment | not modelled | 45.3 | 50<br><b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative chromatin binding protein;<br><b>PDBTitle:</b> crystal structure of chaetomium thermophilum kti12 in complex with2 adp-alf3  |
| 118 | <a href="#">c4bzbB_</a> | Alignment | not modelled | 45.2 | 25<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional enzyme cysn/cysc;<br><b>PDBTitle:</b> structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp   |
| 119 | <a href="#">d1uf9a_</a> | Alignment | not modelled | 45.0 | 36<br><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   |
| 120 | <a href="#">d1jmx1</a>  | Alignment | not modelled | 45.0 | 24<br><b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2   |