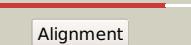
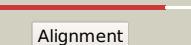
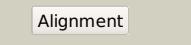
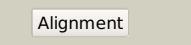
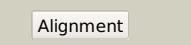
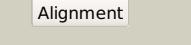
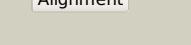
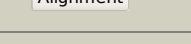


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD0295c_(-)_358945_359748
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	2720586f3fe8a435

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zq5A_	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
2	c2z6vA_	Alignment		100.0	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of sulfotransferase stf9 from2 mycobacterium avium
3	d1texa_	Alignment		100.0	69	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
4	c3ap3A_	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine sulfotransferase 2; <b>PDBTitle:</b> crystal structure of human tyrosylprotein sulfotransferase-2 complexed2 with pap
5	c4gbmA_	Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> curm sulfotransferase; <b>PDBTitle:</b> sulfotransferase domain from the curacin biosynthetic pathway
6	c4goxA_	Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase; <b>PDBTitle:</b> sulfotransferase domain from the synechococcus pcc 7002 olefin2 synthase
7	d1vkja_	Alignment		99.9	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
8	c1vkjA_	Alignment		99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate (glucosamine) 3-o-sulfotransferase 1; <b>PDBTitle:</b> crystal structure of heparan sulfate 3-o-sulfotransferase isoform 1 in2 the presence of pap
9	d1t8ta_	Alignment		99.9	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
10	c3rnIA_	Alignment		99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase; <b>PDBTitle:</b> crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius
11	c1nstA_	Alignment		99.9	11	<b>PDB header:</b> sulfotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate n-deacetylase/n-sulfotransferase; <b>PDBTitle:</b> the sulfotransferase domain of human heparin sulfate n-deacetylase/n-2 sulfotransferase

12	<a href="#">d1nsta_</a>			99.9	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
13	<a href="#">c3bd9A_</a>			99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> heparan sulfate glucosamine 3-o-sulfotransferase <b>PDBTitle:</b> human 3-o-sulfotransferase isoform 5 with bound pap
14	<a href="#">d1fmja_</a>			99.9	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
15	<a href="#">c2gwhA_</a>			99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase 1c2; <b>PDBTitle:</b> human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
16	<a href="#">c3mg9A_</a>			99.9	12	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> teg12; <b>PDBTitle:</b> teg 12 binary structure complexed with the teicoplanin aglycone
17	<a href="#">d1j99a_</a>			99.9	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
18	<a href="#">d1xv1a_</a>			99.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
19	<a href="#">d1ls6a_</a>			99.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
20	<a href="#">c3u3oA_</a>			99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase 1a1; <b>PDBTitle:</b> crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
21	<a href="#">c5x2bK_</a>		not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> sulfotransferase; <b>PDBTitle:</b> crystal structure of mouse sulfotransferase sult7a1 complexed with pap
22	<a href="#">c2ovfA_</a>		not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stal; <b>PDBTitle:</b> crystal structure of stal-pap complex
23	<a href="#">c1q1qA_</a>		not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase family, cytosolic, 2b, member 1 isoform a; <b>PDBTitle:</b> crystal structure of human pregnenolone sulfotransferase (sult2b1a) in2 the presence of pap
24	<a href="#">d1q20a_</a>		not modelled	99.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
25	<a href="#">c2zvpX_</a>		not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> tyrosine-ester sulfotransferase; <b>PDBTitle:</b> crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
26	<a href="#">d1g3ma_</a>		not modelled	99.9	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
27	<a href="#">d2a3ra1</a>		not modelled	99.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
28	<a href="#">c3mgba_</a>		not modelled	99.9	12	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> teg12; <b>PDBTitle:</b> teg 12 ternary structure complexed with pap and the teicoplanin2 aglycone

29	<a href="#">d3bfxa1</a>		Alignment	not modelled	99.9	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
30	<a href="#">c5mekA</a>		Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic sulfotransferase 18; <b>PDBTitle:</b> sulphotransferase-18 from arabidopsis thaliana in complex with 3'-2' phosphoadenosine 5'-phosphate (pap)
31	<a href="#">d1aqua</a>		Alignment	not modelled	99.8	8	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
32	<a href="#">c1zd1B</a>		Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfotransferase 4a1; <b>PDBTitle:</b> human sulfotransferase sult4a1
33	<a href="#">d1q44a</a>		Alignment	not modelled	99.8	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> PAPS sulfotransferase
34	<a href="#">c2h8kA</a>		Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sult1c3 splice variant d; <b>PDBTitle:</b> human sulfotranferase sult1c3 in complex with pap
35	<a href="#">c5tizA</a>		Alignment	not modelled	99.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase; <b>PDBTitle:</b> schistosoma japonicum (blood fluke) sulfotransferase
36	<a href="#">c4mubA</a>		Alignment	not modelled	99.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase; <b>PDBTitle:</b> schistosoma mansoni (blood fluke) sulfotransferase/oxamquine complex
37	<a href="#">c5x56A</a>		Alignment	not modelled	91.0	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii repair protein psb27-h1, chloroplastic; <b>PDBTitle:</b> crystal structure of psb27 from arabidopsis thaliana
38	<a href="#">c2y6xA</a>		Alignment	not modelled	83.1	15	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii 11 kd protein; <b>PDBTitle:</b> structure of psb27 from thermosynechococcus elongatus
39	<a href="#">c2kmfA</a>		Alignment	not modelled	77.2	16	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii 11 kda protein; <b>PDBTitle:</b> solution structure of psb27 from cyanobacterial photosystem2 ii
40	<a href="#">c3neyC</a>		Alignment	not modelled	74.2	11	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> 55 kda erythrocyte membrane protein; <b>PDBTitle:</b> crystal structure of the kinase domain of mpp1/p55
41	<a href="#">c6gyeB</a>		Alignment	not modelled	71.8	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinamide-nucleotide adenyllyltransferase nadr family / <b>PDBTitle:</b> crystal structure of nadr protein in complex with nr
42	<a href="#">d1kjwa2</a>		Alignment	not modelled	71.0	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
43	<a href="#">d1kgda</a>		Alignment	not modelled	67.1	7	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
44	<a href="#">c2qorA</a>		Alignment	not modelled	66.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of plasmodium vivax guanylate kinase
45	<a href="#">c3x1dA</a>		Alignment	not modelled	65.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atlastin; <b>PDBTitle:</b> crystal structure of atlastin from drosophila melanogaster
46	<a href="#">c5ca8A</a>		Alignment	not modelled	65.5	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein sey1; <b>PDBTitle:</b> structures of the yeast dynamin-like gtpase sey1p in complex with gdp
47	<a href="#">d2bcgy1</a>		Alignment	not modelled	65.3	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
48	<a href="#">c2if2C</a>		Alignment	not modelled	64.4	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dephospho-coa kinase; <b>PDBTitle:</b> crystal structure of the putative dephospho-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.
49	<a href="#">c3q5eG</a>		Alignment	not modelled	61.1	32	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atlastin-1; <b>PDBTitle:</b> crystal structure of human atlastin-1 (residues 1-447) bound to gdp,2 crystal form 2
50	<a href="#">d1lw7a2</a>		Alignment	not modelled	60.9	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
51	<a href="#">c1lw7A</a>		Alignment	not modelled	59.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator nadr; <b>PDBTitle:</b> nadr protein from haemophilus influenzae
52	<a href="#">c4xrpa</a>		Alignment	not modelled	58.4	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pnkp1; <b>PDBTitle:</b> structure of the pnkp1/rnl/hen1 rna repair complex
53	<a href="#">d1p3da1</a>		Alignment	not modelled	57.5	21	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
54	<a href="#">c4y0aA</a>		Alignment	not modelled	56.5	12	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> shikimate kinase from acinetobacter baumannii in complex with2 shikimate
55	<a href="#">c3f5fA</a>		Alignment	not modelled	53.5	13	<b>PDB header:</b> transport, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, heparan sulfate 2-o-sulfotransferase <b>PDBTitle:</b> crystal structure of heparan sulfate 2-o-sulfotransferase

						from gallus2 gallus as a maltose binding protein fusion.
56	<a href="#">c3tlxA</a>	Alignment	not modelled	53.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 2; <b>PDBTitle:</b> crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
57	<a href="#">d2erya1</a>	Alignment	not modelled	53.4	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
58	<a href="#">d1yzna1</a>	Alignment	not modelled	52.6	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
59	<a href="#">d1j6ua1</a>	Alignment	not modelled	51.6	8	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
60	<a href="#">c3lh5A</a>	Alignment	not modelled	50.9	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> crystal structure of the sh3-guanylate kinase core domain of zo-1
61	<a href="#">c2oiIA</a>	Alignment	not modelled	50.1	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein rab-25; <b>PDBTitle:</b> crystal structure of human rab25 in complex with gdp
62	<a href="#">c1zuiA</a>	Alignment	not modelled	49.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
63	<a href="#">d1viaa</a>	Alignment	not modelled	48.5	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
64	<a href="#">c6cauA</a>	Alignment	not modelled	47.2	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylumuramate--l-alanine ligase; <b>PDBTitle:</b> udp-n-acetylumuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
65	<a href="#">d1lvga</a>	Alignment	not modelled	46.7	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
66	<a href="#">d2bmea1</a>	Alignment	not modelled	44.5	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
67	<a href="#">c4nu0B</a>	Alignment	not modelled	44.3	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from streptococcus pneumoniae2 with ap5a
68	<a href="#">d1rkba</a>	Alignment	not modelled	43.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
69	<a href="#">c3bh1A</a>	Alignment	not modelled	42.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0371 protein dip2346; <b>PDBTitle:</b> crystal structure of protein dip2346 from corynebacterium diphtheriae
70	<a href="#">c1kjwA</a>	Alignment	not modelled	41.7	13	<b>PDB header:</b> neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> postsynaptic density protein 95; <b>PDBTitle:</b> sh3-guanylate kinase module from psd-95
71	<a href="#">c3uatA</a>	Alignment	not modelled	41.6	11	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> disks large homolog 1; <b>PDBTitle:</b> guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules
72	<a href="#">d1nija1</a>	Alignment	not modelled	41.4	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
73	<a href="#">d2hmva1</a>	Alignment	not modelled	41.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
74	<a href="#">c1gqaA</a>	Alignment	not modelled	40.9	20	<b>PDB header:</b> cell wall biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylumuramate-l-alanine ligase; <b>PDBTitle:</b> murc - crystal structure of the apo-enzyme from haemophilus influenzae
75	<a href="#">d1g6oa</a>	Alignment	not modelled	40.4	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
76	<a href="#">d1ak2a1</a>	Alignment	not modelled	40.3	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
77	<a href="#">d1s3ga1</a>	Alignment	not modelled	40.1	5	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
78	<a href="#">c1z6gA</a>	Alignment	not modelled	38.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of guanylate kinase from plasmodium falciparum
79	<a href="#">d2fga1</a>	Alignment	not modelled	37.7	6	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
80	<a href="#">c5d0nA</a>	Alignment	not modelled	37.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate, phosphate dikinase regulatory protein, <b>PDBTitle:</b> crystal structure of maize pdrp bound with amp
81	<a href="#">c3r3pb</a>	Alignment	not modelled	37.3	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mobile intron protein; <b>PDBTitle:</b> homing endonuclease i-bth0305i catalytic domain
82	<a href="#">d1r5ba3</a>	Alignment	not modelled	37.1	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

					<b>Family:</b> G proteins
83	<a href="#">d1m8pa3</a>	Alignment	not modelled	36.6	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ATP sulfurylase C-terminal domain
84	<a href="#">c3akyA</a>	Alignment	not modelled	36.3	<b>PDB header:</b> adenylate kinase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> stability, activity and structure of adenylate kinase2 mutants
85	<a href="#">c4ag5A</a>	Alignment	not modelled	36.2	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type iv secretory pathway virb4 components-like protein; <b>PDBTitle:</b> structure of virb4 of thermoanaerobacter pseudethanolicus
86	<a href="#">c4j7cA</a>	Alignment	not modelled	34.9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ktr system potassium uptake protein a; <b>PDBTitle:</b> ktrab potassium transporter from bacillus subtilis
87	<a href="#">c4nh0A</a>	Alignment	not modelled	34.3	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell divisionftskspoiiie; <b>PDBTitle:</b> cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
88	<a href="#">d1yzga1</a>	Alignment	not modelled	33.3	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
89	<a href="#">c4ii7D</a>	Alignment	not modelled	33.0	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> flai atpase; <b>PDBTitle:</b> archaellum assembly atpase flai
90	<a href="#">d1akya1</a>	Alignment	not modelled	32.6	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
91	<a href="#">c2v65A</a>	Alignment	not modelled	31.9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase a chain; <b>PDBTitle:</b> apo ldh from the psychrophile c. gunnari
92	<a href="#">c2c99A</a>	Alignment	not modelled	31.9	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator; <b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
93	<a href="#">d1qf9a</a>	Alignment	not modelled	30.8	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
94	<a href="#">c1lys4A</a>	Alignment	not modelled	30.4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> structure of aspartate-semialdehyde dehydrogenase from methanococcus2 jannaschii
95	<a href="#">c1nijA</a>	Alignment	not modelled	30.1	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
96	<a href="#">c5butG</a>	Alignment	not modelled	29.9	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> ktr system potassium uptake protein a,ktr system potassium <b>PDBTitle:</b> crystal structure of inactive conformation of ktrab k+ transporter
97	<a href="#">d1zina1</a>	Alignment	not modelled	29.6	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
98	<a href="#">c3hr1A</a>	Alignment	not modelled	29.6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease-like protein; <b>PDBTitle:</b> crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
99	<a href="#">c4kblA</a>	Alignment	not modelled	29.4	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase arih1; <b>PDBTitle:</b> structure of hhari, a ring-ibr-ring ubiquitin ligase: autoinhibition2 of an ariadne-family e3 and insights into ligation mechanism
100	<a href="#">c3bbpA</a>	Alignment	not modelled	29.1	<b>PDB header:</b> protein transport/splicing <b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein rab-6a; <b>PDBTitle:</b> rab6-gtp:gcc185 rab binding domain complex
101	<a href="#">c2gedB</a>	Alignment	not modelled	29.0	<b>PDB header:</b> protein transport, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor beta subunit; <b>PDBTitle:</b> signal recognition particle receptor beta-subunit in nucleotide-free2 dimerized form
102	<a href="#">d1j09a2</a>	Alignment	not modelled	28.8	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
103	<a href="#">c2ak2A</a>	Alignment	not modelled	28.7	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase isoenzyme-2; <b>PDBTitle:</b> adenylate kinase isoenzyme-2
104	<a href="#">c3vaaC</a>	Alignment	not modelled	28.4	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of shikimate kinase from2 bacteroides thetaiotaomicron
105	<a href="#">c5uj7B</a>	Alignment	not modelled	28.3	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
106	<a href="#">c3t76A</a>	Alignment	not modelled	28.2	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
107	<a href="#">c1znyA</a>	Alignment	not modelled	27.9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
					<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

108	<a href="#">d1pjqa1</a>	Alignment	not modelled	27.7	15	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
109	<a href="#">c4cw7A</a>	Alignment	not modelled	27.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative adenylate kinase; <b>PDBTitle:</b> structure of the fap7-rps14 complex in complex with atp
110	<a href="#">d1khta</a>	Alignment	not modelled	27.4	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
111	<a href="#">c2ak3B</a>	Alignment	not modelled	27.2	7	<b>PDB header:</b> transferase (phosphotransferase) <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate kinase isoenzyme-3; <b>PDBTitle:</b> the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution
112	<a href="#">c3tr0A</a>	Alignment	not modelled	27.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> structure of guanylate kinase (gmk) from coxiella burnetii
113	<a href="#">d1l8qa2</a>	Alignment	not modelled	27.0	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
114	<a href="#">c5vvwA</a>	Alignment	not modelled	26.9	21	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetyl muramate-l-alanine ligase; <b>PDBTitle:</b> structure of murc from pseudomonas aeruginosa
115	<a href="#">d1jiva</a>	Alignment	not modelled	26.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
116	<a href="#">d1teva</a>	Alignment	not modelled	26.3	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
117	<a href="#">c1s3ga</a>	Alignment	not modelled	25.8	5	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from bacillus2 globisporus
118	<a href="#">c2eu8B</a>	Alignment	not modelled	25.6	10	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of a thermostable mutant of bacillus2 subtilis adenylate kinase (q199r)
119	<a href="#">c3h0kA</a>	Alignment	not modelled	25.2	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> upf0200 protein sso1041; <b>PDBTitle:</b> crystal structure of an adenylated kinase related protein from2 sulfolobus solfataricus to 3.25a
120	<a href="#">c2bovA</a>	Alignment	not modelled	25.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ras-related protein ral-a; <b>PDBTitle:</b> molecular recognition of an adp-ribosylating clostridium2 botulinum c3 exoenzyme by rala gtpase