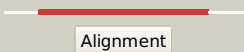

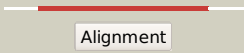



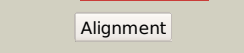



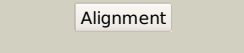
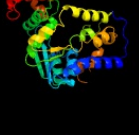
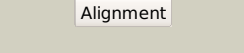



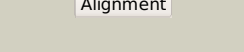

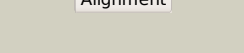
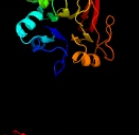
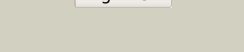







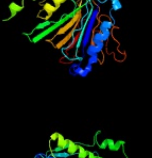

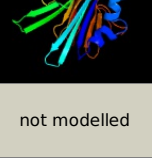


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2201_(asnB)_2465005_2466963
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	514741f93e0343af

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ct9D_</a>	 Alignment		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> asparagine synthetase b; <b>PDBTitle:</b> crystal structure of asparagine synthetase b from2 escherichia coli
2	<a href="#">c1q15A_</a>	 Alignment		100.0	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> cara; <b>PDBTitle:</b> carbapenam synthetase
3	<a href="#">c1mlzB_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-lactam synthetase; <b>PDBTitle:</b> beta-lactam synthetase apo enzyme
4	<a href="#">d1ct9a1</a>	 Alignment		100.0	29	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
5	<a href="#">d1jgta1</a>	 Alignment		100.0	28	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
6	<a href="#">d1q15a1</a>	 Alignment		100.0	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
7	<a href="#">d1ct9a2</a>	 Alignment		100.0	38	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
8	<a href="#">d1q15a2</a>	 Alignment		100.0	18	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
9	<a href="#">c1lecjB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate <b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
10	<a href="#">d1jgta2</a>	 Alignment		100.0	24	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
11	<a href="#">c1gph1_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> 1; <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase; <b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis

12	<a href="#">d1gph12</a>	Alignment		100.0	27	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
13	<a href="#">c1jxaA</a>	Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine 6-phosphate synthase; <b>PDBTitle:</b> glucosamine 6-phosphate synthase with glucose 6-phosphate
14	<a href="#">d1ecfa2</a>	Alignment		100.0	26	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
15	<a href="#">d1xffa</a>	Alignment		100.0	28	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
16	<a href="#">d1ofda3</a>	Alignment		99.8	29	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
17	<a href="#">d1te5a</a>	Alignment		99.8	17	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
18	<a href="#">d1ea0a3</a>	Alignment		99.7	29	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
19	<a href="#">d1xnqa1</a>	Alignment		99.7	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
20	<a href="#">c4zfb</a>	Alignment		99.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase egtc; <b>PDBTitle:</b> ergothioneine-biosynthetic ntn hydrolase egtc, apo form
21	<a href="#">c3fiuD</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nmN synthetase from francisella tularensis
22	<a href="#">c3mdnD</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine aminotransferase class-ii domain protein; <b>PDBTitle:</b> structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
23	<a href="#">c3p52B</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
24	<a href="#">c2e18B</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of project ph0182 from pyrococcus horikoshii ot3
25	<a href="#">c3k32D</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mj0690; <b>PDBTitle:</b> the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
26	<a href="#">d2pg3a1</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
27	<a href="#">d1k92a1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
28	<a href="#">c5udwB</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel

29	<a href="#">c3bl5E</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> queuosine biosynthesis protein quec; <b>PDBTitle:</b> crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
30	<a href="#">c5khaA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad+ synthetase; <b>PDBTitle:</b> structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
31	<a href="#">c5ghaC</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
32	<a href="#">c5hujB</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nade from streptococcus pyogenes
33	<a href="#">c2ywcC</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
34	<a href="#">dlj20a1</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
35	<a href="#">c2hmaA</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna (5-methylaminomethyl-2-thiouridylate)- <b>PDBTitle:</b> the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
36	<a href="#">c1k97A</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
37	<a href="#">c2vx0B</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
38	<a href="#">c2derA</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
39	<a href="#">dlwy5a1</a>	Alignment	not modelled	98.7	10	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
40	<a href="#">dlgpm1</a>	Alignment	not modelled	98.7	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
41	<a href="#">c4q16C</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad+ synthetase from deinococcus radiodurans
42	<a href="#">c4f4hA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine dependent nad+ synthetase; <b>PDBTitle:</b> crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
43	<a href="#">dlkqpa</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
44	<a href="#">dlvl2a1</a>	Alignment	not modelled	98.6	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
45	<a href="#">c4xfdA</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
46	<a href="#">c3vrhA</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
47	<a href="#">c2e21A</a>	Alignment	not modelled	98.5	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
48	<a href="#">d2c5sa1</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
49	<a href="#">c3n05B</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
50	<a href="#">c4u7jB</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
51	<a href="#">c1gpmD</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate
52	<a href="#">c2nz2A</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
53	<a href="#">dlni5a1</a>	Alignment	not modelled	98.5	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
54	<a href="#">c1vl2C</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780)

						from2 thermotoga maritima at 1.65 a resolution
55	<a href="#">c1kh2D_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
56	<a href="#">c2vdcF_</a>	Alignment	not modelled	98.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadph] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
57	<a href="#">c3dpiA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+ synthetase; <b>PDBTitle:</b> crystal structure of nad+ synthetase from burkholderia pseudomallei
58	<a href="#">c4nzpA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
59	<a href="#">c3uowB_</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
60	<a href="#">c5tw7E_</a>	Alignment	not modelled	98.4	22	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
61	<a href="#">d1wxia1</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
62	<a href="#">c4kr7A_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna sulfurtransferase; <b>PDBTitle:</b> crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
63	<a href="#">c1lm1A_</a>	Alignment	not modelled	98.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
64	<a href="#">c3tqiB_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
65	<a href="#">c3a2kB_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
66	<a href="#">c2dplA_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
67	<a href="#">d1sura_</a>	Alignment	not modelled	98.3	8	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
68	<a href="#">c3q4gA_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad synthetase from vibrio cholerae
69	<a href="#">c2c5sA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiamine biosynthesis protein thii; <b>PDBTitle:</b> crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
70	<a href="#">c1ni5A_</a>	Alignment	not modelled	98.1	11	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
71	<a href="#">c2o8vA_</a>	Alignment	not modelled	98.0	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> paps reductase in a covalent complex with thioredoxin c35a
72	<a href="#">c3dlaD_</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
73	<a href="#">c2goyC_</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
74	<a href="#">c5udtD_</a>	Alignment	not modelled	97.8	33	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
75	<a href="#">c3ilvA_</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
76	<a href="#">d1zuna1</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
77	<a href="#">c4bvvB_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine-phosphosulphate reductase; <b>PDBTitle:</b> structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
78	<a href="#">c1zunA_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenyllyltransferase subunit 2; <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae

79	<a href="#">d1ru8a_</a>	Alignment	not modelled	97.2	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
80	<a href="#">c2oq2B_</a>	Alignment	not modelled	97.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of yeast paps reductase with pap, a product complex
81	<a href="#">d2d13a1</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
82	<a href="#">d1vbka1</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
83	<a href="#">c2wsiA_</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fad synthetase; <b>PDBTitle:</b> crystal structure of yeast fad synthetase (fad1) in complex2 with fad
84	<a href="#">c3g59A_</a>	Alignment	not modelled	94.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn adenyltransferase; <b>PDBTitle:</b> crystal structure of candida glabrata fmn adenyltransferase in2 complex with atp
85	<a href="#">c1vbka_</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1313; <b>PDBTitle:</b> crystal structure of ph1313 from pyrococcus horikoshii ot3
86	<a href="#">c3sbtB_</a>	Alignment	not modelled	82.6	8	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> a1 cistron-splicing factor aar2; <b>PDBTitle:</b> crystal structure of a aar2-prp8 complex
87	<a href="#">c6mx4_</a>	Alignment	not modelled	46.0	40	<b>PDB header:</b> virus <b>Chain:</b> J: <b>PDB Molecule:</b> e1; <b>PDBTitle:</b> cryoem structure of chimeric eastern equine encephalitis virus
88	<a href="#">c4i43A_</a>	Alignment	not modelled	44.5	11	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> a1 cistron-splicing factor aar2; <b>PDBTitle:</b> crystal structure of prp8:aar2 complex
89	<a href="#">c3o1B_</a>	Alignment	not modelled	42.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
90	<a href="#">c3rfuC_</a>	Alignment	not modelled	42.0	24	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> copper efflux atpase; <b>PDBTitle:</b> crystal structure of a copper-transporting pib-type atpase
91	<a href="#">c3lwdA_</a>	Alignment	not modelled	41.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
92	<a href="#">d1dv5a_</a>	Alignment	not modelled	39.6	13	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> apo-D-alanyl carrier protein
93	<a href="#">c3nwpA_</a>	Alignment	not modelled	39.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
94	<a href="#">c3muwE_</a>	Alignment	not modelled	38.7	40	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> structural polyprotein; <b>PDBTitle:</b> pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
95	<a href="#">c2xfbF_</a>	Alignment	not modelled	37.9	28	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
96	<a href="#">c2xfcD_</a>	Alignment	not modelled	37.9	28	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> the chikungunya e1 e2 envelope glycoprotein complex fit into2 the semliki forest virus cryo-em map
97	<a href="#">c3n42F_</a>	Alignment	not modelled	37.8	28	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> crystal structures of the mature envelope glycoprotein complex (furin2 cleavage) of chikungunya virus.
98	<a href="#">c3j0fG_</a>	Alignment	not modelled	37.6	40	<b>PDB header:</b> virus <b>Chain:</b> G: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> sindbis virion
99	<a href="#">c3j0cG_</a>	Alignment	not modelled	37.1	36	<b>PDB header:</b> virus <b>Chain:</b> G: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
100	<a href="#">c2alaA_</a>	Alignment	not modelled	36.8	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> structural polyprotein (p130); <b>PDBTitle:</b> crystal structure of the semliki forest virus envelope protein e1 in2 its monomeric conformation.
101	<a href="#">c5mrwF_</a>	Alignment	not modelled	35.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> potassium-transporting atpase atp-binding subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
102	<a href="#">c1ld4O_</a>	Alignment	not modelled	35.4	40	<b>PDB header:</b> virus <b>Chain:</b> O: <b>PDB Molecule:</b> spike glycoprotein e1; <b>PDBTitle:</b> placement of the structural proteins in sindbis virus
103	<a href="#">c6nk6B_</a>	Alignment	not modelled	35.3	24	<b>PDB header:</b> virus like particle/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> e1 glycoprotein; <b>PDBTitle:</b> electron cryo-microscopy of chikungunya vlp in complex with mouse2 mxra8 receptor
104	<a href="#">c3i08A_</a>	Alignment	not modelled	34.7	17	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a;



104	<a href="#">c3jv0A_</a>	Alignment	not modelled	34.7	17	<b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
105	<a href="#">d2alaa2</a>	Alignment	not modelled	32.5	24	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
106	<a href="#">c1y8aA_</a>	Alignment	not modelled	32.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1437; <b>PDBTitle:</b> structure of gene product af1437 from archaeoglobus fulgidus
107	<a href="#">c1z8yE_</a>	Alignment	not modelled	32.0	40	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> spike glycoprotein e1; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
108	<a href="#">c2kncA_</a>	Alignment	not modelled	30.4	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> platelet integrin afaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
109	<a href="#">c2yewB_</a>	Alignment	not modelled	30.2	33	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> e1 envelope glycoprotein; <b>PDBTitle:</b> modeling barmah forest virus structural proteins
110	<a href="#">c3muuA_</a>	Alignment	not modelled	29.6	40	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> structural polyprotein; <b>PDBTitle:</b> crystal structure of the sindbis virus e2-e1 heterodimer at low ph
111	<a href="#">d1md6a_</a>	Alignment	not modelled	29.5	26	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Cytokine <b>Family:</b> Interleukin-1 (IL-1)
112	<a href="#">d1mj4a_</a>	Alignment	not modelled	29.5	6	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
113	<a href="#">d1hkoa_</a>	Alignment	not modelled	28.1	12	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
114	<a href="#">c3icoA_</a>	Alignment	not modelled	26.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from mycobacterium2 tuberculosis
115	<a href="#">c3w7bB_</a>	Alignment	not modelled	24.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
116	<a href="#">d1iccc_</a>	Alignment	not modelled	24.4	18	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
117	<a href="#">c6gmaA_</a>	Alignment	not modelled	24.1	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rb1-inducible coiled-coil protein 1; <b>PDBTitle:</b> crystal structure of the fip200 c-terminal region
118	<a href="#">c3lhiA_</a>	Alignment	not modelled	24.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-phosphogluconolactonase(y_p_207848.1)2 from neisseria gonorrhoeae fa 1090 at 1.33 a resolution
119	<a href="#">c3obiC_</a>	Alignment	not modelled	24.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
120	<a href="#">d1soxa2</a>	Alignment	not modelled	23.4	6	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5