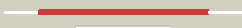



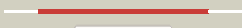




















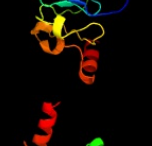

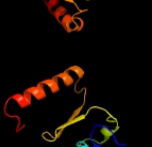
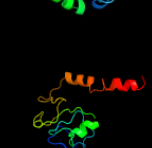

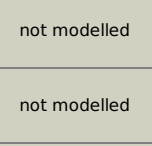


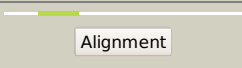
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1127c_(ppdK)_1249937_1251409
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	3c394d296d7e169d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1kblA_</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase
2	<a href="#">c1h6zA_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase; <b>PDBTitle:</b> 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
3	<a href="#">c1vvhA_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate,orthophosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase with bound mg-pep from maize
4	<a href="#">c2olsA_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate synthase; <b>PDBTitle:</b> the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
5	<a href="#">c5fbtA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate synthase; <b>PDBTitle:</b> crystal structure of rifampin phosphotransferase rph-Im from listeria2 monocytogenes in complex with rifampin
6	<a href="#">d1kbla3</a>	 Alignment		100.0	40	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Pyruvate phosphate dikinase, N-terminal domain
7	<a href="#">d1vbgA3</a>	 Alignment		100.0	41	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Pyruvate phosphate dikinase, N-terminal domain
8	<a href="#">d1h6za3</a>	 Alignment		100.0	37	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Pyruvate phosphate dikinase, N-terminal domain
9	<a href="#">d1kbla2</a>	 Alignment		100.0	44	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
10	<a href="#">d1vbgA2</a>	 Alignment		100.0	40	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
11	<a href="#">d1h6za2</a>	 Alignment		100.0	41	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain

12	<a href="#">d1zyna2</a>	Alignment		99.9	25	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
13	<a href="#">c3t07D_</a>	Alignment		99.9	23	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
14	<a href="#">c2e28A_</a>	Alignment		99.9	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
15	<a href="#">c5woyA_</a>	Alignment		99.9	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> nmr solution structure of enzyme i (neit) protein using two 4d-spectra
16	<a href="#">c2hwgA_</a>	Alignment		99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
17	<a href="#">c1ezaA_</a>	Alignment		99.9	21	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> enzyme i; <b>PDBTitle:</b> amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
18	<a href="#">c5t1oB_</a>	Alignment		99.8	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase ptsp; <b>PDBTitle:</b> solution-state nmr and saxs structural ensemble of npr (1-85) in2 complex with ein-ntr (170-424)
19	<a href="#">c2hroA_</a>	Alignment		99.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
20	<a href="#">d2hi6a1</a>	Alignment		96.4	17	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IIVD-like <b>Family:</b> AF0055-like
21	<a href="#">c5ym0A_</a>	Alignment	not modelled	94.3	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the crystal structure of dhad
22	<a href="#">d2gp4a1</a>	Alignment	not modelled	92.7	26	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IIVD-like <b>Family:</b> IIVD/EDD C-terminal domain-like
23	<a href="#">c5oybB_</a>	Alignment	not modelled	90.4	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydratase, ilvd/edd family; <b>PDBTitle:</b> crystal structure of d-xylonate dehydratase in holo-form
24	<a href="#">c2gp4B_</a>	Alignment	not modelled	89.8	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
25	<a href="#">c2pkpA_</a>	Alignment	not modelled	88.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> homoaconitase small subunit; <b>PDBTitle:</b> crystal structure of 3-isopropylmalate dehydratase (leud)2 from methanocaldococcus jannaschii dsm2661 (mj1271)
26	<a href="#">c2gp4A_</a>	Alignment	not modelled	85.6	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
27	<a href="#">d1v7la_</a>	Alignment	not modelled	79.0	34	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IIVD-like <b>Family:</b> LeuD-like
28	<a href="#">c3vbaE_</a>	Alignment	not modelled	76.9	18	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> isopropylmalate/citramalate isomerase small subunit; <b>PDBTitle:</b> crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit

29	<a href="#">c5ze4A</a>	 Alignment	not modelled	75.7	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
30	<a href="#">c5j84A</a>	 Alignment	not modelled	73.7	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form
31	<a href="#">d5easa1</a>	 Alignment	not modelled	67.9	20	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases <b>Family:</b> Terpenoid cyclase N-terminal domain
32	<a href="#">d1l5ja2</a>	 Alignment	not modelled	67.6	31	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> LeuD-like
33	<a href="#">c1m6vE</a>	 Alignment	not modelled	66.6	18	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of 2 carbamoyl phosphate synthetase
34	<a href="#">c3ln7A</a>	 Alignment	not modelled	63.5	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from 2 pasteurella multocida
35	<a href="#">d1uc8a2</a>	 Alignment	not modelled	62.1	24	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> Lysine biosynthesis enzyme LysX ATP-binding domain
36	<a href="#">c1w2wJ</a>	 Alignment	not modelled	57.8	22	<b>PDB header:</b> isomerase <b>Chain:</b> J: <b>PDB Molecule:</b> 5-methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> crystal structure of yeast ypr118w, a methylthioribose-1-phosphate 2 isomerase related to regulatory eif2b subunits
37	<a href="#">c3wvqA</a>	 Alignment	not modelled	56.3	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pgm1; <b>PDBTitle:</b> structure of atp grasp protein
38	<a href="#">c2zkrf</a>	 Alignment	not modelled	55.7	13	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> rna expansion segment es7 part iii; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex 2 obtained by docking homology models of the rna and proteins into an 3.8.7 a cryo-em map
39	<a href="#">c3ln6A</a>	 Alignment	not modelled	53.3	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthesis bifunctional protein gshab; <b>PDBTitle:</b> crystal structure of a bifunctional glutathione synthetase from 2 streptococcus agalactiae
40	<a href="#">c3r23B</a>	 Alignment	not modelled	52.8	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine--d-alanine ligase from bacillus 2 anthracis
41	<a href="#">c2yvka</a>	 Alignment	not modelled	50.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> crystal structure of 5-methylthioribose 1-phosphate 2 isomerase product complex from bacillus subtilis
42	<a href="#">c2hcuA</a>	 Alignment	not modelled	49.6	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydratase small subunit; <b>PDBTitle:</b> crystal structure of smu.1381 (or leud) from streptococcus mutans
43	<a href="#">d1kska3</a>	 Alignment	not modelled	42.2	39	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsuA N-terminal domain
44	<a href="#">c6a34B</a>	 Alignment	not modelled	41.5	26	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> crystal structure of 5-methylthioribose 1-phosphate isomerase from 2 pyrococcus horikoshii ot3 - form i
45	<a href="#">c1hx9A</a>	 Alignment	not modelled	41.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-epi-aristolochene synthase; <b>PDBTitle:</b> crystal structure of teas w273s form 1
46	<a href="#">c3iz5H</a>	 Alignment	not modelled	40.0	10	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 60s ribosomal protein l7a (l7ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
47	<a href="#">d1iowa2</a>	 Alignment	not modelled	37.5	25	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
48	<a href="#">c3u9sA</a>	 Alignment	not modelled	36.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase 2 (mcc) 750 kd holoenzyme, coa complex
49	<a href="#">c4gaxA</a>	 Alignment	not modelled	35.8	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> amomorpha-4,11-diene synthase; <b>PDBTitle:</b> crystal structure of an alpha-bisabolol synthase mutant
50	<a href="#">c3g4dB</a>	 Alignment	not modelled	33.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> (+)-delta-cadinene synthase isozyme xc1; <b>PDBTitle:</b> crystal structure of (+)-delta-cadinene synthase from gossypium 2 arboreum and evolutionary divergence of metal binding motifs for 3 catalysis
51	<a href="#">c2h1fB</a>	 Alignment	not modelled	32.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide heptosyltransferase-1; <b>PDBTitle:</b> e. coli heptosyltransferase waac with adp
52	<a href="#">c4a1eF</a>	 Alignment	not modelled	32.1	10	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> rpl7a; <b>PDBTitle:</b> t. thermophila 60s ribosomal subunit in complex with 2 initiation factor 6. this file contains 5s rna, 5.8s rna 3 and proteins of molecule 1

53	<a href="#">d1n1ba1</a>	Alignment	not modelled	31.5	16	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases <b>Family:</b> Terpenoid cyclase N-terminal domain
54	<a href="#">c3j39G</a>	Alignment	not modelled	31.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l7a; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
55	<a href="#">c1ehiB</a>	Alignment	not modelled	30.9	7	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine:d-lactate ligase; <b>PDBTitle:</b> d-alanine:d-lactate ligase (Imddl2) of vancomycin-resistant2 leuconostoc mesenteroides
56	<a href="#">c2zbtB</a>	Alignment	not modelled	30.7	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
57	<a href="#">c2rkbE</a>	Alignment	not modelled	30.7	37	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> serine dehydratase-like; <b>PDBTitle:</b> serine dehydratase like-1 from human cancer cells
58	<a href="#">c5b04B</a>	Alignment	not modelled	30.7	15	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
59	<a href="#">c3zf7x</a>	Alignment	not modelled	30.0	13	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 60s ribosomal protein l23a; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
60	<a href="#">d1ehia2</a>	Alignment	not modelled	30.0	5	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
61	<a href="#">c3tovB</a>	Alignment	not modelled	29.5	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9; <b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
62	<a href="#">d1vkza3</a>	Alignment	not modelled	28.9	9	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
63	<a href="#">c3n6rK</a>	Alignment	not modelled	28.6	16	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
64	<a href="#">c2hjwA</a>	Alignment	not modelled	28.6	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> crystal structure of the bc domain of acc2
65	<a href="#">c5h80A</a>	Alignment	not modelled	28.5	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylase; <b>PDBTitle:</b> biotin carboxylase domain of single-chain bacterial carboxylase
66	<a href="#">c3femB</a>	Alignment	not modelled	28.5	17	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxine biosynthesis protein snz1; <b>PDBTitle:</b> structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
67	<a href="#">c4zhtB</a>	Alignment	not modelled	28.4	6	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional udp-n-acetylglucosamine 2-epimerase/n- <b>PDBTitle:</b> crystal structure of udp-glcna2-2-epimerase
68	<a href="#">c2i80B</a>	Alignment	not modelled	28.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine-d-alanine ligase; <b>PDBTitle:</b> allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
69	<a href="#">c5ig9H</a>	Alignment	not modelled	27.8	14	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> atp grasp ligase; <b>PDBTitle:</b> crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc
70	<a href="#">c5mlkA</a>	Alignment	not modelled	27.8	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
71	<a href="#">c5dmxC</a>	Alignment	not modelled	27.5	24	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
72	<a href="#">d1iwpG</a>	Alignment	not modelled	27.5	27	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Diol dehydratase, gamma subunit <b>Family:</b> Diol dehydratase, gamma subunit
73	<a href="#">c3j61G</a>	Alignment	not modelled	26.9	10	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l8e; <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
74	<a href="#">d1k4ia</a>	Alignment	not modelled	26.9	14	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
75	<a href="#">c3tqtB</a>	Alignment	not modelled	26.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> structure of the d-alanine-d-alanine ligase from coxiella burnetii
76	<a href="#">d2cqaa1</a>	Alignment	not modelled	26.8	30	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TIP49 domain
77	<a href="#">c1uc5M</a>	Alignment	not modelled	26.4	24	<b>PDB header:</b> lyase <b>Chain:</b> M: <b>PDB Molecule:</b> diol dehydrase gamma subunit; <b>PDBTitle:</b> structure of diol dehydratase complexed with (r)-1,2-2 propanediol
78	<a href="#">d1eexg</a>	Alignment	not modelled	26.4	24	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Diol dehydratase, gamma subunit <b>Family:</b> Diol dehydratase, gamma subunit <b>PDB header:</b> ribosome

79	<a href="#">c3zch_H</a>	Alignment	not modelled	26.2	13	<b>Chain:</b> H: <b>PDB Molecule:</b> 60s ribosomal protein rpl8 (l7ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
80	<a href="#">c5i47A</a>	Alignment	not modelled	26.2	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> rimk domain protein atp-grasp; <b>PDBTitle:</b> crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745
81	<a href="#">d3etja3</a>	Alignment	not modelled	26.0	17	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
82	<a href="#">c3u9sE</a>	Alignment	not modelled	25.9	18	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
83	<a href="#">c3i12A</a>	Alignment	not modelled	25.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
84	<a href="#">c3u5iG</a>	Alignment	not modelled	25.6	13	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l8-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
85	<a href="#">c3u9sl</a>	Alignment	not modelled	25.3	16	<b>PDB header:</b> ligase <b>Chain:</b> I: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
86	<a href="#">c3a11D</a>	Alignment	not modelled	25.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b, delta subunit; <b>PDBTitle:</b> crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
87	<a href="#">d1e4ea2</a>	Alignment	not modelled	25.2	13	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> ATP-binding domain of peptide synthetases
88	<a href="#">c3vpbC</a>	Alignment	not modelled	25.1	19	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> putative acetylornithine deacetylase; <b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
89	<a href="#">c4xz7A</a>	Alignment	not modelled	25.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a tgase
90	<a href="#">c3m3hA</a>	Alignment	not modelled	24.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
91	<a href="#">c5b04G</a>	Alignment	not modelled	24.5	15	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
92	<a href="#">d1gsoa3</a>	Alignment	not modelled	24.3	27	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> BC ATP-binding domain-like
93	<a href="#">c3se7A</a>	Alignment	not modelled	23.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> vana; <b>PDBTitle:</b> ancient vana
94	<a href="#">c1w96B</a>	Alignment	not modelled	23.7	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
95	<a href="#">c3j3bG</a>	Alignment	not modelled	23.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l7a; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
96	<a href="#">c2nv2U</a>	Alignment	not modelled	22.7	15	<b>PDB header:</b> lyase/transferase <b>Chain:</b> U: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
97	<a href="#">c4yakD</a>	Alignment	not modelled	22.2	13	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> beta subunit of acyl-coa synthetase (ndp forming); <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 in complex with coenzyme a, acetyl-coenzyme a and with3 phosphorylated phosphohistidine segment (site i orientation)
98	<a href="#">c5dboA</a>	Alignment	not modelled	21.4	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b-like protein; <b>PDBTitle:</b> crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
99	<a href="#">c5ax7A</a>	Alignment	not modelled	21.2	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvyl transferase 1; <b>PDBTitle:</b> yeast pyruvyltransferase pvg1p
100	<a href="#">d1pswa</a>	Alignment	not modelled	21.1	33	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
101	<a href="#">c6hxgE</a>	Alignment	not modelled	20.7	13	<b>PDB header:</b> plant protein <b>Chain:</b> E: <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase-like subunit pdx1.2; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (intermediate) <b>PDB header:</b> transferase/transferase

102	<a href="#">c4adsF_</a>	Alignment	not modelled	20.6	13	<b>Chain:</b> F; <b>PDB Molecule:</b> pyridoxine biosynthetic enzyme pdx1 homologue, putative; <b>PDBTitle:</b> crystal structure of plasmodial plp synthase complex
103	<a href="#">c5xvsA_</a>	Alignment	not modelled	20.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gdp/udp-n,n'-diacetylbaicillosamine 2-epimerase <b>PDBTitle:</b> crystal structure of udp-glcnac 2-epimerase neuc complexed with udp
104	<a href="#">d2vv5a1</a>	Alignment	not modelled	20.3	23	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Mechanosensitive channel protein MscS (YggB), middle domain
105	<a href="#">c1ulzA_</a>	Alignment	not modelled	20.3	20	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> pyruvate carboxylase n-terminal domain; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase