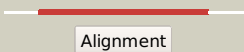

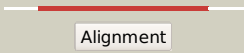



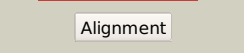



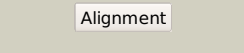

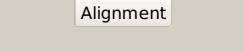



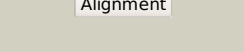

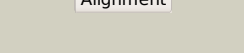

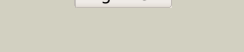
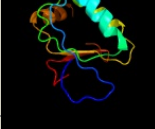











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1707_(-)_1934889_1936349
Date	Fri Aug 2 13:30:30 BST 2019
Unique Job ID	7dc8882c5927b57b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6rtfA_	 Alignment		100.0	21	PDB header: membrane protein Chain: A; PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
2	c5da0A_	 Alignment		100.0	30	PDB header: transport protein Chain: A; PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
3	c4yzfA_	 Alignment		100.0	22	PDB header: immune system Chain: A; PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the anion exchanger domain of human erythrocyte2 band 3
4	c5sv9B_	 Alignment		100.0	17	PDB header: transport protein Chain: B; PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
5	c6caaA_	 Alignment		100.0	18	PDB header: transport protein Chain: A; PDB Molecule: electrogenic sodium bicarbonate cotransporter 1; PDBTitle: cryoem structure of human slc4a4 sodium-coupled acid-base transporter2 nbce1
6	c3qe7A_	 Alignment		100.0	15	PDB header: transport protein Chain: A; PDB Molecule: uracil permease; PDBTitle: crystal structure of uracil transporter--uraa
7	c5i6cB_	 Alignment		100.0	15	PDB header: transport protein Chain: B; PDB Molecule: uric acid-xanthine permease; PDBTitle: the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
8	c5ezbB_	 Alignment		99.8	20	PDB header: transport protein Chain: B; PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
9	c3lloA_	 Alignment		99.8	17	PDB header: motor protein Chain: A; PDB Molecule: prestin; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
10	c3mglA_	 Alignment		99.7	20	PDB header: transport protein Chain: A; PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
11	c3ny7A_	 Alignment		99.7	22	PDB header: membrane protein Chain: A; PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp

12	c3oirA_	Alignment		99.7	23	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolfinella2 succinogenes
13	c2klnA_	Alignment		99.7	19	PDB header: transport protein Chain: A: PDB Molecule: probable sulphate-transport transmembrane protein, cog0659; PDBTitle: solution structure of stas domain of rv1739c from m. tuberculosis
14	c5l25A_	Alignment		99.6	17	PDB header: transport protein Chain: A: PDB Molecule: boron transporter 1; PDBTitle: crystal structure of arabidopsis thaliana bor1
15	c3klkB_	Alignment		99.6	25	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
16	c2vy9A_	Alignment		99.5	20	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
17	d1lauza_	Alignment		99.4	15	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
18	d1th8b_	Alignment		99.4	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
19	c3f43A_	Alignment		99.4	13	PDB header: transcription Chain: A: PDB Molecule: putative anti-sigma factor antagonist tm1081; PDBTitle: crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
20	d1vc1a_	Alignment		99.4	22	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
21	c4hylB_	Alignment	not modelled	99.3	18	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
22	c4xs5D_	Alignment	not modelled	99.1	16	PDB header: transport protein Chain: D: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from dyadobacter fermentans dsm 18053
23	c3t6oA_	Alignment	not modelled	99.0	11	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
24	d1h4xa_	Alignment	not modelled	98.9	13	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
25	c6ic4K_	Alignment	not modelled	98.3	14	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
26	c3ih9A_	Alignment	not modelled	96.0	24	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
27	c4hluC_	Alignment	not modelled	79.0	15	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
28	c5x40A_	Alignment	not modelled	75.8	23	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp

29	c1yqtA_	Alignment	not modelled	74.6	16	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
30	c3bezC_	Alignment	not modelled	64.8	14	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
31	c4rnhA_	Alignment	not modelled	64.6	14	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
32	d1b0ua_	Alignment	not modelled	62.4	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
33	c5xgdA_	Alignment	not modelled	59.8	13	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
34	c2dfwA_	Alignment	not modelled	59.7	21	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
35	c3bl4B_	Alignment	not modelled	58.9	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
36	c4lykB_	Alignment	not modelled	57.9	8	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase yaha; PDBTitle: crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++
37	c3hvbB_	Alignment	not modelled	56.8	8	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
38	c4rvcA_	Alignment	not modelled	56.8	12	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
39	c5xu1A_	Alignment	not modelled	56.3	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
40	d2q3la1	Alignment	not modelled	55.6	15	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
41	c3kc2A_	Alignment	not modelled	54.5	5	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
42	c2pcjB_	Alignment	not modelled	53.3	11	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
43	c3a1yG_	Alignment	not modelled	52.7	14	PDB header: ribosomal protein Chain: G: PDB Molecule: acidic ribosomal protein p0; PDBTitle: the structure of archaeal ribosomal stalk p1/p0 complex
44	c2it1B_	Alignment	not modelled	52.1	12	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
45	c3ghfA_	Alignment	not modelled	51.4	8	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
46	c2nq2C_	Alignment	not modelled	50.8	12	PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
47	c3gfbB_	Alignment	not modelled	49.1	13	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
48	d1dnpa2	Alignment	not modelled	48.4	6	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
49	c4eogA_	Alignment	not modelled	48.4	22	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of csx1 of pyrococcus furiosus
50	d1l7vc_	Alignment	not modelled	48.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
51	c2yz2B_	Alignment	not modelled	48.2	17	PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
52	d1vm6a3	Alignment	not modelled	47.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	c4wbsA_	Alignment	not modelled	47.2	13	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum
54	c5m3cB_	Alignment	not modelled	47.1	16	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575

						from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
55	c3hv9A_	Alignment	not modelled	44.8	8	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
56	c4u02C_	Alignment	not modelled	44.8	11	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
57	d1g6ha_	Alignment	not modelled	43.8	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
58	d2j07a2	Alignment	not modelled	43.4	9	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
59	c5yrpB_	Alignment	not modelled	42.5	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: sensory box/response regulator; PDBTitle: crystal structure of the eal domain of mycobacterium smegmatis dcpa
60	c2deoA_	Alignment	not modelled	42.3	13	PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfd protein; PDBTitle: 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
61	c5d3mF_	Alignment	not modelled	42.0	18	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
62	c2olkD_	Alignment	not modelled	41.9	11	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
63	c4fokA_	Alignment	not modelled	41.1	9	PDB header: protein binding Chain: A: PDB Molecule: fimx; PDBTitle: 1.8 a crystal structure of the fimx eal domain in complex with c-digmp
64	c2d3wB_	Alignment	not modelled	39.9	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcc; PDBTitle: crystal structure of escherichia coli sufcc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
65	d1vp1a_	Alignment	not modelled	39.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
66	c1f2uD_	Alignment	not modelled	39.3	20	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
67	d1ji0a_	Alignment	not modelled	39.1	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
68	c5nikK_	Alignment	not modelled	39.1	16	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
69	c2qy6A_	Alignment	not modelled	39.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0209 protein yfck; PDBTitle: crystal structure of the n-terminal domain of upf0209 protein yfck2 from escherichia coli o157:h7
70	c4hu4B_	Alignment	not modelled	38.4	13	PDB header: signaling protein,hydrolase Chain: B: PDB Molecule: oxygen sensor protein dosp; PDBTitle: crystal structure of eal domain of the e. coli dosp - dimeric form
71	c2pr7A_	Alignment	not modelled	38.2	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
72	c4q6jB_	Alignment	not modelled	38.0	13	PDB header: unknown function Chain: B: PDB Molecule: lmo0131 protein; PDBTitle: crystal structure of eal domain protein from listeria monocytogenes2 egd-e
73	c1vciA_	Alignment	not modelled	37.9	14	PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
74	c4ymuJ_	Alignment	not modelled	37.5	12	PDB header: protein binding/transport protein Chain: J: PDB Molecule: abc-type polar amino acid transport system, atpase PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps
75	c3fb3A_	Alignment	not modelled	37.1	15	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase; PDBTitle: crystal structure of trypanosoma brucei acetyltransferase,2 tb11.01.2886
76	c5m1tB_	Alignment	not modelled	36.8	13	PDB header: signaling protein Chain: B: PDB Molecule: mucr phosphodiesterase; PDBTitle: pamucr phosphodiesterase, c-di-gmp complex
77	c3pfmA_	Alignment	not modelled	35.5	8	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
78	c3jipA_	Alignment	not modelled	35.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
						PDB header: transport protein

79	c1oxtB	Alignment	not modelled	34.5	14	Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
80	d1udxa3	Alignment	not modelled	34.0	18	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
81	c2mwigB	Alignment	not modelled	33.7	15	PDB header: protein binding Chain: B: PDB Molecule: blue-light photoreceptor; PDBTitle: full-length solution structure of ytvA, a lov-photoreceptor protein2 and regulator of bacterial stress response
82	c6amxA	Alignment	not modelled	33.3	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucleotide binding domain of o-antigen2 polysaccharide abc-transporter
83	c3j21k	Alignment	not modelled	32.6	10	PDB header: ribosome Chain: K: PDB Molecule: 50s ribosomal protein l14e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
84	d1qsrA	Alignment	not modelled	31.8	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
85	d2j8ga2	Alignment	not modelled	31.3	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: 1,4-beta-N-acetyl muramidase
86	c5x5yB	Alignment	not modelled	31.2	16	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
87	c4hjfA	Alignment	not modelled	30.6	13	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++
88	c4p31B	Alignment	not modelled	30.5	18	PDB header: hydrolase Chain: B: PDB Molecule: lipopolysaccharide export system atp-binding protein lptb; PDBTitle: crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium
89	c4f48A	Alignment	not modelled	30.3	8	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of firmexal-c-di-gmp-pilz complexes from2 xanthomonas campestris
90	d1np7a2	Alignment	not modelled	29.1	13	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
91	c5x7kB	Alignment	not modelled	29.1	25	PDB header: transport protein Chain: B: PDB Molecule: lipase b; PDBTitle: crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system
92	d1oxxk2	Alignment	not modelled	28.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
93	c2r6oB	Alignment	not modelled	28.5	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative diguanylate cyclase/phosphodiesterase (ggdef & eal) PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
94	c2d2fA	Alignment	not modelled	28.4	12	PDB header: protein binding Chain: A: PDB Molecule: sufoC protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufoC from thermus2 thermophilus hb8
95	c2b5oA	Alignment	not modelled	28.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: ferredoxin-nadp reductase
96	c2pzfB	Alignment	not modelled	28.0	9	PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
97	c5nj3B	Alignment	not modelled	27.4	22	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
98	c3pjwA	Alignment	not modelled	26.8	9	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
99	c5ws4A	Alignment	not modelled	26.4	11	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
100	c5do7B	Alignment	not modelled	26.2	17	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
101	d2hyda1	Alignment	not modelled	26.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
102	c4hziA	Alignment	not modelled	26.1	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of the leptospira interrogans atpase subunit of an2 orphan abc transporter
103	c3dhwC	Alignment	not modelled	26.0	12	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni

104	c2basa1	Alignment	not modelled	25.9	14	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
105	c3bk7A_	Alignment	not modelled	25.7	18	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein from2 pyrococcus abysii
106	c5ugjC_	Alignment	not modelled	25.6	11	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
107	d1g2912	Alignment	not modelled	25.5	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
108	c4m1bA_	Alignment	not modelled	25.2	14	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
109	d1a9xa3	Alignment	not modelled	25.0	23	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
110	d1owla2	Alignment	not modelled	24.8	13	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
111	c4ywjB_	Alignment	not modelled	24.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
112	c3j16B_	Alignment	not modelled	24.3	14	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
113	c2vytA_	Alignment	not modelled	24.0	14	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
114	c4o9uB_	Alignment	not modelled	24.0	22	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
115	d1u3da2	Alignment	not modelled	23.9	11	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
116	c5lj7B_	Alignment	not modelled	23.3	15	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
117	c2kl8A_	Alignment	not modelled	23.1	20	PDB header: de novo protein Chain: A: PDB Molecule: or15; PDBTitle: solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
118	c1z47B_	Alignment	not modelled	23.1	16	PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius
119	c4us3A_	Alignment	not modelled	22.9	13	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
120	c6k4fU_	Alignment	not modelled	22.8	25	PDB header: biosynthetic protein Chain: U: PDB Molecule: duf1987 domain-containing protein; PDBTitle: siac of pseudomonas aeruginosa