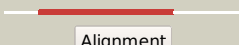



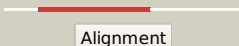

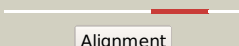

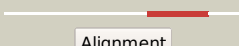

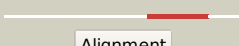

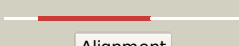

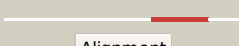









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3273 (-) _3654634_3656928
Date	Thu Aug 8 16:20:48 BST 2019
Unique Job ID	27811589fd78beba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6rtfA_	 Alignment		100.0	16	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	25	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	17	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	c1ddzA_	 Alignment		100.0	24	PDB header: lyase Chain: A; PDB Molecule: carbonic anhydrase; PDBTitle: x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
5	d1ddz1	 Alignment		100.0	23	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
6	d1ddz2	 Alignment		100.0	24	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
7	c5sv9B_	 Alignment		100.0	11	PDB header: transport protein Chain: B; PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
8	d1ekja_	 Alignment		100.0	22	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
9	c5swcE_	 Alignment		100.0	23	PDB header: lyase Chain: E; PDB Molecule: carbonic anhydrase; PDBTitle: the structure of the beta-carbonic anhydrase ccaa
10	c2w3nA_	 Alignment		100.0	24	PDB header: lyase Chain: A; PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
11	c5cxkG_	 Alignment		100.0	25	PDB header: lyase Chain: G; PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of beta carbonic anhydrase from vibrio cholerae

12	d1i6pa_	Alignment		100.0	22	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
13	c3ucoB_	Alignment		100.0	26	PDB header: lyase/lyase inhibitor Chain: B; PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide
14	c2a8cE_	Alignment		100.0	24	PDB header: lyase Chain: E; PDB Molecule: carbonic anhydrase 2; PDBTitle: haemophilus influenzae beta-carbonic anhydrase
15	c3qe7A_	Alignment		100.0	14	PDB header: transport protein Chain: A; PDB Molecule: uracil permease; PDBTitle: crystal structure of uracil transporter--uraa
16	c4o1kA_	Alignment		100.0	24	PDB header: lyase Chain: A; PDB Molecule: carbonic anhydrase; PDBTitle: crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
17	c4rxvA_	Alignment		100.0	25	PDB header: lyase Chain: A; PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of the beta carbonic anhydrase psca3 isolated from2 pseudomonas aeruginosa
18	c4o1jB_	Alignment		100.0	26	PDB header: lyase Chain: B; PDB Molecule: carbonic anhydrase; PDBTitle: crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
19	c6caaA_	Alignment		100.0	13	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
20	c2a5vB_	Alignment		100.0	25	PDB header: lyase Chain: B; PDB Molecule: carbonic anhydrase (carbonate dehydratase) (carbonic PDBTitle: crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
21	c6gwuB_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: B; PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase cance103p from candida albicans
22	c3eyxB_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: B; PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
23	c3vrkA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: carbonyl sulfide hydrolase; PDBTitle: crystal structutre of thiobacillus thioparus thi115 carbonyl sulfide2 hydrolase / thiocyanate complex
24	c3lasA_	Alignment	not modelled	100.0	27	PDB header: lyase Chain: A; PDB Molecule: putative carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
25	c3tenD_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D; PDB Molecule: cs2 hydrolase; PDBTitle: holo form of carbon disulfide hydrolase
26	c1ylkA_	Alignment	not modelled	100.0	21	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein rv1284/mt1322; PDBTitle: crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
27	c5ztpB_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B; PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase from glaciozyma antarctica
28	d1g5ca_	Alignment	not modelled	100.0	23	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
						PDB header: transport protein

29	c5i6cB_	Alignment	not modelled	100.0	14	Chain: B: PDB Molecule: uric acid-xanthine permease; PDBTitle: the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
30	c5j25A_	Alignment	not modelled	99.5	13	PDB header: transport protein Chain: A: PDB Molecule: boron transporter 1; PDBTitle: crystal structure of arabidopsis thaliana bor1
31	c3lkIB_	Alignment	not modelled	99.2	17	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
32	c5ezbB_	Alignment	not modelled	99.1	15	PDB header: transport protein Chain: B: PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
33	c3mgIA_	Alignment	not modelled	99.0	13	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
34	c3lloA_	Alignment	not modelled	99.0	11	PDB header: motor protein Chain: A: PDB Molecule: prestin; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
35	c2klnA_	Alignment	not modelled	98.9	16	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
36	c3ny7A_	Alignment	not modelled	98.9	13	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
37	c3oirA_	Alignment	not modelled	98.9	21	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinnella2 succinogenes
38	d1th8b_	Alignment	not modelled	98.6	20	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
39	c4hylB_	Alignment	not modelled	98.6	12	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
40	d1vc1a_	Alignment	not modelled	98.5	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
41	d1auza_	Alignment	not modelled	98.5	18	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
42	c3f43A_	Alignment	not modelled	98.5	15	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
43	c2vy9A_	Alignment	not modelled	98.3	18	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
44	c4xs5D_	Alignment	not modelled	98.0	11	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
45	c3t6oA_	Alignment	not modelled	97.9	16	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.
46	d1h4xa_	Alignment	not modelled	97.8	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
47	c6ic4K_	Alignment	not modelled	97.1	9	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
48	c3ih9A_	Alignment	not modelled	92.7	24	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
49	c6azoC_	Alignment	not modelled	79.6	13	PDB header: hydrolase Chain: C: PDB Molecule: putative amidase; PDBTitle: structural and biochemical characterization of a non-canonical biuret2 hydrolase (biuh) from the cyanuric acid catabolism pathway of3 rhizobium leguminosorum bv. viciae 3841
50	c3o93A_	Alignment	not modelled	78.2	14	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
51	c3ot4F_	Alignment	not modelled	76.2	20	PDB header: hydrolase Chain: F: PDB Molecule: putative isochorismatase; PDBTitle: structure and catalytic mechanism of bordetella bronchiseptica nicf
52	c2hwkA_	Alignment	not modelled	73.8	30	PDB header: hydrolase Chain: A: PDB Molecule: helicase nsp2; PDBTitle: crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
53	c3tb4A_	Alignment	not modelled	68.7	17	PDB header: hydrolase Chain: A: PDB Molecule: vibriobactin-specific isochorismatase;

						PDBTitle: crystal structure of the isc domain of vibb
54	d1zo0a1	Alignment	not modelled	67.7	33	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Ornithine decarboxylase antizyme-like
55	d1nf9a_	Alignment	not modelled	66.2	13	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
56	c3ojcD_	Alignment	not modelled	65.5	7	PDB header: isomerase Chain: D: PDB Molecule: putative aspartate/glutamate racemase; PDBTitle: crystal structure of a putative asp/glu racemase from yersinia pestis
57	c3hu5B_	Alignment	not modelled	64.9	11	PDB header: hydrolase Chain: B: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
58	c3oqpB_	Alignment	not modelled	63.5	23	PDB header: hydrolase Chain: B: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
59	d1j2ra_	Alignment	not modelled	62.9	13	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
60	c3oqpA_	Alignment	not modelled	62.8	23	PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
61	c3ux8A_	Alignment	not modelled	61.5	14	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc, a subunit; PDBTitle: crystal structure of uvra
62	c1vqtA_	Alignment	not modelled	58.8	17	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
63	d1im5a_	Alignment	not modelled	57.4	16	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
64	c3pihA_	Alignment	not modelled	56.8	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
65	c3iruA_	Alignment	not modelled	55.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phoshonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phoshonoacetaldehyde hydrolase like protein from2 oleispira antarctica
66	c6n9lA_	Alignment	not modelled	53.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
67	c6nplA_	Alignment	not modelled	51.9	12	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride) PDBTitle: cryo-em structure of nkcc1
68	c4rvca_	Alignment	not modelled	50.9	11	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
69	c3zqjC_	Alignment	not modelled	47.4	13	PDB header: dna binding protein Chain: C: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
70	c5ha8A_	Alignment	not modelled	47.3	22	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: structure of a cysteine hydrolase
71	c2wtaA_	Alignment	not modelled	46.2	10	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: acinetobacter baumannii nicotinamidase pyrazinamidase
72	c2a67C_	Alignment	not modelled	44.8	12	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein
73	c3d89A_	Alignment	not modelled	44.3	10	PDB header: electron transport Chain: A: PDB Molecule: rieske domain-containing protein; PDBTitle: crystal structure of a soluble rieske ferredoxin from mus musculus
74	c3rstH_	Alignment	not modelled	43.0	14	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
75	c4nfaA_	Alignment	not modelled	41.6	37	PDB header: signaling protein Chain: A: PDB Molecule: eds1; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
76	c5wxvL_	Alignment	not modelled	39.4	14	PDB header: lyase Chain: L: PDB Molecule: isochorismate lyase; PDBTitle: the crystal structure of vabb-icl domain from vibrio anguillarum 775
77	d1vpla_	Alignment	not modelled	39.3	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
78	d1e8ca1	Alignment	not modelled	38.0	43	Fold: MurF and HprK N-domain-like Superfamily: MurE/MurF N-terminal domain Family: MurE/MurF N-terminal domain
79	c4u02C_	Alignment	not modelled	37.8	14	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein;

						PDBTitle: crystal structure of apo-ttha1159
80	c2vf7B_	Alignment	not modelled	37.1	17	PDB header: dna binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
81	d1fqta_	Alignment	not modelled	36.5	23	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
82	c3zqjF_	Alignment	not modelled	36.2	17	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
83	c2deoA_	Alignment	not modelled	35.3	6	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
84	c2ygrD_	Alignment	not modelled	35.3	8	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
85	c2de7E_	Alignment	not modelled	35.3	23	PDB header: oxidoreductase Chain: E: PDB Molecule: ferredoxin component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
86	c3bezC_	Alignment	not modelled	34.7	15	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
87	c5x40A_	Alignment	not modelled	34.2	13	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
88	c2olkD_	Alignment	not modelled	33.8	11	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
89	d2de6a1	Alignment	not modelled	33.3	3	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
90	c4eogA_	Alignment	not modelled	32.9	17	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of csx1 of pyrococcus furiosus
91	c6cl4A_	Alignment	not modelled	32.0	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
92	c5d3mF_	Alignment	not modelled	31.2	14	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
93	d1gg4a3	Alignment	not modelled	30.9	36	Fold: MurF and HprK N-domain-like Superfamily: MurE/MurF N-terminal domain Family: MurE/MurF N-terminal domain
94	d2jo6a1	Alignment	not modelled	30.9	17	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
95	d1rkba_	Alignment	not modelled	30.8	7	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
96	c3irvA_	Alignment	not modelled	30.6	13	PDB header: hydrolase Chain: A: PDB Molecule: cysteine hydrolase; PDBTitle: crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
97	d2fh5b1	Alignment	not modelled	30.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
98	c3vr1B_	Alignment	not modelled	30.2	7	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
99	c2rauA_	Alignment	not modelled	30.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
100	c5gleA_	Alignment	not modelled	29.9	16	PDB header: lyase Chain: A: PDB Molecule: isochorismate lyase; PDBTitle: the structure of vibrio anguillarum775 angb-icl
101	c3gceA_	Alignment	not modelled	29.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin component of carbazole 1,9a- PDBTitle: ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
102	c3hb7G_	Alignment	not modelled	29.2	12	PDB header: hydrolase Chain: G: PDB Molecule: isochorismatase hydrolase; PDBTitle: the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
103	d1nrjb_	Alignment	not modelled	28.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
104	c4wbsA_	Alignment	not modelled	27.1	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum
105	d2jzaa1	Alignment	not modelled	26.9	20	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
106	c6amxA_	Alignment	not modelled	26.6	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-

						antigen2 polysaccharide abc-transporter
107	d1ji0a_	Alignment	not modelled	26.2	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
108	c3w5iB_	Alignment	not modelled	25.9	8	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferriformans
109	c4aayH_	Alignment	not modelled	25.7	17	PDB header: oxidoreductase Chain: H: PDB Molecule: arob; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
110	c2r8bA_	Alignment	not modelled	25.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
111	c3bk7A_	Alignment	not modelled	25.3	21	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 abyssi
112	d1z01a1	Alignment	not modelled	24.9	17	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
113	c6fgzA_	Alignment	not modelled	24.9	20	PDB header: lipid binding protein Chain: A: PDB Molecule: dynamin; PDBTitle: cyanidioschyzon merolae dnm1 (cmdnm1)
114	d1uuya_	Alignment	not modelled	24.8	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
115	c3i8sC_	Alignment	not modelled	24.8	9	PDB header: transport protein Chain: C: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
116	c1z01D_	Alignment	not modelled	24.6	27	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase PDBTitle: 2-oxoquinoline 8-monooxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
117	c2dfwA_	Alignment	not modelled	24.5	18	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
118	c4p31B_	Alignment	not modelled	24.5	14	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
119	c5gw8A_	Alignment	not modelled	24.3	26	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
120	c1qgeD_	Alignment	not modelled	24.0	15	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase