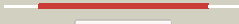



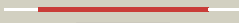




















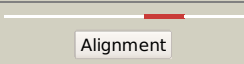
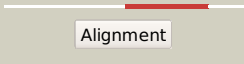
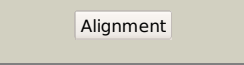
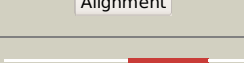
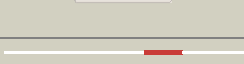




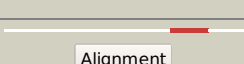
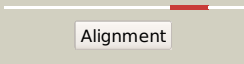
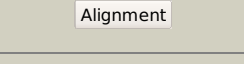
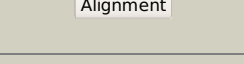
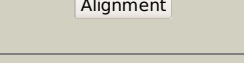
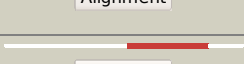
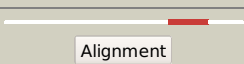
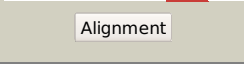
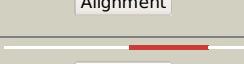
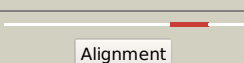
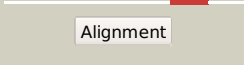

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3270_(ctpC)_3650523_3652679
Date	Thu Aug 8 16:20:47 BST 2019
Unique Job ID	3613c5f8c0afe08b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j09A_	 Alignment		100.0	33	PDB header: hydrolase, metal transport Chain: A; PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
2	c3rfuC_	 Alignment		100.0	36	PDB header: hydrolase, membrane protein Chain: C; PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
3	c3j08A_	 Alignment		100.0	35	PDB header: hydrolase, metal transport Chain: A; PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
4	c4umwA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A; PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
5	c5mrwF_	 Alignment		100.0	25	PDB header: hydrolase Chain: F; PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
6	c1mhsA_	 Alignment		100.0	24	PDB header: membrane protein, proton transport Chain: A; PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
7	c2zxeA_	 Alignment		100.0	23	PDB header: hydrolase/transport protein Chain: A; PDB Molecule: na, k-atpase alpha subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
8	c3b9bA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
9	c3ixzA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
10	c3b8eC_	 Alignment		100.0	24	PDB header: hydrolase/transport protein Chain: C; PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
11	c6a69A_	 Alignment		100.0	24	PDB header: structural protein Chain: A; PDB Molecule: plasma membrane calcium-transporting atpase 1; PDBTitle: cryo-em structure of a p-type atpase

12	c3b8cB_	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
13	c6roiA_	Alignment		100.0	20	PDB header: lipid transport Chain: A: PDB Molecule: probable phospholipid-transporting atpase drs2; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p
14	c3skyA_	Alignment		100.0	43	PDB header: hydrolase Chain: A: PDB Molecule: copper-exporting p-type atpase b; PDBTitle: 2.1a crystal structure of the phosphate bound atp binding domain of f2 archaeoglobus fulgidus copb
15	c2b8eB_	Alignment		100.0	40	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
16	c2iyeC_	Alignment		100.0	35	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
17	c3p96A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
18	d1wpga2	Alignment		100.0	37	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
19	d2b8ea1	Alignment		100.0	39	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
20	c3n28A_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
21	d1y8aa1	Alignment	not modelled	99.9	25	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
22	c2hc8A_	Alignment	not modelled	99.9	38	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
23	c2kijA_	Alignment	not modelled	99.9	36	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the actuator domain of the copper-2 transporting atpase atp7a
24	c2kmvA_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form
25	d1wpga1	Alignment	not modelled	99.8	24	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
26	c2koyA_	Alignment	not modelled	99.8	23	PDB header: metal transport Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
27	c2arfA_	Alignment	not modelled	99.7	26	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
28	c4ezeB_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family hydrolase t0658 from salmonella2 enterica subsp. enterica serovar typhi (target efi-501419)

29	c5lbkA	 Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase paa2, chloroplastic; PDBTitle: crystal structure of the n-domain of hma8, a copper-transporting p-2 type atpase
30	d2a29a1	 Alignment	not modelled	99.7	18	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
31	c2r8zC	 Alignment	not modelled	99.6	25	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
32	c3mmzA	 Alignment	not modelled	99.6	24	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
33	d1k1ea	 Alignment	not modelled	99.5	24	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi
34	c3l7yA	 Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
35	d2b8ea2	 Alignment	not modelled	99.5	32	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
36	c3n07B	 Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: B: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
37	c4umfC	 Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; PDBTitle: crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
38	c4qjbB	 Alignment	not modelled	99.5	28	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
39	c5lbdB	 Alignment	not modelled	99.5	22	PDB header: hydrolase Chain: B: PDB Molecule: copper-transporting atpase paa1, chloroplastic; PDBTitle: crystal structure of the n-domain of hma6, a copper-transporting p-2 type atpase
40	c2p9jH	 Alignment	not modelled	99.5	15	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
41	c3mn1B	 Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: B: PDB Molecule: probable yrbi family phosphatase; PDBTitle: crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
42	c3ewiB	 Alignment	not modelled	99.4	12	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidylyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
43	c3e8mD	 Alignment	not modelled	99.4	25	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidylyltransferase; PDBTitle: structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
44	c4hgnB	 Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: B: PDB Molecule: 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate PDBTitle: crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
45	c4navB	 Alignment	not modelled	99.3	22	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
46	d2b30a1	 Alignment	not modelled	99.3	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
47	c3n1uA	 Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, had superfamily, subfamily iii a; PDBTitle: structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
48	d1rkqa	 Alignment	not modelled	99.2	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
49	d1wr8a	 Alignment	not modelled	99.2	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
50	d1nnla	 Alignment	not modelled	99.2	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
51	c3m1yA	Alignment	not modelled	99.2	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
52	d1l6ra	Alignment	not modelled	99.2	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof

53	d1kvja_	Alignment	not modelled	99.2	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
54	c2kkhA_	Alignment	not modelled	99.2	15	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
55	d1p6ta2	Alignment	not modelled	99.1	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
56	c3daoB_	Alignment	not modelled	99.1	26	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from 2 eubacterium rectale at 1.80 a resolution
57	d1j97a_	Alignment	not modelled	99.1	23	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
58	c2ofgX_	Alignment	not modelled	99.1	19	PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
59	c4zexA_	Alignment	not modelled	99.1	29	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
60	d1q8la_	Alignment	not modelled	99.1	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
61	d1afia_	Alignment	not modelled	99.1	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
62	d1cpza_	Alignment	not modelled	99.1	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
63	d1osda_	Alignment	not modelled	99.1	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
64	d1s6ua_	Alignment	not modelled	99.1	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
65	c2l3mA_	Alignment	not modelled	99.1	21	PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from 2 bacillus anthracis str. ames
66	d1p6ta1	Alignment	not modelled	99.1	22	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
67	d2qifa1	Alignment	not modelled	99.1	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
68	c2n7yA_	Alignment	not modelled	99.1	19	PDB header: metal binding protein Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: nmr structure of metal-binding domain 1 of atp7b
69	d1nrwa_	Alignment	not modelled	99.0	39	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
70	c3dxsX_	Alignment	not modelled	99.0	21	PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1; PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase
71	c2ofhX_	Alignment	not modelled	99.0	21	PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
72	c1y3kA_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of 2 menkes protein
73	c1yjrA_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
74	c2ropA_	Alignment	not modelled	99.0	20	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
75	c2lqbA_	Alignment	not modelled	99.0	21	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: metal binding repeat 2 of the wilson disease protein (atp7b)
76	c2ldiA_	Alignment	not modelled	99.0	24	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaa sub mutant
77	d2aw0a_	Alignment	not modelled	99.0	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
78	c6ff2A_	Alignment	not modelled	99.0	22	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone copz; PDBTitle: copz metallochaperone
79	d1rlma_	Alignment	not modelled	99.0	27	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof

80	d1mwza_	Alignment	not modelled	99.0	30	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
81	d2ggpb1	Alignment	not modelled	98.9	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
82	c2kt2A_	Alignment	not modelled	98.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
83	c2qyhD_	Alignment	not modelled	98.9	32	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical conserved protein, gk1056; PDBTitle: crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
84	c1yg0A_	Alignment	not modelled	98.9	20	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
85	c3r4cA_	Alignment	not modelled	98.9	36	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like hydrolase; PDBTitle: divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
86	c2ew9A_	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
87	c3pgvB_	Alignment	not modelled	98.9	30	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
88	c4u9rA_	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: A: PDB Molecule: czcp cation efflux p1-atpase; PDBTitle: structure of the n-terminal extension from cupriavidus metallidurans2 czcp
89	c3fzqA_	Alignment	not modelled	98.9	33	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
90	d1rkua_	Alignment	not modelled	98.9	21	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
91	c2ga7A_	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
92	c2gcfA_	Alignment	not modelled	98.9	23	PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the coppeter(i) atpase2 pacs in its apo form
93	c3dnpA_	Alignment	not modelled	98.9	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stress response protein yhax; PDBTitle: crystal structure of stress response protein yhax from bacillus2 subtilis
94	d1wpga4	Alignment	not modelled	98.9	21	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
95	c3niwA_	Alignment	not modelled	98.8	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
96	c2rmlA_	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting p-type atpase copa; PDBTitle: solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
97	c2rogA_	Alignment	not modelled	98.8	28	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
98	c2kyzA_	Alignment	not modelled	98.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
99	c4y2iA_	Alignment	not modelled	98.8	24	PDB header: metal transport Chain: A: PDB Molecule: putative metal-binding transport protein; PDBTitle: gold ion bound to golb
100	d2feaa1	Alignment	not modelled	98.8	14	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
101	d2rbka1	Alignment	not modelled	98.7	38	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
102	c2k2pA_	Alignment	not modelled	98.7	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
103	d1nf2a_	Alignment	not modelled	98.7	32	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
104	c2aj1A_	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada PDB header: metal binding protein

105	c6fp6X_	Alignment	not modelled	98.6	21	Chain: X: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: complex of human cu,zn sod1 with the human copper chaperone for sod12 in a compact conformation
106	c3fryB_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: B: PDB Molecule: probable copper-exporting p-type atpase a; PDBTitle: crystal structure of the copa c-terminal metal binding domain
107	c4b6jA_	Alignment	not modelled	98.6	28	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
108	d1sb6a_	Alignment	not modelled	98.5	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
109	c3fvvA_	Alignment	not modelled	98.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
110	d1qupa2	Alignment	not modelled	98.5	7	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
111	c3kd3A_	Alignment	not modelled	98.5	17	PDB header: unknown function Chain: A: PDB Molecule: phosphoserine phosphohydrolase-like protein; PDBTitle: crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
112	d1q3ja_	Alignment	not modelled	98.5	14	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
113	c1jk9D_	Alignment	not modelled	98.4	8	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yso1 and yccs
114	c1qupA_	Alignment	not modelled	98.4	8	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
115	d1wzca1	Alignment	not modelled	98.4	34	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
116	c3gygA_	Alignment	not modelled	98.4	25	PDB header: hydrolase Chain: A: PDB Molecule: ntd biosynthesis operon putative hydrolase ntdb; PDBTitle: crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
117	d1cc8a_	Alignment	not modelled	98.3	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
118	c2crlA_	Alignment	not modelled	98.3	23	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase
119	d1fe0a_	Alignment	not modelled	98.3	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
120	d1s2oa1	Alignment	not modelled	98.3	26	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof