







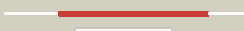















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1992c_(ctpG)_2234999_2237314
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	3d937a759e1ce56b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j09A_	 Alignment		100.0	31	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	31	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	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
4	c4umwA_	 Alignment		100.0	37	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	24	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	24	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	c3ixzA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
9	c3b9bA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
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	25	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	26	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	40	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 of2 archaeoglobus fulgidus copb
15	c2b8eB_	Alignment		100.0	37	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
16	c2iyeC_	Alignment		100.0	30	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	d2b8ea1	Alignment		99.9	40	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
19	d1wpga2	Alignment		99.9	36	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
20	c3n28A_	Alignment		99.9	23	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	19	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
22	c2hc8A_	Alignment	not modelled	99.9	40	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	37	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	d1wpga1	Alignment	not modelled	99.8	23	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
25	c2kmvA_	Alignment	not modelled	99.7	23	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
26	c4ezeB_	Alignment	not modelled	99.6	22	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)
27	c2koyA_	Alignment	not modelled	99.6	33	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
28	c2r8zC_	Alignment	not modelled	99.5	30	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
29	c2arfA_	Alignment	not modelled	99.5	37	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
30	c3mmzA_	Alignment	not modelled	99.5	28	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomycetes2 avermitilis ma-4680
31	d1k1ea_	Alignment	not modelled	99.4	29	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
32	c4qjbB_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
33	d2a29a1	Alignment	not modelled	99.4	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
34	c3n07B_	Alignment	not modelled	99.4	17	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
35	c4umfC_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kds; 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
36	c5lbaA_	Alignment	not modelled	99.4	34	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
37	c2p9jH_	Alignment	not modelled	99.4	12	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
38	c3mn1B_	Alignment	not modelled	99.4	22	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
39	c5lbdB_	Alignment	not modelled	99.4	29	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	c3l7yA_	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
41	c3ewiB_	Alignment	not modelled	99.3	11	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidylyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
42	c3e8mD_	Alignment	not modelled	99.3	15	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
43	c4hgnB_	Alignment	not modelled	99.2	14	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
44	c4navB_	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
45	c3n1uA_	Alignment	not modelled	99.2	22	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
46	d1wr8a_	Alignment	not modelled	99.2	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
47	d1rkqa_	Alignment	not modelled	99.2	23	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
48	d2b8ea2	Alignment	not modelled	99.2	28	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
49	d1nna_	Alignment	not modelled	99.2	22	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
50	d1l6ra_	Alignment	not modelled	99.1	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
51	c3m1yA_	Alignment	not modelled	99.1	24	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
52	c3daoB_	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution

53	c2ofgX	Alignment	not modelled	99.0	15	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
54	d1j97a	Alignment	not modelled	99.0	25	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
55	c2kkhA	Alignment	not modelled	99.0	13	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
56	d1wpga4	Alignment	not modelled	99.0	20	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
57	c4zexA	Alignment	not modelled	99.0	17	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
58	d2b30a1	Alignment	not modelled	99.0	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
59	d1nrwa	Alignment	not modelled	99.0	27	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
60	c2l3mA	Alignment	not modelled	99.0	18	PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
61	d1p6ta2	Alignment	not modelled	99.0	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
62	d1kvja	Alignment	not modelled	99.0	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
63	d1p6ta1	Alignment	not modelled	99.0	25	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
64	d2qifa1	Alignment	not modelled	99.0	24	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
65	d1s6ua	Alignment	not modelled	98.9	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
66	d1cpza	Alignment	not modelled	98.9	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
67	d1afia	Alignment	not modelled	98.9	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
68	d1rlma	Alignment	not modelled	98.9	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
69	d1q8la	Alignment	not modelled	98.9	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
70	c2n7yA	Alignment	not modelled	98.9	15	PDB header: metal binding protein Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: nmr structure of metal-binding domain 1 of atp7b
71	d1osda	Alignment	not modelled	98.9	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
72	c6ff2A	Alignment	not modelled	98.9	14	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone copz; PDBTitle: copz metallochaperone
73	c3dxxX	Alignment	not modelled	98.9	18	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
74	c2ropA	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
75	d2aw0a	Alignment	not modelled	98.9	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
76	c4u9rA	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: A: PDB Molecule: czcp cation efflux p1-atpase; PDBTitle: structure of the n-terminal extension from cupriavidus metallidurans2 czcp
77	c2lqbA	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: metal binding repeat 2 of the wilson disease protein (atp7b)
78	c1yjrA	Alignment	not modelled	98.9	21	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
79	c2ofhX	Alignment	not modelled	98.9	15	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 PDB header: structural genomics, unknown function

80	c2qyhD	Alignment	not modelled	98.9	24	Chain: D: PDB Molecule: hypothetical conserved protein, gk1056; PDBTitle: crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
81	c2ga7A	Alignment	not modelled	98.9	13	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)
82	c1y3kA	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of2 menkes protein
83	c3dnpA	Alignment	not modelled	98.9	20	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
84	c2ldiA	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaan sub mutant
85	c3fzqA	Alignment	not modelled	98.8	26	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
86	c2ew9A	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
87	c3r4cA	Alignment	not modelled	98.8	27	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
88	c1yg0A	Alignment	not modelled	98.8	20	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
89	c2kt2A	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
90	d1mwza	Alignment	not modelled	98.8	26	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
91	d2ggpb1	Alignment	not modelled	98.8	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
92	c3pgvB	Alignment	not modelled	98.7	24	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
93	c3niwA	Alignment	not modelled	98.7	23	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
94	c4y2iA	Alignment	not modelled	98.7	20	PDB header: metal transport Chain: A: PDB Molecule: putative metal-binding transport protein; PDBTitle: gold ion bound to golb
95	d1rkua	Alignment	not modelled	98.7	22	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
96	d2feaa1	Alignment	not modelled	98.7	17	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
97	c2rmIA	Alignment	not modelled	98.7	14	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
98	c2gcfA	Alignment	not modelled	98.7	22	PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the copper(i) atpase2 pacs in its apo form
99	c2rogA	Alignment	not modelled	98.7	16	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
100	c2k2pA	Alignment	not modelled	98.6	24	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
101	d2rbka1	Alignment	not modelled	98.6	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
102	c2kyzA	Alignment	not modelled	98.6	9	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
103	c2aj1A	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
104	d1nf2a	Alignment	not modelled	98.6	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
						PDB header: metal binding protein

105	c6fp6X_	Alignment	not modelled	98.5	11	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	c4b6jA_	Alignment	not modelled	98.4	28	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
107	d1sb6a_	Alignment	not modelled	98.4	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
108	c3fryB_	Alignment	not modelled	98.4	13	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
109	c3fvvA_	Alignment	not modelled	98.4	30	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	98.3	8	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
111	c3kd3A_	Alignment	not modelled	98.3	13	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	c1jk9D_	Alignment	not modelled	98.3	8	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yso1 and yccs
113	c1qupA_	Alignment	not modelled	98.3	10	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
114	d1wzca1	Alignment	not modelled	98.3	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
115	c2crlA_	Alignment	not modelled	98.3	12	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
116	d1s2oa1	Alignment	not modelled	98.2	27	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
117	c3gygA_	Alignment	not modelled	98.2	20	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
118	d1cc8a_	Alignment	not modelled	98.2	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
119	d1fe0a_	Alignment	not modelled	98.1	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
120	d2vkqa1	Alignment	not modelled	98.1	14	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)