



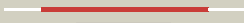

















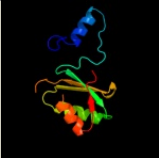


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j09A_	 Alignment		100.0	33	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
2	c3rfuC_	 Alignment		100.0	34	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	c1mhsA_	 Alignment		100.0	26	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
5	c2zxeA_	 Alignment		100.0	26	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
6	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
7	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
8	c3b8eC_	 Alignment		100.0	25	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
9	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
10	c2b8eB_	 Alignment		100.0	42	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
11	c2iyeC_	 Alignment		100.0	32	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b

12	c3p96A_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
13	c3n28A_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
14	d1wpga2	Alignment		100.0	35	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
15	d2b8ea1	Alignment		100.0	41	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
16	d1y8aa1	Alignment		99.9	24	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
17	c2hc8A_	Alignment		99.9	27	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
18	c2kijA_	Alignment		99.9	29	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
19	d1wpga1	Alignment		99.8	30	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
20	c2kmvA_	Alignment		99.8	19	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
21	c2koyA_	Alignment	not modelled	99.7	21	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
22	c2arfA_	Alignment	not modelled	99.7	25	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
23	c2r8zC_	Alignment	not modelled	99.7	26	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
24	c3l7yA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
25	d2a29a1	Alignment	not modelled	99.6	19	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
26	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
27	d1k1ea_	Alignment	not modelled	99.6	30	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi
28	c3mn1B_	Alignment	not modelled	99.6	26	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
29	c3n07B_	Alignment	not modelled	99.5	19 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
30	c2p9jH_	Alignment	not modelled	99.5	20 PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
31	c3n1uA_	Alignment	not modelled	99.5	23 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
32	d2b30a1	Alignment	not modelled	99.5	16 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
33	d1rkqa_	Alignment	not modelled	99.5	17 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
34	c3ewiB_	Alignment	not modelled	99.5	17 PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
35	d2b8ea2	Alignment	not modelled	99.4	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	d1wr8a_	Alignment	not modelled	99.4	18 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
37	c3e8mD_	Alignment	not modelled	99.4	20 PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidyltransferase; 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
38	d1mwza_	Alignment	not modelled	99.4	100 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
39	c2kkhA_	Alignment	not modelled	99.4	20 PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
40	c2ew9A_	Alignment		99.3	23 PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
41	d1kvja_	Alignment	not modelled	99.3	16 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
42	d1q8la_	Alignment	not modelled	99.3	17 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
43	d1p6ta2	Alignment	not modelled	99.3	27 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
44	d1afia_	Alignment	not modelled	99.3	31 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
45	c2l3mA_	Alignment	not modelled	99.3	28 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
46	c3r4cA_	Alignment	not modelled	99.3	19 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
47	d1s6ua_	Alignment	not modelled	99.3	18 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
48	d2qifa1	Alignment	not modelled	99.3	30 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
49	d1p6ta1	Alignment	not modelled	99.3	33 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
50	d1osda_	Alignment	not modelled	99.3	31 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
51	c2kt2A_	Alignment	not modelled	99.2	23 PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmer, the n-terminal hma domain of tn501 mercuric2 reductase
52	c2ropA_	Alignment	not modelled	99.2	19 PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
53	c2dvaX_	Alignment	not modelled	99.2	26 PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1;

53	c3u3aA_	Alignment	not modelled	99.2	20	PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase 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
54	c1y3kA_	Alignment	not modelled	99.2	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
55	d1cpza_	Alignment	not modelled	99.2	32	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
56	c2ofhX_	Alignment	not modelled	99.2	30	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
57	c1yg0A_	Alignment	not modelled	99.2	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
58	d1l6ra_	Alignment	not modelled	99.2	24	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphatse; PDBTitle: crystal structure of a putative phosphatse (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
59	c3daoB_	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
60	d2aw0a_	Alignment	not modelled	99.2	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
61	d2ggpb1_	Alignment	not modelled	99.2	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
62	d1nnla_	Alignment	not modelled	99.2	24	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
63	c1yjrA_	Alignment	not modelled	99.2	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
64	c2kyzA_	Alignment	not modelled	99.2	26	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaan sub mutant
65	c2k2pA_	Alignment	not modelled	99.2	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
66	c2ldiA_	Alignment	not modelled	99.2	33	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)
67	c3m1yA_	Alignment	not modelled	99.2	25	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
68	c2ga7A_	Alignment	not modelled	99.2	16	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
69	c2rogA_	Alignment	not modelled	99.2	27	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
70	d1j97a_	Alignment	not modelled	99.2	29	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
71	c2gcfA_	Alignment	not modelled	99.2	33	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
72	c2rmlA_	Alignment	not modelled	99.1	23	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
73	c2aj1A_	Alignment	not modelled	99.1	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
74	d1nrwa_	Alignment	not modelled	99.1	37	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
75	c3fryB_	Alignment	not modelled	99.1	23	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
76	c2qyhD_	Alignment	not modelled	99.0	23	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
77	d1rkua_	Alignment	not modelled	99.0	17	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
78	d1sb6a_	Alignment	not modelled	99.0	25	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
						Fold: HAD-like

79	d1rlma_	Alignment	not modelled	99.0	28	Superfamily: HAD-like Family: Predicted hydrolases Cof
80	c3dnpA_	Alignment	not modelled	99.0	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
81	d1qupa2	Alignment	not modelled	99.0	10	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
82	d1wpga4	Alignment	not modelled	99.0	26	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
83	c3fzqA_	Alignment	not modelled	99.0	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
84	c1qupA_	Alignment	not modelled	99.0	10	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
85	c1jk9D_	Alignment	not modelled	99.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yso1 and yccs
86	c3pgvB_	Alignment	not modelled	98.9	27	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
87	c3niwA_	Alignment	not modelled	98.9	31	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
88	d1cc8a_	Alignment	not modelled	98.9	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
89	d2rbka1	Alignment	not modelled	98.9	28	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
90	d2feaa1	Alignment	not modelled	98.8	14	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
91	d1fe0a_	Alignment	not modelled	98.8	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
92	c2crlA_	Alignment	not modelled	98.8	19	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
93	d1nf2a_	Alignment	not modelled	98.7	30	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
94	c3fvvA_	Alignment	not modelled	98.6	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
95	c3kd3A_	Alignment	not modelled	98.5	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
96	d1s2oa1	Alignment	not modelled	98.4	29	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
97	c3gygA_	Alignment	not modelled	98.4	22	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
98	d2vkqa1	Alignment	not modelled	98.4	12	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
99	d1wzca1	Alignment	not modelled	98.4	26	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
100	d1q3ia_	Alignment	not modelled	98.2	19	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
101	c1xviA_	Alignment	not modelled	98.2	28	PDB header: hydrolase Chain: A: PDB Molecule: putative mannosyl-3-phosphoglycerate phosphatase; PDBTitle: crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
102	d1xvia_	Alignment	not modelled	98.2	28	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
103	c1y8aA_	Alignment	not modelled	98.1	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
						PDB header: isomerase

104	c2i55C_	Alignment	not modelled	98.0	26	Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
105	c3iruA_	Alignment	not modelled	97.9	19	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
106	c3mc1A_	Alignment	not modelled	97.8	19	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
107	d2bdua1	Alignment	not modelled	97.8	14	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
108	d1zs9a1	Alignment	not modelled	97.8	22	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
109	d1qyia_	Alignment	not modelled	97.8	26	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
110	d2fuea1	Alignment	not modelled	97.8	24	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
111	d1swva_	Alignment	not modelled	97.7	22	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
112	d1u02a_	Alignment	not modelled	97.7	28	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
113	d2ah5a1	Alignment	not modelled	97.7	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
114	c3gwiA_	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: A: PDB Molecule: magnesium-transporting atpase, p-type 1; PDBTitle: crystal structure of mg-atpase nucleotide binding domain
115	d2amya1	Alignment	not modelled	97.5	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
116	c3s6jC_	Alignment	not modelled	97.5	18	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
117	c2odaB_	Alignment	not modelled	97.4	18	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
118	d1mo7a_	Alignment	not modelled	97.4	23	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
119	c3mpoD_	Alignment	not modelled	97.4	33	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
120	d1te2a_	Alignment	not modelled	97.3	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like