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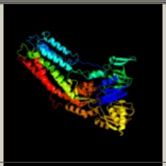
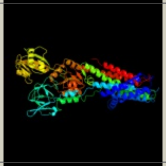
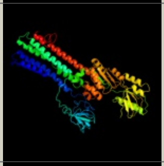
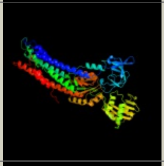
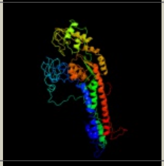
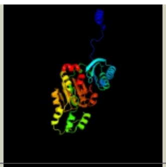
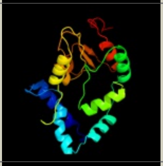
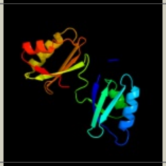
Description	Q59385
Date	Thu Jan 5 12:37:17 GMT 2012
Unique Job ID	daa1eeada2b81464

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j09A_	Alignment		100.0	38	**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	45	**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	39	**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	25	**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	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
6	c3ixzA_	Alignment		100.0	22	**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	22	**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	23	**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	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b

12	c3p96A_	Alignment		100.0	18	**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	20	**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	36	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
15	d2b8ea1	Alignment		100.0	46	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
16	d1y8aa1	Alignment		99.9	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**AF1437-like
17	c2hc8A_	Alignment		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
18	c2kijA_	Alignment		99.9	41	**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	c2ew9A_	Alignment		99.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
20	c2ropA_	Alignment		99.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
21	c2rmlA_	Alignment		99.9	29	**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
22	c2kmvA_	Alignment	not modelled	99.8	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
23	d1wpga1	Alignment	not modelled	99.8	22	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
24	c2koyA_	Alignment	not modelled	99.8	22	**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
25	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
26	d2a29a1	Alignment	not modelled	99.7	16	**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
27	c2r8zC_	Alignment	not modelled	99.7	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

28	c3mmzA_	Alignment	not modelled	99.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
29	d1k1ea_	Alignment	not modelled	99.6	31	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
30	c3n07B_	Alignment	not modelled	99.6	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
31	c2p9jH_	Alignment	not modelled	99.6	15	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
32	c3l7yA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1108c; **PDBTitle:** the crystal structure of smu.1108c from streptococcus mutans ua159
33	c3mn1B_	Alignment	not modelled	99.5	21	**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
34	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
35	d2b8ea2	Alignment	not modelled	99.5	31	**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	c3e8mD_	Alignment	not modelled	99.5	23	**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
37	c3ewiB_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
38	d2b30a1	Alignment	not modelled	99.4	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
39	c2kkhA_	Alignment	not modelled	99.4	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
40	d1kvja_	Alignment	not modelled	99.3	27	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
41	d1nnla_	Alignment	not modelled	99.3	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
42	d1rkqa_	Alignment	not modelled	99.3	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
43	d1wr8a_	Alignment	not modelled	99.3	27	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
44	d1s6ua_	Alignment	not modelled	99.3	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
45	d1q8la_	Alignment	not modelled	99.3	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
46	c3m1yA_	Alignment	not modelled	99.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
47	d1p6ta2	Alignment	not modelled	99.3	33	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
48	d1afia_	Alignment	not modelled	99.3	34	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
49	d1l6ra_	Alignment	not modelled	99.3	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
50	c3dxsX_	Alignment	not modelled	99.3	33	**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
51	c2rogA_	Alignment	not modelled	99.3	48	**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
52	c1yjrA_	Alignment	not modelled	99.3	27	**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
53	d1cpza_	Alignment	not modelled	99.2	33	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain

54	d1osda_	Alignment	not modelled	99.2	31	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
55	c3daoB_	Alignment	not modelled	99.2	25	**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
56	d1j97a_	Alignment	not modelled	99.2	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
57	c2l3mA_	Alignment	not modelled	99.2	32	**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
58	c2kt2A_	Alignment	not modelled	99.2	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
59	d1p6ta1	Alignment	not modelled	99.2	35	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
60	d1mwza_	Alignment	not modelled	99.2	29	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
61	d2qifa1	Alignment	not modelled	99.2	33	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
62	d2ggpb1	Alignment	not modelled	99.2	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
63	c3r4cA_	Alignment	not modelled	99.2	15	**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
64	d2aw0a_	Alignment	not modelled	99.2	31	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
65	c2k2pA_	Alignment	not modelled	99.2	21	**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
66	c1y3kA_	Alignment	not modelled	99.2	28	**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
67	c2gcfA_	Alignment	not modelled	99.2	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
68	c2ofhX_	Alignment	not modelled	99.2	27	**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
69	c2kyzA_	Alignment	not modelled	99.2	23	**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
70	c2ldiA_	Alignment	not modelled	99.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
71	d1nrwa_	Alignment	not modelled	99.1	35	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
72	c1yg0A_	Alignment	not modelled	99.1	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
73	c2ga7A_	Alignment	not modelled	99.1	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)
74	d1rlma_	Alignment	not modelled	99.1	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
75	d1qupa2	Alignment	not modelled	99.1	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
76	c2qyhD_	Alignment	not modelled	99.1	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
77	c1qupA_	Alignment	not modelled	99.1	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
78	d1rkua_	Alignment	not modelled	99.1	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase;

79	c3fzqA_	Alignment	not modelled	99.1	33	**PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
80	c2aj1A_	Alignment	not modelled	99.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
81	d1sb6a_	Alignment	not modelled	99.0	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
82	c3dnpA_	Alignment	not modelled	99.0	28	**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
83	c3pgvB_	Alignment	not modelled	99.0	25	**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
84	c1jk9D_	Alignment	not modelled	99.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
85	c3fryB_	Alignment	not modelled	99.0	33	**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
86	c2crlA_	Alignment	not modelled	99.0	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
87	c3niwA_	Alignment	not modelled	98.9	34	**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	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
90	d2feaa1	Alignment	not modelled	98.9	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**MtnX-like
91	d1fe0a_	Alignment	not modelled	98.9	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
92	d2rbka1	Alignment	not modelled	98.9	37	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
93	d1nf2a_	Alignment	not modelled	98.8	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
94	c3fvvA_	Alignment	not modelled	98.7	23	**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	c3gygA_	Alignment	not modelled	98.6	23	**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
96	c3kd3A_	Alignment	not modelled	98.6	16	**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
97	d1q3ia_	Alignment	not modelled	98.6	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
98	d1s2oa1	Alignment	not modelled	98.5	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
99	d1wzca1	Alignment	not modelled	98.5	31	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
100	d2vkqa1	Alignment	not modelled	98.3	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
101	c1xviA_	Alignment	not modelled	98.3	32	**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	98.3	32	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
103	c3gwiA_	Alignment	not modelled	98.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**magnesium-transporting atpase, p-type 1; **PDBTitle:** crystal structure of mg-atpase nucleotide binding domain
						Fold:HAD-like

104	d1qyia_	Alignment	not modelled	98.1	23	**Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
105	c2i55C_	Alignment	not modelled	98.1	30	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
106	c3iruA_	Alignment	not modelled	98.1	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
107	c1y8aA_	Alignment	not modelled	98.1	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1437; **PDBTitle:** structure of gene product af1437 from archaeoglobus fulgidus
108	d1zs9a1	Alignment	not modelled	98.1	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
109	d1mo7a_	Alignment	not modelled	97.9	16	**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
110	d1swva_	Alignment	not modelled	97.9	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
111	d2fuea1	Alignment	not modelled	97.8	32	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
112	c3mc1A_	Alignment	not modelled	97.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted phosphatase, had family; **PDBTitle:** crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
113	d1u02a_	Alignment	not modelled	97.6	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
114	c3s6jC_	Alignment	not modelled	97.6	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas syringae
115	c3mpoD_	Alignment	not modelled	97.6	34	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
116	d2bdua1	Alignment	not modelled	97.5	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
117	c2odaB_	Alignment	not modelled	97.5	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**hypothetical protein pspto_2114; **PDBTitle:** crystal structure of pspto_2114
118	c3m9lA_	Alignment	not modelled	97.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** crystal structure of probable had family hydrolase from2 pseudomonas fluorescens pf-5
119	c3ib6B_	Alignment	not modelled	97.4	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
120	d2amya1	Alignment	not modelled	97.3	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof