Phyre2

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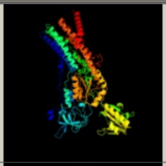
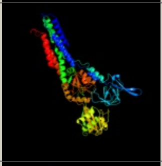
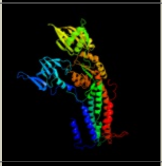
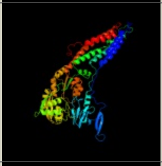
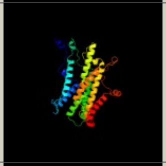
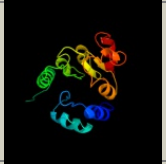
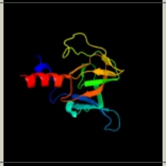
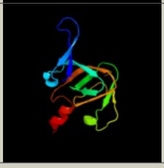
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zxeA_	Alignment		100.0	22	**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
2	c3ixzA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
3	c1mhsA_	Alignment		100.0	21	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
4	c3b9bA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
5	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
6	c3rfuC_	Alignment		100.0	23	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
7	c3b8cB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
8	c3j09A_	Alignment		100.0	27	**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
9	c3j08A_	Alignment		100.0	27	**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
10	c2b8eB_	Alignment		100.0	31	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain
11	c2iyeC_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b

12	d1wpga2	Alignment		100.0	35	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
13	d2b8ea1	Alignment		100.0	34	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
14	c3p96A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
15	d1wpga4	Alignment		100.0	23	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
16	d1y8aa1	Alignment		100.0	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**AF1437-like
17	c3n28A_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase; **PDBTitle:** crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
18	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
19	c2kijA_	Alignment		99.8	33	**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
20	d1wpga1	Alignment		99.8	24	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
21	d1mo7a_	Alignment	not modelled	99.6	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
22	c3n07B_	Alignment	not modelled	99.6	13	**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
23	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
24	d2a29a1	Alignment	not modelled	99.6	100	**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
25	d1q3ia_	Alignment	not modelled	99.5	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
26	c2r8zC_	Alignment	not modelled	99.5	15	**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
27	c3mmzA_	Alignment	not modelled	99.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
28	c3mn1B_	Alignment	not modelled	99.5	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
29	d1k1ea_	Alignment	not modelled	99.5	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
30	c3gwiA_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**magnesium-transporting atpase, p-type 1; **PDBTitle:** crystal structure of mg-atpase nucleotide binding domain
31	c3l7yA_	Alignment	not modelled	99.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1108c; **PDBTitle:** the crystal structure of smu.1108c from streptococcus mutans ua159
32	c3ewiB_	Alignment	not modelled	99.5	13	**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
33	d1wpga3	Alignment	not modelled	99.5	13	**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	c3e8mD_	Alignment	not modelled	99.4	17	**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
35	c3n1uA_	Alignment	not modelled	99.4	14	**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
36	d1wr8a_	Alignment	not modelled	99.4	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
37	d1rkqa_	Alignment	not modelled	99.4	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
38	d1l6ra_	Alignment	not modelled	99.4	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
39	c3m1yA_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
40	c3daoB_	Alignment	not modelled	99.3	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
41	d1j97a_	Alignment	not modelled	99.3	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
42	c2koyA_	Alignment	not modelled	99.3	17	**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
43	c2kmvA_	Alignment	not modelled	99.2	12	**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
44	d1nrwa_	Alignment	not modelled	99.2	29	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
45	d1rlma_	Alignment	not modelled	99.2	27	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
46	d2b30a1	Alignment	not modelled	99.2	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
47	c3r4cA_	Alignment	not modelled	99.2	26	**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
48	d1nnla_	Alignment	not modelled	99.1	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
49	d1rkua_	Alignment	not modelled	99.1	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
50	c3dnpA_	Alignment	not modelled	99.1	25	**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
51	c2qyhD_	Alignment	not modelled	99.1	21	**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
52	c3pgvB_	Alignment	not modelled	99.1	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
53	c3fzqA_	Alignment	not modelled	99.1	24	**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
54	d2rbka1	Alignment	not modelled	99.0	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
55	d2feaa1	Alignment	not modelled	99.0	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**MtnX-like
56	c3niwA_	Alignment	not modelled	99.0	22	**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
57	d1nf2a_	Alignment	not modelled	98.9	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
58	c3fvvA_	Alignment	not modelled	98.7	18	**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
59	c2arfA_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wilson disease atpase; **PDBTitle:** solution structure of the wilson atpase n-domain in the2 presence of atp
60	d1s2oa1	Alignment	not modelled	98.7	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
61	c3kd3A_	Alignment	not modelled	98.7	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
62	c3gygA_	Alignment	not modelled	98.7	18	**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
63	d1wzca1	Alignment	not modelled	98.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
64	d1xvia_	Alignment	not modelled	98.4	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
65	c1xviA_	Alignment	not modelled	98.4	24	**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
66	c2i55C_	Alignment	not modelled	98.3	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
67	d2b8ea2	Alignment	not modelled	98.3	21	**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
68	d2vkqa1	Alignment	not modelled	98.2	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
69	d1qyia_	Alignment	not modelled	98.2	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
70	d1zs9a1	Alignment	not modelled	98.1	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
71	c3iruA_	Alignment	not modelled	98.0	20	**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
72	d1swva_	Alignment	not modelled	97.9	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
73	d2fuea1	Alignment	not modelled	97.8	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
74	c1y8aA_	Alignment	not modelled	97.8	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1437; **PDBTitle:** structure of gene product af1437 from archaeoglobus fulgidus
75	d1u02a_	Alignment	not modelled	97.8	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
76	c3mpoD_	Alignment	not modelled	97.8	34	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
77	c3s6jC_	Alignment	not modelled	97.7	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas syringae
78	d2amya1	Alignment	not modelled	97.7	16	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: Predicted hydrolases Cof
79	c3mc1A_	Alignment	not modelled	97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted phosphatase, had family; **PDBTitle:** crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
80	d2bdua1	Alignment	not modelled	97.6	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
81	c2voyH_	Alignment	not modelled	97.6	28	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
82	c2pibA_	Alignment	not modelled	97.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphorylated carbohydrates phosphatase tm_1254; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
83	c3m9lA_	Alignment	not modelled	97.4	18	**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
84	c2odaB_	Alignment	not modelled	97.3	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**hypothetical protein pspto_2114; **PDBTitle:** crystal structure of pspto_2114
85	c2yy6B_	Alignment	not modelled	97.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphoglycolate phosphatase; **PDBTitle:** crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
86	c3d6jA_	Alignment	not modelled	97.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
87	d2hsza1	Alignment	not modelled	97.1	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
88	c2voyK_	Alignment	not modelled	97.1	16	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
89	c3pdwA_	Alignment	not modelled	97.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized hydrolase yutf; **PDBTitle:** crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
90	d2gmwa1	Alignment	not modelled	97.1	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
91	c3dv9A_	Alignment	not modelled	97.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** putative beta-phosphoglucomutase from bacteroides vulgatus.
92	d1u7pa_	Alignment	not modelled	97.0	8	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
93	c2hi0B_	Alignment	not modelled	97.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphoglycolate phosphatase; **PDBTitle:** crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
94	c2hx1D_	Alignment	not modelled	97.0	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
95	d2fdra1	Alignment	not modelled	97.0	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
96	c3esqA_	Alignment	not modelled	96.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d,d-heptose 1,7-bisphosphate phosphatase; **PDBTitle:** crystal structure of calcium-bound d,d-heptose 1.7-2 bisphosphate phosphatase from e. coli
97	c2qltA_	Alignment	not modelled	96.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(dl)-glycerol-3-phosphatase 1; **PDBTitle:** crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
98	d2ah5a1	Alignment	not modelled	96.9	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
99	d1te2a_	Alignment	not modelled	96.9	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
100	c3ib6B_	Alignment	not modelled	96.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
101	c2pr7A_	Alignment	not modelled	96.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
102	d2go7a1	Alignment	not modelled	96.6	19	**Fold:**HAD-like **Superfamily:**HAD-like

						Family:beta-Phosphoglucomutase-like
103	d2hcfa1	Alignment	not modelled	96.6	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
104	c3sd7A_	Alignment	not modelled	96.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphatase; **PDBTitle:** 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
105	c3l8hC_	Alignment	not modelled	96.6	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of d,d-heptose 1.7-bisphosphate phosphatase from b.2 bronchiseptica complexed with magnesium and phosphate
106	d1zrna_	Alignment	not modelled	96.6	9	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
107	c2hoqA_	Alignment	not modelled	96.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had-hydrolase ph1655; **PDBTitle:** crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
108	c2no5B_	Alignment	not modelled	96.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**(s)-2-haloacid dehalogenase iva; **PDBTitle:** crystal structure analysis of a dehalogenase with intermediate complex
109	c2cftA_	Alignment	not modelled	96.3	20	**PDB header:**phosphatase **Chain:** A: **PDB Molecule:**pyridoxal phosphate phosphatase; **PDBTitle:** crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
110	d1vjra_	Alignment	not modelled	96.3	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
111	d1wvia_	Alignment	not modelled	96.2	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
112	d2fi1a1	Alignment	not modelled	96.1	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
113	d1zd3a1	Alignment	not modelled	96.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
114	c1zjjA_	Alignment	not modelled	95.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ph1952; **PDBTitle:** crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
115	c3l5kA_	Alignment	not modelled	95.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain- **PDBTitle:** the crystal structure of human haloacid dehalogenase-like2 hydrolase domain containing 1a (hdhd1a)
116	d1z5ga1	Alignment	not modelled	95.9	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Class B acid phosphatase, AphA
117	d1ydfa1	Alignment	not modelled	95.7	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
118	c3cnhA_	Alignment	not modelled	95.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase family protein; **PDBTitle:** crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
119	d1cr6a1	Alignment	not modelled	95.6	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
120	d1x42a1	Alignment	not modelled	95.5	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related