Phyre2

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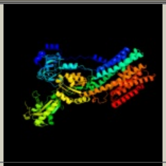
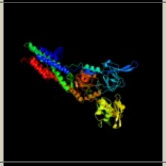
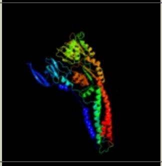
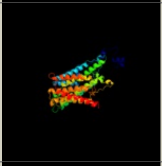
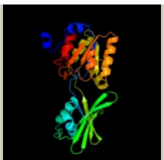
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zxeA_	Alignment		100.0	28	**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	c3b9bA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
3	c3ixzA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
4	c3b8eC_	Alignment		100.0	27	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
5	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
6	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
7	c3rfuC_	Alignment		100.0	24	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
8	c3j09A_	Alignment		100.0	25	**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	25	**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	d1wpga4	Alignment		100.0	28	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
11	c2b8eB_	Alignment		100.0	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain

12	c2iyeC_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b
13	d1wpga2	Alignment		100.0	31	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
14	d2b8ea1	Alignment		100.0	41	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
15	d1y8aa1	Alignment		100.0	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**AF1437-like
16	c3p96A_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
17	c3gwiA_	Alignment		99.9	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**magnesium-transporting atpase, p-type 1; **PDBTitle:** crystal structure of mg-atpase nucleotide binding domain
18	d1mo7a_	Alignment		99.9	25	**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
19	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
20	d1wpga1	Alignment		99.9	33	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
21	d1wpga3	Alignment	not modelled	99.9	22	**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	d1q3ia_	Alignment	not modelled	99.9	24	**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
23	c2hc8A_	Alignment	not modelled	99.9	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
24	c2kijA_	Alignment	not modelled	99.8	25	**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
25	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
26	c2r8zC_	Alignment	not modelled	99.5	18	**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	c2p9jH_	Alignment	not modelled	99.5	22	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
28	c3mmzA_	Alignment	not modelled	99.5	18	**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	c3mn1B_	Alignment	not modelled	99.5	24	**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
30	d1k1ea_	Alignment	not modelled	99.4	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
31	c3l7yA_	Alignment	not modelled	99.4	18	**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	99.4	16	**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	d1l6ra_	Alignment	not modelled	99.4	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
34	d1wr8a_	Alignment	not modelled	99.3	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
35	c3n1uA_	Alignment	not modelled	99.3	21	**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	d1rkqa_	Alignment	not modelled	99.3	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
37	c3e8mD_	Alignment	not modelled	99.3	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
38	c3m1yA_	Alignment	not modelled	99.2	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
39	c3daoB_	Alignment	not modelled	99.2	20	**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
40	d1j97a_	Alignment	not modelled	99.2	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
41	d1rlma_	Alignment	not modelled	99.2	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
42	d1nrwa_	Alignment	not modelled	99.2	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
43	c2qyhD_	Alignment	not modelled	99.2	24	**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
44	d2b30a1	Alignment	not modelled	99.1	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
45	c3dnpA_	Alignment	not modelled	99.1	27	**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
46	c3r4cA_	Alignment	not modelled	99.1	24	**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	c3pgvB_	Alignment	not modelled	99.1	19	**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
48	c3fzqA_	Alignment	not modelled	99.1	18	**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
49	d2rbka1	Alignment	not modelled	99.0	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
50	c3niwA_	Alignment	not modelled	99.0	25	**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
51	d1rkua_	Alignment	not modelled	99.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
52	d1nnla_	Alignment	not modelled	98.9	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
53	d1nf2a_	Alignment	not modelled	98.9	22	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: Predicted hydrolases Cof
54	c2kmvA_	Alignment	not modelled	98.8	15	**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
55	d2feaa1	Alignment	not modelled	98.8	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**MtnX-like
56	c3gygA_	Alignment	not modelled	98.6	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
57	d1s2oa1	Alignment	not modelled	98.6	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
58	c3fvvA_	Alignment	not modelled	98.6	25	**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	c2koyA_	Alignment	not modelled	98.6	15	**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
60	d2a29a1	Alignment	not modelled	98.5	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
61	d1xvia_	Alignment	not modelled	98.4	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
62	c1xviA_	Alignment	not modelled	98.4	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
63	d1wzca1	Alignment	not modelled	98.4	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
64	c3kd3A_	Alignment	not modelled	98.4	9	**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
65	c2i55C_	Alignment	not modelled	98.3	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
66	d2vkqa1	Alignment	not modelled	98.1	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
67	c1y8aA_	Alignment	not modelled	98.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1437; **PDBTitle:** structure of gene product af1437 from archaeoglobus fulgidus
68	c2voyH_	Alignment	not modelled	98.0	32	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
69	c2voyB_	Alignment	not modelled	98.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
70	c3iruA_	Alignment	not modelled	97.8	21	**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
71	d1u02a_	Alignment	not modelled	97.8	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
72	d2fuea1	Alignment	not modelled	97.8	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
73	d1qyia_	Alignment	not modelled	97.7	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
74	d1zs9a1	Alignment	not modelled	97.7	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
75	d1swva_	Alignment	not modelled	97.7	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
76	d2amya1	Alignment	not modelled	97.6	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
77	c3mpoD_	Alignment	not modelled	97.6	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
						Fold:HAD-like

78	d2bdua1	Alignment	not modelled	97.6	18	**Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
79	c3s6jC_	Alignment	not modelled	97.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas syringae
80	c2odaB_	Alignment	not modelled	97.4	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**hypothetical protein pspto_2114; **PDBTitle:** crystal structure of pspto_2114
81	c2arfA_	Alignment	not modelled	97.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wilson disease atpase; **PDBTitle:** solution structure of the wilson atpase n-domain in the2 presence of atp
82	c3mc1A_	Alignment	not modelled	97.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted phosphatase, had family; **PDBTitle:** crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
83	c3m9lA_	Alignment	not modelled	97.1	17	**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	c2voyK_	Alignment	not modelled	97.1	35	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
85	c3dv9A_	Alignment	not modelled	97.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** putative beta-phosphoglucomutase from bacteroides vulgatus.
86	c2pibA_	Alignment	not modelled	96.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphorylated carbohydrates phosphatase tm_1254; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
87	c3pdwA_	Alignment	not modelled	96.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized hydrolase yutf; **PDBTitle:** crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
88	c3d6jA_	Alignment	not modelled	96.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
89	c2yy6B_	Alignment	not modelled	96.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphoglycolate phosphatase; **PDBTitle:** crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
90	c3ib6B_	Alignment	not modelled	96.6	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
91	d1u7pa_	Alignment	not modelled	96.6	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
92	c2hx1D_	Alignment	not modelled	96.5	16	**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
93	c2hi0B_	Alignment	not modelled	96.4	16	**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	d2hsza1	Alignment	not modelled	96.4	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
95	d2go7a1	Alignment	not modelled	96.2	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
96	d2gmwa1	Alignment	not modelled	96.2	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
97	c3esqA_	Alignment	not modelled	96.2	20	**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
98	d2ah5a1	Alignment	not modelled	96.2	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
99	c2qltA_	Alignment	not modelled	96.2	20	**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
100	d1z5ga1	Alignment	not modelled	96.1	27	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Class B acid phosphatase, AphA
101	c2no5B_	Alignment	not modelled	95.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**(s)-2-haloacid dehalogenase iva; **PDBTitle:** crystal structure analysis of a dehalogenase with intermediate complex
102	d1te2a_	Alignment	not modelled	95.8	21	**Fold:**HAD-like **Superfamily:**HAD-like

						Family:beta-Phosphoglucomutase-like
103	c2cftA_	Alignment	not modelled	95.8	22	**PDB header:**phosphatase **Chain:** A: **PDB Molecule:**pyridoxal phosphate phosphatase; **PDBTitle:** crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
104	c3et4A_	Alignment	not modelled	95.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**outer membrane protein p4, nadp phosphatase; **PDBTitle:** structure of recombinant haemophilus influenzae e(p4) acid phosphatase
105	c3pctA_	Alignment	not modelled	95.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class c acid phosphatase; **PDBTitle:** structure of the class c acid phosphatase from pasteurella multocida
106	c2pr7A_	Alignment	not modelled	95.6	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
107	d1zrna_	Alignment	not modelled	95.5	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
108	d1wvia_	Alignment	not modelled	95.4	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
109	d2fdra1	Alignment	not modelled	95.4	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
110	d1zd3a1	Alignment	not modelled	95.4	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
111	c2hoqA_	Alignment	not modelled	95.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had-hydrolase ph1655; **PDBTitle:** crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
112	d2hcfa1	Alignment	not modelled	95.2	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
113	d2fi1a1	Alignment	not modelled	95.1	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
114	d1vjra_	Alignment	not modelled	95.0	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
115	d1ydfa1	Alignment	not modelled	95.0	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
116	d1cr6a1	Alignment	not modelled	95.0	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
117	d2b82a1	Alignment	not modelled	94.9	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Class B acid phosphatase, AphA
118	d1x42a1	Alignment	not modelled	94.8	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
119	c1zjjA_	Alignment	not modelled	94.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ph1952; **PDBTitle:** crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
120	c3l5kA_	Alignment	not modelled	94.2	13	**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)