

Phyre2

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Description	RVBD1225c_(-)_1367897_1368727
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cftA_	Alignment		100.0	26	PDB header: phosphatase Chain: A; PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
2	c3qgmC_	Alignment		100.0	24	PDB header: hydrolase Chain: C; PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
3	c3pdwA_	Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
4	c1zjzA_	Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
5	d1ys9a1	Alignment		100.0	22	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
6	d1wvia_	Alignment		100.0	22	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
7	d1ydfa1	Alignment		100.0	25	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
8	c4ig4A_	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
9	d1yv9a1	Alignment		100.0	24	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
10	d2c4na1	Alignment		100.0	23	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
11	c4i9gB_	Alignment		100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: glycerol 3-phosphate phosphatase; PDBTitle: crystal structure of glycerol phosphate phosphatase rv1692 from2 mycobacterium tuberculosis in complex with magnesium

12	d1vjra_	Alignment		100.0	23	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
13	c2ho4A_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127
14	c2x4dA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
15	c2hx1D_	Alignment		100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had superfamily; PDBTitle: crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
16	c3kc2A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
17	c3dv9A_	Alignment		100.0	15	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
18	c3qnmA_	Alignment		100.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: haloalkane dehalogenase family member from bacteroides2 thetaiotaomicron of unknown function
19	c3mc1A_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
20	d2hsza1	Alignment		99.9	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
21	c3iruA_	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phosphonoacetaldehyde hydrolase like protein from2 oleispira antarctica
22	c2hi0B_	Alignment	not modelled	99.9	14	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
23	c3d6jA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
24	c3vayB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: had-superfamily hydrolase; PDBTitle: crystal structure of 2-haloacid dehalogenase from pseudomonas syringae2 pv. tomato dc3000
25	d1swva_	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
26	d2fdra1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
27	c2hoqA_	Alignment	not modelled	99.9	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
						Fold: HAD-like

28	d1qq5a_	Alignment	not modelled	99.9	13	Superfamily: HAD-like Family: HAD-related
29	c4ex7A_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
30	c4uasA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
31	c3ddhA_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like family hydrolase; PDBTitle: the structure of a putative haloacid dehalogenase-like family2 hydrolase from bacteroides thetaiotaomicron vpi-5482
32	c3umcC_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase pa0810
33	d1te2a_	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
34	c3umbA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase rsc1362
35	c4g9bA_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: crystal structure of beta-phosphoglucomutase homolog from escherichia2 coli, target efi-501172, with bound mg, open lid
36	c2yy6B_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
37	c2x4dB_	Alignment	not modelled	99.9	32	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
38	c3umgD_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 rha0230
39	c3qypB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
40	c3um9A_	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530
41	c2om6A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
42	d2gfha1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
43	c3s6jC_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
44	c4uavA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidopsis thaliana
45	c3nuqA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
46	d1zs9a1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
47	c4gibA_	Alignment	not modelled	99.9	15	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
48	d1x42a1	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
49	c3e58A_	Alignment	not modelled	99.9	15	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
50	d2ah5a1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
51	c3k1zA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of human haloacid dehalogenase-like hydrolase domain2 containing 3 (hdhd3)
52	c6f2xA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)

53	c3l8hC_	Alignment	not modelled	99.9	24	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
54	d1zrna_	Alignment	not modelled	99.9	11	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
55	d2hdoa1	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
56	d2go7a1	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
57	c4rn3B_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: had superfamily hydrolase; PDBTitle: crystal structure of a had-superfamily hydrolase, subfamily ia,2 variant 1 (gsu2069) from geobacter sulfurreducens pca at 2.15 a3 resolution
58	d2gmwa1	Alignment	not modelled	99.9	25	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
59	c3ed5A_	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yfnb; PDBTitle: the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
60	c4eekA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-phosphoglucomutase-related protein; PDBTitle: crystal structure of a had family hydrolase dr_1622 from deinococcus2 radiodurans r1 (target efi-501256) with bound phosphate and sodium
61	c3esqA_	Alignment	not modelled	99.9	25	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-bisphosphate2 phosphatase from e. coli
62	c2pibA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
63	d1o08a_	Alignment	not modelled	99.9	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
64	c2no5B_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
65	c3sd7A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
66	c2ympB_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: l-haloacid dehalogenase; PDBTitle: chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
67	d2hcfA1	Alignment	not modelled	99.9	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
68	c4ygsA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase; PDBTitle: crystal structure of had phosphatase from thermococcus onnurineus
69	c2pkeA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: haloacid delahogenase-like family hydrolase; PDBTitle: crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
70	c2qltA_	Alignment	not modelled	99.9	15	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
71	c3m9lA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: crystal structure of probable had family hydrolase from pseudomonas2 fluorescens pf-5
72	d2o2xa1	Alignment	not modelled	99.9	22	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
73	c3l5kA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: the crystal structure of human haloacid dehalogenase-like hydrolase2 domain containing 1a (hdhd1a)
74	d1qyia_	Alignment	not modelled	99.9	23	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
75	c3kd3A_	Alignment	not modelled	99.9	11	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
76	c3cmvA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: s(-)-azetidine-2-carboxylate hydrolase;

76	c3slwA	Alignment	not modelled	99.9	11	PDBTitle: x-ray crystal structure of l-azetidine-2-carboxylate hydrolase PDB header: hydrolase
77	c2g80C	Alignment	not modelled	99.9	12	Chain: C; PDB Molecule: protein utr4; PDBTitle: crystal structure of utr4 protein (unknown transcript 4 protein)2 (yei038w) from saccharomyces cerevisiae at 2.28 a resolution
78	c2w11B	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B; PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
79	c3fzqA	Alignment	not modelled	99.9	14	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
80	c3i28A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
81	c4jb3A	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of bt_0970, a had family phosphatase from2 bacteroides thetaiotaomicron vpi-5482, target efi-501083, with bound3 sodium and glycerol, closed lid, ordered loop
82	d2g80a1	Alignment	not modelled	99.8	11	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
83	c3cnhA	Alignment	not modelled	99.8	17	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
84	c4zexA	Alignment	not modelled	99.8	9	PDB header: unknown function Chain: A; PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
85	c3dnpA	Alignment	not modelled	99.8	14	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
86	d1zd3a1	Alignment	not modelled	99.8	16	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
87	c2i6xA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A; PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the structure of a predicted had-like family hydrolase from2 porphyromonas gingivalis.
88	d1cr6a1	Alignment	not modelled	99.8	26	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
89	c1cr6A	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
90	d2fi1a1	Alignment	not modelled	99.8	18	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
91	c4uw9A	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A; PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structural of archaeal beta-phosphoglucomutase2 from hyper-thermophilic pyrococcus sp. strain st 04
92	c4jyrG	Alignment	not modelled	99.8	34	PDB header: hydrolase Chain: G; PDB Molecule: d,d-heptose 1,7-bisphosphate phosphatase; PDBTitle: crystal structure of d,d-heptose 1,7-bisphosphate phosphatase from2 burkholderia thailandensis
93	d1nrwa	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
94	c3nasA	Alignment	not modelled	99.8	16	PDB header: isomerase Chain: A; PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
95	c3niwA	Alignment	not modelled	99.8	12	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
96	d1rkqa	Alignment	not modelled	99.8	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
97	c2p11A	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bx_e_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
98	c2qyhD	Alignment	not modelled	99.8	16	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
99	c3r4cA	Alignment	not modelled	99.8	12	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 PDB header: hydrolase

100	c4dfdB	Alignment	not modelled	99.8	15	Chain: B: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family enzyme bt-2542 (target efi-501088)2 from bacteroides thetaiotaomicron, magnesium complex
101	c2odaB	Alignment	not modelled	99.8	27	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
102	d1nf2a	Alignment	not modelled	99.8	10	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
103	c3kzxA	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: had-superfamily hydrolase, subfamily ia, variant 1; PDBTitle: crystal structure of a had-superfamily hydrolase from ehrlichia2 chaffeensis at 1.9a resolution
104	d1wr8a	Alignment	not modelled	99.8	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
105	d1l6ra	Alignment	not modelled	99.8	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
106	c4qjbB	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
107	d1wzca1	Alignment	not modelled	99.8	11	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
108	d1u7pa	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
109	d2b0ca1	Alignment	not modelled	99.8	15	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
110	c3daoB	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
111	d2rbka1	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
112	c3pgvB	Alignment	not modelled	99.8	16	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
113	c3m1yA	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
114	c3ib6B	Alignment	not modelled	99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
115	c3gygA	Alignment	not modelled	99.8	10	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
116	c1xviA	Alignment	not modelled	99.7	12	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
117	d1xvia	Alignment	not modelled	99.7	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
118	d1rlma	Alignment	not modelled	99.7	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
119	d2b30a1	Alignment	not modelled	99.7	9	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
120	d1j97a	Alignment	not modelled	99.7	11	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase