
















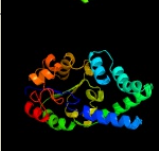
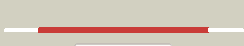





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3376 (-)_3790336_3790989
Date	Fri Aug 9 18:20:04 BST 2019
Unique Job ID	e9e6775f356c2c87

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iruA_	 Alignment		100.0	14	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
2	d1swva_	 Alignment		100.0	16	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
3	d2go7a1	 Alignment		99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
4	c3dv9A_	 Alignment		99.9	15	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
5	d2hsza1	 Alignment		99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
6	d2fdra1	 Alignment		99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
7	c3d6jA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
8	c3qypB_	 Alignment		99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
9	c3qnmA_	 Alignment		99.9	15	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
10	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
11	c4eekA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-phosphoglucomutase-related protein; PDBTitle: crystal structure of had family hydrolase dr_1622 from deinococcus2 radiodurans r1 (target efi-501256) with bound phosphate and sodium

12	d1te2a_	Alignment		99.9	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
13	c2yy6B_	Alignment		99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
14	c4ex7A_	Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
15	d2ah5a1	Alignment		99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
16	c4g9bA_	Alignment		99.9	18	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
17	c3m9IA_	Alignment		99.9	24	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
18	c3s6jC_	Alignment		99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
19	c3umcC_	Alignment		99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase pa0810
20	c3umbA_	Alignment		99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase rsc1362
21	c6f2xA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
22	c3um9A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530
23	c3l5kA_	Alignment	not modelled	99.9	16	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)
24	c3umgD_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 rha0230
25	c3i28A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
26	c2pibA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
27	d2hdoa1	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
28	c2no5B_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with

					intermediate complex
29	c4uasA	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
30	c3nuqA	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
31	c3e58A	Alignment	not modelled	99.9	17 PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
32	c2qltA	Alignment	not modelled	99.9	16 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
33	d1zs9a1	Alignment	not modelled	99.9	21 Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
34	d1zrna	Alignment	not modelled	99.9	27 Fold: HAD-like Superfamily: HAD-like Family: HAD-related
35	d1qq5a	Alignment	not modelled	99.9	23 Fold: HAD-like Superfamily: HAD-like Family: HAD-related
36	c2om6A	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
37	d1zd3a1	Alignment	not modelled	99.9	20 Fold: HAD-like Superfamily: HAD-like Family: YihX-like
38	c2hi0B	Alignment	not modelled	99.9	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
39	c4rn3B	Alignment	not modelled	99.9	16 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
40	c4uavA	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidobis thaliana
41	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
42	c4gibA	Alignment	not modelled	99.9	16 PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
43	d1o08a	Alignment	not modelled	99.9	21 Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
44	c3sd7A	Alignment	not modelled	99.9	14 PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
45	c3ddhA	Alignment	not modelled	99.9	14 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
46	c2hoqA	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
47	d2hcfa1	Alignment	not modelled	99.9	13 Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
48	d1x42a1	Alignment	not modelled	99.9	21 Fold: HAD-like Superfamily: HAD-like Family: HAD-related
49	d2gfha1	Alignment	not modelled	99.9	18 Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
50	c4uw9A	Alignment	not modelled	99.9	13 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
51	c3nasA	Alignment	not modelled	99.9	15 PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
52	c2ympB	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: B: PDB Molecule: l-haloacid dehalogenase; PDBTitle: chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
					Fold: HAD-like

53	d2fi1a1	Alignment	not modelled	99.9	16	Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
54	c3cnhA	Alignment	not modelled	99.9	18	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
55	c2g80C	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: C: PDB Molecule: protein utr4; PDBTitle: crystal structure of utr4 protein (unknown transcript 4 protein)2 (yel038w) from saccharomyces cerevisiae at 2.28 a resolution
56	c4ygsA	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase; PDBTitle: crystal structure of had phosphatase from thermococcus onnurineus
57	c3vayB	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: had-superfamily hydrolase; PDBTitle: crystal structure of 2-haloacid dehalogenase from pseudomonas syringae2 pv. tomato dc3000
58	c3k1zA	Alignment	not modelled	99.9	19	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)
59	c3ed5A	Alignment	not modelled	99.9	15	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	c3smvA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: s(-)-azetidine-2-carboxylate hydrolase; PDBTitle: x-ray crystal structure of l-azetidine-2-carboxylate hydrolase
61	d2g80a1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
62	c2i6xA	Alignment	not modelled	99.9	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.
63	d2b0ca1	Alignment	not modelled	99.8	22	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
64	d2gmwa1	Alignment	not modelled	99.8	25	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
65	c4jb3A	Alignment	not modelled	99.8	18	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
66	c3esqA	Alignment	not modelled	99.8	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
67	c2ho4A	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127
68	c3l8hC	Alignment	not modelled	99.8	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
69	c3pdwA	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
70	c2w11B	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
71	d2o2xa1	Alignment	not modelled	99.8	25	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
72	c4dfdB	Alignment	not modelled	99.8	16	PDB header: hydrolase 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
73	c1cr6A	Alignment	not modelled	99.8	25	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
74	c3kzxA	Alignment	not modelled	99.8	9	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
75	c3qgmC	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
76	d2c4na1	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: NagD-like

77	d1u7pa_	Alignment	not modelled	99.8	18	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
78	c2x4dB_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
79	d1qvia_	Alignment	not modelled	99.8	24	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
80	d1vjra_	Alignment	not modelled	99.8	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
81	d1cr6a1	Alignment	not modelled	99.8	24	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
82	c4ig4A_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
83	c2x4dA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
84	c3kd3A_	Alignment	not modelled	99.8	8	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
85	d1wvia_	Alignment	not modelled	99.8	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
86	c4b6jA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
87	c2zg6A_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein st2620; PDBTitle: crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfobolus tokodaii
88	c2p11A_	Alignment	not modelled	99.7	16	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
89	d1yv9a1	Alignment	not modelled	99.7	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
90	d1ys9a1	Alignment	not modelled	99.7	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
91	d2fpwa1	Alignment	not modelled	99.7	24	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
92	d1ydfa1	Alignment	not modelled	99.7	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
93	c2cftA_	Alignment	not modelled	99.7	20	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
94	c4i9gB_	Alignment	not modelled	99.7	17	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
95	c2odaB_	Alignment	not modelled	99.7	27	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
96	c4jyrG_	Alignment	not modelled	99.7	25	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
97	c3m1yA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
98	d2feaa1	Alignment	not modelled	99.7	10	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
99	c1zjzA_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
100	c3ib6B_	Alignment	not modelled	99.6	22	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	d1j97a_	Alignment	not modelled	99.6	11	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase

102	d1nnla_	Alignment	not modelled	99.6	13	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
103	c2hx1D_	Alignment	not modelled	99.5	16	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
104	c2pr7A_	Alignment	not modelled	99.4	26	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
105	c3kc2A_	Alignment	not modelled	99.4	31	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
106	d1rkua_	Alignment	not modelled	99.4	15	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
107	d1q92a_	Alignment	not modelled	99.2	18	Fold: HAD-like Superfamily: HAD-like Family: 5'(3')-deoxyribonucleotidase (dnt-2)
108	c2i7dB_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: B: PDB Molecule: 5'(3')-deoxyribonucleotidase, cytosolic type; PDBTitle: structure of human cytosolic deoxyribonucleotidase in2 complex with deoxyuridine, alf4 and mg2+
109	c4ezeB_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family hydrolase t0658 from salmonella2 enterica subsp. enterica serovar typhi (target efi-501419)
110	c3fvvA_	Alignment	not modelled	99.2	14	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
111	c4hgnB_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: B: PDB Molecule: 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate PDBTitle: crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
112	c3p96A_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
113	d1wr8a_	Alignment	not modelled	99.1	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
114	c3mn1B_	Alignment	not modelled	99.0	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
115	c3e8mD_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidyltransferase; PDBTitle: structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
116	c4umfC_	Alignment	not modelled	99.0	20	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; PDBTitle: crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
117	d1k1ea_	Alignment	not modelled	99.0	19	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi
118	c3n28A_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
119	c2r8zC_	Alignment	not modelled	98.9	21	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
120	c3n07B_	Alignment	not modelled	98.9	14	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