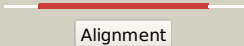

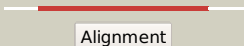

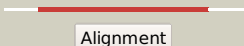







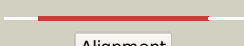











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3400_(-)_3817419_3818207
Date	Fri Aug 9 18:20:07 BST 2019
Unique Job ID	606f002d6264782b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iruA_	 Alignment		100.0	17	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
2	d1swva_	 Alignment		100.0	14	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
3	c3d6jA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
4	d2hsza1	 Alignment		99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
5	c3dv9A_	 Alignment		99.9	22	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
6	c3qypB_	 Alignment		99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
7	d1te2a_	 Alignment		99.9	22	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
8	c4ex7A_	 Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
9	c4uavA_	 Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidobsis thaliana
10	c4eekA_	 Alignment		99.9	26	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
11	d2fdra1	 Alignment		99.9	22	Fold: HAD-like Superfamily: HAD-liike Family: beta-Phosphoglucomutase-like

12	c3s6jC_	Alignment		99.9	26	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
13	c3mc1A_	Alignment		99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
14	c2hi0B_	Alignment		99.9	19	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
15	c4uasA_	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
16	d1zs9a1	Alignment		99.9	17	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
17	d2ah5a1	Alignment		99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
18	c2yy6B_	Alignment		99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
19	c3umgD_	Alignment		99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 rha0230
20	c3nuqA_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
21	c3umcC_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the I-2-haloacid dehalogenase pa0810
22	c2qltA_	Alignment	not modelled	99.9	18	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 PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
23	c3e58A_	Alignment	not modelled	99.9	23	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
24	d2hdoa1	Alignment	not modelled	99.9	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
25	c4g9bA_	Alignment	not modelled	99.9	26	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
26	c6f2xA_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
27	c4uw9A_	Alignment	not modelled	99.9	23	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
28	c3l5kA_	Alignment	not modelled	99.9	23	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)

29	c4gibA	Alignment	not modelled	99.9	26	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
30	c3sd7A	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
31	c2pibA	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
32	c3umbA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase rsc1362
33	d2hcfa1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
34	c2no5B	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
35	d2go7a1	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
36	d2gfha1	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
37	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
38	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
39	c3qnmA	Alignment	not modelled	99.9	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
40	c3qgmC	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
41	d1o08a	Alignment	not modelled	99.9	26	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
42	d1zrna	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
43	c2hoqA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
44	c3um9A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530
45	c3nasA	Alignment	not modelled	99.9	29	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
46	c3i28A	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
47	c3vayB	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: had-superfamily hydrolase; PDBTitle: crystal structure of 2-haloacid dehalogenase from pseudomonas syringae2 pv. tomato dc3000
48	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
49	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
50	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
51	c3k1zA	Alignment	not modelled	99.9	18	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	d1x42a1	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
53	c3m9IA	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

54	d1qq5a_	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
55	d1qyia_	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
56	c3pdwA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
57	d1zd3a1	Alignment	not modelled	99.9	12	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
58	d1vjra_	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
59	c2ho4A_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127
60	d2g80a1	Alignment	not modelled	99.9	10	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
61	c4ygsA_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase; PDBTitle: crystal structure of had phosphatase from thermococcus onnurineus
62	c2cftA_	Alignment	not modelled	99.8	17	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
63	c2pkeA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like family hydrolase; PDBTitle: crystal structure of haloacid dehalogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
64	d2gmwa1	Alignment	not modelled	99.8	26	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
65	c3smvA_	Alignment	not modelled	99.8	10	PDB header: hydrolase Chain: A: PDB Molecule: s(-)-azetidine-2-carboxylate hydrolase; PDBTitle: x-ray crystal structure of l-azetidine-2-carboxylate hydrolase
66	c3l8hC_	Alignment	not modelled	99.8	26	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
67	c2w11B_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfobolus2 tokodaii
68	c3esqA_	Alignment	not modelled	99.8	26	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
69	c4ig4A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
70	c2g80C_	Alignment	not modelled	99.8	9	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
71	c2p11A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bxe_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
72	d1ys9a1	Alignment	not modelled	99.8	11	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
73	d1wvia_	Alignment	not modelled	99.8	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
74	d2fi1a1	Alignment	not modelled	99.8	19	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
75	c4i9gB_	Alignment	not modelled	99.8	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
76	d2o2xa1	Alignment	not modelled	99.8	23	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
77	c2x4dA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp PDB header: unknown function

78	c3kd3A	Alignment	not modelled	99.8	13	Chain: A: PDB Molecule: phosphoserine phosphohydrolase-like protein; PDBTitle: crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
79	c3cnhA	Alignment	not modelled	99.8	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
80	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.
81	d2c4na1	Alignment	not modelled	99.8	10	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
82	d1yv9a1	Alignment	not modelled	99.8	12	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
83	c4jb3A	Alignment	not modelled	99.8	13	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
84	d1ydfa1	Alignment	not modelled	99.8	12	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
85	c3kzxA	Alignment	not modelled	99.8	13	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
86	c4dfdB	Alignment	not modelled	99.8	11	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
87	d1nlna	Alignment	not modelled	99.8	16	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
88	d1u7pa	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
89	c1cr6A	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
90	c2x4dB	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
91	d2b0ca1	Alignment	not modelled	99.7	12	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
92	c2odaB	Alignment	not modelled	99.7	21	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
93	c1zjA	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
94	c2hx1D	Alignment	not modelled	99.7	13	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
95	c4jyrG	Alignment	not modelled	99.7	22	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
96	d1cr6a1	Alignment	not modelled	99.7	16	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
97	d1j97a	Alignment	not modelled	99.7	16	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
98	c4b6jA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
99	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
100	d2fpwa1	Alignment	not modelled	99.7	24	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
101	c3ib6B	Alignment	not modelled	99.6	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

102	c2zg6A_	Alignment	not modelled	99.6	18	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
103	d2feaa1	Alignment	not modelled	99.6	13	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
104	d1rkua_	Alignment	not modelled	99.6	11	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
105	c3kc2A_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
106	c2pr7A_	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_59989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
107	c3p96A_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
108	c4hgnB_	Alignment	not modelled	99.3	17	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
109	d1wr8a_	Alignment	not modelled	99.3	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
110	c2r8zC_	Alignment	not modelled	99.3	22	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
111	c4zexA_	Alignment	not modelled	99.3	10	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
112	d1l6ra_	Alignment	not modelled	99.2	11	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
113	c2i7dB_	Alignment	not modelled	99.2	13	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+
114	c4ezeB_	Alignment	not modelled	99.2	9	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)
115	d1k1ea_	Alignment	not modelled	99.2	25	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
116	c3n28A_	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
117	c4umfC_	Alignment	not modelled	99.2	22	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
118	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
119	c3n07B_	Alignment	not modelled	99.2	21	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
120	c4qjbB_	Alignment	not modelled	99.1	11	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum