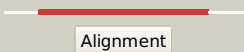

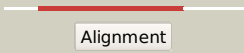

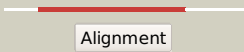

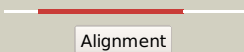

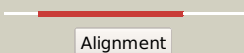

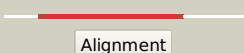

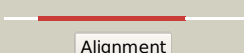





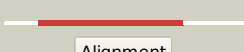

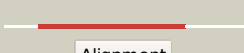









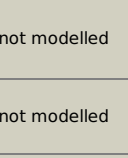


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1692_(-)_1916705_1917766
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	289a95a94ea68559

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4i9gB_	 Alignment		100.0	100	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
2	c3kc2A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
3	c2ho4A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127
4	c4ig4A_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearotherophilus
5	d1wvia_	 Alignment		100.0	30	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
6	d1ydfa1	 Alignment		100.0	33	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
7	c3qgmC_	 Alignment		100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
8	d1ys9a1	 Alignment		100.0	29	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
9	c2cftA_	 Alignment		100.0	33	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
10	d1yv9a1	 Alignment		100.0	33	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
11	c1zjzA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3

12	d2c4na1	Alignment		100.0	27	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
13	c3pdwA	Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
14	d1vjra	Alignment		100.0	28	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
15	c2x4dA	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
16	c2hx1D	Alignment		100.0	24	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
17	c2x4dB	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
18	d2fdra1	Alignment		99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
19	c3iruA	Alignment		99.9	17	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
20	c3d6jA	Alignment		99.9	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
21	c3dv9A	Alignment	not modelled	99.9	15	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
22	d2hsza1	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
23	c3umgD	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 rha0230
24	c3nuqA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
25	d2hdoa1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
26	c2hi0B	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphoglycolate phosphatase; PDBTitle: crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
27	d1swva	Alignment	not modelled	99.9	12	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
28	c3s6jC	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas

						syringae
29	c3qypB_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
30	c3umcC_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: C: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase pa0810
31	c4ex7A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
32	d1qvia_	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
33	c3mc1A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
34	c3qnmA_	Alignment	not modelled	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
35	c4g9bA_	Alignment	not modelled	99.9	14	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	c2om6A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
37	c2hogA_	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
38	c4eekA_	Alignment	not modelled	99.9	20	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
39	c3umbA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase rsc1362
40	d2ah5a1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
41	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
42	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
43	d1zs9a1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
44	d1zrna_	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
45	c3ed5A_	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yfnb; PDBTitle: the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
46	c3i28A_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
47	d2gfha1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
48	c3um9A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530
49	d1qq5a_	Alignment	not modelled	99.9	19	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
50	c4uavA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidobsis thaliana
51	d1te2a_	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
52	c3sd7A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
53	c3k1zA_	Alignment	not modelled	99.9	20	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)
						PDB header: hydrolase

54	c3l5kA	Alignment	not modelled	99.9	16	Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: the crystal structure of human haloacid dehalogenase-like hydrolase2 domain containing 1a (hdhd1a)
55	d2g80a1	Alignment	not modelled	99.9	10	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
56	c4uasA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
57	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
58	c2pibA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
59	c6f2xA	Alignment	not modelled	99.9	21	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
60	c2g80C	Alignment	not modelled	99.9	10	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
61	c2yy6B	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
62	d2hcfa1	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
63	d1x42a1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
64	d2o2xa1	Alignment	not modelled	99.9	22	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
65	c3ddhA	Alignment	not modelled	99.9	13	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
66	c3l8hC	Alignment	not modelled	99.9	25	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	c4rn3B	Alignment	not modelled	99.9	20	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
68	d2fi1a1	Alignment	not modelled	99.9	21	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
69	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
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	d2gmwa1	Alignment	not modelled	99.9	20	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
72	c3e58A	Alignment	not modelled	99.9	12	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
73	d2go7a1	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
74	c4gibA	Alignment	not modelled	99.9	12	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
75	c3esqA	Alignment	not modelled	99.9	18	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
76	c2p11A	Alignment	not modelled	99.9	9	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
77	c3m9lA	Alignment	not modelled	99.9	16	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
78	d1o08a_	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
79	c4uw9A_	Alignment	not modelled	99.9	12	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
80	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
81	d1zd3a1	Alignment	not modelled	99.8	12	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
82	c2w11B_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
83	c3cnhA_	Alignment	not modelled	99.8	14	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	c3ib6B_	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
85	c4ygsA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase; PDBTitle: crystal structure of had phosphatase from thermococcus onnurineus
86	c1cr6A_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
87	c2i6xA_	Alignment	not modelled	99.8	11	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	c4dfdB_	Alignment	not modelled	99.8	14	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
89	c4jb3A_	Alignment	not modelled	99.8	11	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
90	c3nasA_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
91	d1cr6a1	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
92	d1u7pa_	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
93	d2b0ca1	Alignment	not modelled	99.8	10	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
94	c2odaB_	Alignment	not modelled	99.8	18	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
95	c3kzxA_	Alignment	not modelled	99.7	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
96	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
97	c3kd3A_	Alignment	not modelled	99.7	7	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
98	c2pr7A_	Alignment	not modelled	99.6	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
99	c4b6iA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
100	c2zg6A_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein st2620; PDBTitle: crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfolobus tokodaii

101	d2fpwa1	Alignment	not modelled	99.6	28	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
102	d1nna_	Alignment	not modelled	99.5	14	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
103	c3m1yA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
104	d2feaa1	Alignment	not modelled	99.4	12	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
105	d1j97a_	Alignment	not modelled	99.3	13	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
106	d1wr8a_	Alignment	not modelled	99.3	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
107	c4hgnB_	Alignment	not modelled	99.1	30	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
108	d1rkua_	Alignment	not modelled	99.1	13	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
109	d1l6ra_	Alignment	not modelled	99.1	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
110	c4zexA_	Alignment	not modelled	99.0	17	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
111	d1vj5a1	Alignment	not modelled	98.9	39	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
112	c3mn1B_	Alignment	not modelled	98.9	27	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
113	c3n07B_	Alignment	not modelled	98.9	28	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
114	c4qjbB_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
115	c2qyhD_	Alignment	not modelled	98.8	18	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
116	c3zvmA_	Alignment	not modelled	98.8	19	PDB header: hydrolase/transferase/dna phosphatase/kinase; Chain: A: PDB Molecule: bifunctional polynucleotide phosphatase/kinase; PDBTitle: the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
117	c3dnpA_	Alignment	not modelled	98.8	12	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
118	c4umfC_	Alignment	not modelled	98.8	28	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
119	c2r8zC_	Alignment	not modelled	98.8	28	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	c3fzqA_	Alignment	not modelled	98.7	12	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