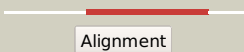

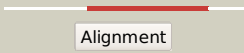

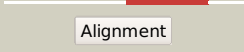

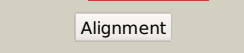



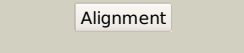

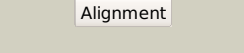



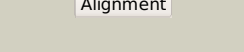

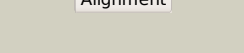

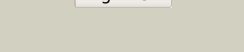












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2006_otsB1_2252010_2255993
Date	Mon Aug 5 13:25:11 BST 2019
Unique Job ID	78a4682eece09ab1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ktrE_	 Alignment		100.0	29	PDB header: transferase Chain: E: PDB Molecule: glycoside hydrolase family 65 central catalytic; PDBTitle: crystal structure of 2-o-alpha-glucosylglycerol phosphorylase in2 complex with isofagomine and glycerol
2	c1h54B_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: maltose phosphorylase; PDBTitle: maltose phosphorylase from lactobacillus brevis
3	d1h54a1	 Alignment		100.0	27	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
4	c2rdyB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: bh0842 protein; PDBTitle: crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
5	c4ufcA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: gh95; PDBTitle: crystal structure of the gh95 enzyme bacova_03438
6	c5gvxA_	 Alignment		100.0	56	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-phosphate phosphatase; PDBTitle: structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
7	c2eacB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-fucosidase; PDBTitle: crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
8	d1h54a2	 Alignment		100.0	21	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
9	c5dx9A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of trehalose-6-phosphate phosphatase from cryptococcus2 neoformans
10	d1v7wa1	 Alignment		100.0	12	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
11	c5husA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: trehalose synthase regulatory protein; PDBTitle: structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain

12	c2cqtA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: cellobiose phosphorylase; PDBTitle: crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
13	c5dxiB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
14	c4zlgA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: putative b-glycan phosphorylase; PDBTitle: cellobionic acid phosphorylase - gluconic acid complex
15	c1v7wA_	Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: chitobiose phosphorylase; PDBTitle: crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
16	c5dxiA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
17	d1u02a_	Alignment		99.9	23	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
18	c3iruA_	Alignment		99.8	15	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
19	d1swva_	Alignment		99.8	14	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
20	c4uw9A_	Alignment		99.8	22	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
21	c3dv9A_	Alignment	not modelled	99.8	16	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
22	c3d6jA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
23	c2qltA_	Alignment	not modelled	99.7	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
24	d1te2a_	Alignment	not modelled	99.7	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
25	c5h42A_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 1,2-beta-oligoglucan phosphorylase from2 lachnoclostridium phytofermentans in complex with alpha-d-glucose-1-3 phosphate
26	c3s6jC_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
27	d1qyia_	Alignment	not modelled	99.7	17	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
28	c3nuvA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase;

28	c1bqa	Alignment	not modelled	99.7	14	PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
29	d2fdra1	Alignment	not modelled	99.7	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
30	d2hsza1	Alignment	not modelled	99.7	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
31	c4ex7A	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
32	d2ah5a1	Alignment	not modelled	99.7	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
33	c3gypB	Alignment	not modelled	99.7	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
34	c2odaB	Alignment	not modelled	99.7	19	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
35	c4g9bA	Alignment	not modelled	99.7	21	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	c4eekA	Alignment	not modelled	99.7	31	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
37	c3mc1A	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
38	c3l5kA	Alignment	not modelled	99.6	15	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)
39	c2pibA	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
40	c4uasA	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
41	c2hi0B	Alignment	not modelled	99.6	20	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
42	d1zs9a1	Alignment	not modelled	99.6	9	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
43	c4uavA	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidopsis thaliana
44	c4gibA	Alignment	not modelled	99.6	17	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
45	c3i28A	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
46	c3e58A	Alignment	not modelled	99.6	19	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
47	c3nasA	Alignment	not modelled	99.6	18	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
48	d2go7a1	Alignment	not modelled	99.6	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
49	c3sd7A	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
50	c6f2xA	Alignment	not modelled	99.5	16	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
51	c5nz8A	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
52	d2hdoa1	Alignment	not modelled	99.5	11	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
						Fold: HAD-like

53	d1o08a_	Alignment	not modelled	99.5	19	Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
54	c2yy6B_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
55	c2hoqA_	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
56	d2gfha1	Alignment	not modelled	99.5	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
57	c3umcC_	Alignment	not modelled	99.5	10	PDB header: hydrolase Chain: C: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the I-2-haloacid dehalogenase pa0810
58	c4rn3B_	Alignment	not modelled	99.5	14	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
59	d2hcfA1	Alignment	not modelled	99.5	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
60	d2g80a1	Alignment	not modelled	99.5	11	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
61	c5nz7A_	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
62	d1zd3a1	Alignment	not modelled	99.5	14	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
63	c3qnmA_	Alignment	not modelled	99.5	10	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
64	c6ggyA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: laminaribiose phosphorylase; PDBTitle: paenibacillus sp. ym1 laminaribiose phosphorylase with sulphate bound
65	c3vayB_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: B: PDB Molecule: had-superfamily hydrolase; PDBTitle: crystal structure of 2-haloacid dehalogenase from pseudomonas syringae2 pv. tomato dc3000
66	c2g80C_	Alignment	not modelled	99.4	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
67	c3umbA_	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the I-2-haloacid dehalogenase rsc1362
68	d1qq5a_	Alignment	not modelled	99.4	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
69	c2no5B_	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
70	c3umgD_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 rha0230
71	d1zrna_	Alignment	not modelled	99.4	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
72	c1cr6A_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
73	c2pkeA_	Alignment	not modelled	99.4	12	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
74	c3um9A_	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 bpro0530
75	c3l8hC_	Alignment	not modelled	99.4	28	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
76	c4ygsA_	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase; PDBTitle: crystal structure of had phosphatase from thermococcus onnurineus
77	d2gmwa1	Alignment	not modelled	99.3	13	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
						PDB header: hydrolase

78	c2ympB_	Alignment	not modelled	99.3	20	Chain: B: PDB Molecule: l-haloacid dehalogenase; PDBTitle: chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
79	c3cnhA_	Alignment	not modelled	99.3	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
80	d1x42a1	Alignment	not modelled	99.3	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
81	c3esqA_	Alignment	not modelled	99.3	13	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
82	d1cr6a1	Alignment	not modelled	99.2	17	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
83	c4zexA_	Alignment	not modelled	99.2	17	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
84	c2w11B_	Alignment	not modelled	99.2	12	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfobolus2 tokodaii
85	c3pgvB_	Alignment	not modelled	99.2	22	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
86	c2x4dB_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
87	c3m9IA_	Alignment	not modelled	99.2	20	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
88	d1s2oa1	Alignment	not modelled	99.2	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
89	d2fi1a1	Alignment	not modelled	99.2	14	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
90	c3ddhA_	Alignment	not modelled	99.2	9	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
91	d2o2xa1	Alignment	not modelled	99.2	18	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
92	c3kd3A_	Alignment	not modelled	99.2	13	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
93	c2i6xA_	Alignment	not modelled	99.2	14	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.
94	c4b6jA_	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
95	c3qgmC_	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
96	c3k1zA_	Alignment	not modelled	99.2	15	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)
97	c3ib6B_	Alignment	not modelled	99.1	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
98	c4i9gB_	Alignment	not modelled	99.1	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
99	c3zupB_	Alignment	not modelled	99.1	26	PDB header: hydrolase Chain: B: PDB Molecule: mannosyl-3-phosphoglycerate phosphatase; PDBTitle: the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
100	c3ed5A_	Alignment	not modelled	99.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yfnb; PDBTitle: the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
101	c3cmvA_	Alignment	not modelled	99.1	7	PDB header: hydrolase Chain: A: PDB Molecule: s(-)-azetidine-2-carboxylate hydrolase;

101	c3niwA_	Alignment	not modelled	99.1	7	PDBTitle: x-ray crystal structure of l-azetidine-2-carboxylate hydrolase
102	d2rbka1	Alignment	not modelled	99.1	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
103	c3niwA_	Alignment	not modelled	99.1	18	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
104	c2om6A_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
105	d2b0ca1	Alignment	not modelled	99.1	14	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
106	d2feaa1	Alignment	not modelled	99.1	8	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
107	c2ho4A_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127
108	d1nf2a_	Alignment	not modelled	99.1	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
109	c6i60B_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha-rhamnosidase; PDBTitle: structure of alpha-l-rhamnosidase from dictyoglumus thermophilum
110	d1u7pa_	Alignment	not modelled	99.1	20	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
111	d1nnla_	Alignment	not modelled	99.1	17	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
112	d1xvia_	Alignment	not modelled	99.1	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
113	c1xviA_	Alignment	not modelled	99.1	18	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
114	c3fzqA_	Alignment	not modelled	99.1	21	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
115	c2zg6A_	Alignment	not modelled	99.1	16	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
116	c3m1yA_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
117	d1j97a_	Alignment	not modelled	99.0	18	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
118	d2c4na1	Alignment	not modelled	99.0	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
119	c3gygA_	Alignment	not modelled	99.0	14	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
120	c2p11A_	Alignment	not modelled	99.0	14	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