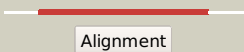

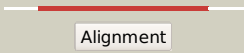



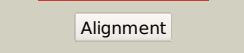



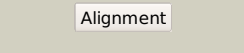

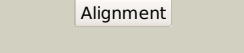



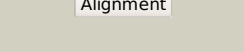

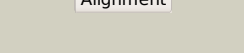

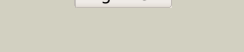



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3113 (-)_3480071_3480739
Date	Thu Aug 8 16:20:29 BST 2019
Unique Job ID	5570670f94ba92d8

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	c3d6jA_	 Alignment		100.0	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
3	d2ah5a1	 Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
4	c4ex7A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
5	d1swva_	 Alignment		100.0	10	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
6	c3s6jC_	 Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
7	c3mc1A_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
8	d2fdra1	 Alignment		100.0	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
9	c6f2xA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
10	d2hsza1	 Alignment		100.0	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
11	c2hi0B_	 Alignment		100.0	15	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

12	c3dv9A_	Alignment		100.0	12	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
13	c3l5kA_	Alignment		100.0	12	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)
14	c2yy6B_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
15	d1te2a_	Alignment		100.0	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
16	c2pibA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
17	c4eekA_	Alignment		100.0	16	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
18	c3qypB_	Alignment		100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
19	d2hdoa1	Alignment		100.0	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
20	c3sd7A_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
21	d2go7a1	Alignment	not modelled	100.0	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
22	c3e58A_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
23	c4uasA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
24	c2hogA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
25	c3nuqA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
26	c2qltA_	Alignment	not modelled	100.0	10	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
27	c3umcC_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase pa0810
28	c4g9bA_	Alignment	not modelled	100.0	12	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 PDB header: hydrolase

29	c3umgD_	Alignment	not modelled	100.0	16	Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 rha0230
30	c4rn3B_	Alignment	not modelled	100.0	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
31	d2hcfal	Alignment	not modelled	100.0	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
32	d1o08a_	Alignment	not modelled	99.9	11	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
33	c3umbA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the I-2-haloacid dehalogenase rsc1362
34	c2no5B_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
35	c4uavA_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidopsis thaliana
36	c3qnmA_	Alignment	not modelled	99.9	14	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
37	c4ygsA_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase; PDBTitle: crystal structure of had phosphatase from thermococcus onnurineus
38	c3ddhA_	Alignment	not modelled	99.9	11	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
39	d1zrna_	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
40	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
41	d1x42a1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
42	c4gibA_	Alignment	not modelled	99.9	13	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
43	d2gfha1	Alignment	not modelled	99.9	12	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
44	c4uw9A_	Alignment	not modelled	99.9	17	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
45	c3um9A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 bpro0530
46	c2ympB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: l-haloacid dehalogenase; PDBTitle: chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
47	d1zs9a1	Alignment	not modelled	99.9	12	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
48	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
49	d2f1a1	Alignment	not modelled	99.9	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
50	c2w11B_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the I-2-haloacid dehalogenase from sulfolobus2 tokodaii
51	c2pkeA_	Alignment	not modelled	99.9	16	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
52	c3ed5A_	Alignment	not modelled	99.9	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
53	c3smvA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: s(-)-azetidine-2-carboxylate hydrolase; PDBTitle: x-ray crystal structure of l-azetidine-2-carboxylate

						hydrolase
54	d1qq5a_	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
55	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)
56	c3vayB_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: had-superfamily hydrolase; PDBTitle: crystal structure of 2-haloacid dehalogenase from pseudomonas syringae2 pv. tomato dc3000
57	c3nasA_	Alignment	not modelled	99.9	13	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
58	c3l8hC_	Alignment	not modelled	99.9	16	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
59	c2x4dB_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
60	c3kd3A_	Alignment	not modelled	99.9	11	PDB header: unknown function Chain: A: PDB Molecule: phosphoserine phosphohydrolase-like protein; PDBTitle: crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
61	c2p11A_	Alignment	not modelled	99.9	10	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
62	c2ho4A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127
63	c3qgmC_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
64	d2g80a1	Alignment	not modelled	99.9	12	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
65	c2g80C_	Alignment	not modelled	99.9	11	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
66	c3cnhA_	Alignment	not modelled	99.9	12	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
67	c3i28A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
68	d1vjra_	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
69	c2x4dA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
70	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
71	d1u7pa_	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
72	c4b6jA_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
73	d2c4na1	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
74	d2gmwa1	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
75	c3kzxA_	Alignment	not modelled	99.9	15	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
76	c3esqA_	Alignment	not modelled	99.9	17	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
						Fold: HAD-like

77	d1wvia_	Alignment	not modelled	99.9	14	Superfamily: HAD-like Family: NagD-like
78	d1zd3a1	Alignment	not modelled	99.9	11	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
79	c4ig4A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
80	c1zjA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
81	d1ydfa1	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
82	d1qyia_	Alignment	not modelled	99.8	15	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
83	d2feaa1	Alignment	not modelled	99.8	12	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
84	d2o2xa1	Alignment	not modelled	99.8	18	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
85	c4jyrG_	Alignment	not modelled	99.8	17	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
86	c2zq6A_	Alignment	not modelled	99.8	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
87	d1yv9a1	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
88	c4i9gB_	Alignment	not modelled	99.8	16	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
89	d1ys9a1	Alignment	not modelled	99.8	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
90	c1cr6A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
91	c2i6xA_	Alignment	not modelled	99.8	12	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.
92	c2cftA_	Alignment	not modelled	99.8	19	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
93	d2b0ca1	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
94	c3m1yA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
95	c2odaB_	Alignment	not modelled	99.8	11	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
96	d1j97a_	Alignment	not modelled	99.8	14	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
97	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
98	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
99	c3ib6B_	Alignment	not modelled	99.8	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
100	d1nna_	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
101	d1cr6a1	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
102	d2fpwa1	Alignment	not modelled	99.8	16	Fold: HAD-like Superfamily: HAD-like

						Family: Histidinol phosphatase-like
103	c2hx1D_	Alignment	not modelled	99.7	12	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	c3kc2A_	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
105	d1rkua_	Alignment	not modelled	99.6	14	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
106	d1q92a_	Alignment	not modelled	99.6	13	Fold: HAD-like Superfamily: HAD-like Family: 5'(3')-deoxyribonucleotidase (dNT-2)
107	c4ezeB_	Alignment	not modelled	99.6	11	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)
108	c2i7dB_	Alignment	not modelled	99.6	14	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	c3p96A_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
110	c2pr7A_	Alignment	not modelled	99.5	16	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
111	c3n28A_	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
112	c4hgnB_	Alignment	not modelled	99.4	11	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
113	c3fvvA_	Alignment	not modelled	99.4	13	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
114	c3mn1B_	Alignment	not modelled	99.4	24	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	c4umfC_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdc5; 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
116	c3e8mD_	Alignment	not modelled	99.3	23	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidylyltransferase; 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
117	d1k1ea_	Alignment	not modelled	99.3	23	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
118	d2vkqa1	Alignment	not modelled	99.3	18	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
119	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
120	c2p9jH_	Alignment	not modelled	99.2	19	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus