

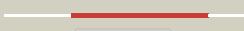














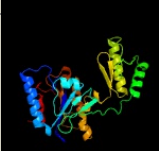



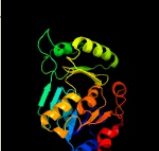


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3372_(otsB2)_3786494_3787669
 Date Fri Aug 9 18:20:03 BST 2019
 Unique Job ID 271c74a05231d146

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gvxA_	 Alignment		100.0	99	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-phosphate phosphatase; PDBTitle: structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
2	c5dx9A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of trehalose-6-phosphate phosphatase from cryptococcus2 neoformans
3	c5dxiB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
4	c5dxIA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
5	c5husA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: trehalose synthase regulatory protein; PDBTitle: structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain
6	d1u02a_	 Alignment		100.0	22	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
7	c3dnpA_	 Alignment		100.0	11	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
8	c4zexA_	 Alignment		100.0	13	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
9	c3gygA_	 Alignment		100.0	15	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
10	c3niwA_	 Alignment		100.0	16	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
11	c3pgvB_	 Alignment		100.0	21	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

12	d1nrwa_	Alignment		100.0	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
13	c3fzqA_	Alignment		100.0	15	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
14	d1nf2a_	Alignment		100.0	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
15	c2qyhD_	Alignment		100.0	17	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
16	d1rlma_	Alignment		100.0	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
17	d1s2oa1	Alignment		100.0	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
18	c3daoB_	Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
19	d2rbka1	Alignment		100.0	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
20	c3zupB_	Alignment		100.0	22	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.
21	c4qjbB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
22	c3r4cA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like hydrolase; PDBTitle: divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
23	c3l7yA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
24	d2b30a1	Alignment	not modelled	100.0	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
25	c4bndB_	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: B: PDB Molecule: alpha-phosphoglucomutase; PDBTitle: structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
26	d1xvia_	Alignment	not modelled	100.0	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
27	c1xviA_	Alignment	not modelled	100.0	15	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 PDB header: isomerase

28	c2i55C_	Alignment	not modelled	100.0	23	Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
29	d2amyA1	Alignment	not modelled	100.0	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
30	d1wr8a_	Alignment	not modelled	100.0	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
31	c6cj0A_	Alignment	not modelled	99.9	15	PDB header: lyase Chain: A: PDB Molecule: trehalose phosphatase; PDBTitle: chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
32	d1rkqa_	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
33	c5ue7A_	Alignment	not modelled	99.9	19	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: crystal structure of the phosphomannomutase pmm1 from candida2 albicans, apoenzyme state
34	c3mpoD_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
35	d2fuea1	Alignment	not modelled	99.9	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
36	d1l6ra_	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
37	d1wzca1	Alignment	not modelled	99.9	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
38	d1k1ea_	Alignment	not modelled	99.8	25	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
39	c2r8zC_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbl phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
40	c4hgnB_	Alignment	not modelled	99.8	19	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
41	c3n07B_	Alignment	not modelled	99.7	26	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
42	c3mn1B_	Alignment	not modelled	99.7	30	PDB header: hydrolase Chain: B: PDB Molecule: probable yrbl family phosphatase; PDBTitle: crystal structure of probable yrbl family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
43	c4umfC_	Alignment	not modelled	99.7	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
44	c3mmzA_	Alignment	not modelled	99.7	29	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
45	c3e8mD_	Alignment	not modelled	99.7	20	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidyltransferase; PDBTitle: structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
46	c3ewiB_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
47	c4navB_	Alignment	not modelled	99.7	28	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
48	c3n1uA_	Alignment	not modelled	99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, had superfamily, subfamily iii a; PDBTitle: structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
49	c2p9jH_	Alignment	not modelled	99.7	21	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
50	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
51	c2cftA_	Alignment	not modelled	99.7	18	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
						PDB header: hydrolase

52	c3p96A	Alignment	not modelled	99.6	16	Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
53	c3n28A	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
54	c3pdwA	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
55	d1j97a	Alignment	not modelled	99.5	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
56	d1yv9a1	Alignment	not modelled	99.5	17	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
57	c4ezeB	Alignment	not modelled	99.5	34	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)
58	c3fvvA	Alignment	not modelled	99.5	17	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
59	d1ydfa1	Alignment	not modelled	99.5	17	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
60	d1wvia	Alignment	not modelled	99.5	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
61	d1rkua	Alignment	not modelled	99.4	15	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
62	c1zja	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
63	c3kd3A	Alignment	not modelled	99.4	18	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
64	d1ys9a1	Alignment	not modelled	99.4	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
65	c3m1yA	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
66	d1nnla	Alignment	not modelled	99.3	23	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
67	c2odaB	Alignment	not modelled	99.2	22	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
68	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
69	c2x4dA	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
70	c4ig4A	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
71	c4b6jA	Alignment	not modelled	99.1	24	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
72	d2c4na1	Alignment	not modelled	99.1	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
73	d1vjra	Alignment	not modelled	99.1	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
74	d2feaa1	Alignment	not modelled	99.1	17	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
75	d2o2xa1	Alignment	not modelled	99.0	19	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
76	d2gmwa1	Alignment	not modelled	99.0	22	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
77	c2iyeC	Alignment	not modelled	99.0	19	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
						PDB header: hydrolase Chain: A: PDB Molecule: d,d-heptose 1,7-bisphosphate

78	c3esqA_	Alignment	not modelled	99.0	23	phosphatase; PDBTitle: crystal structure of calcium-bound d,d-heptose 1,7-bisphosphate2 phosphatase from e. coli PDB header: hydrolase
79	c2ho4A_	Alignment	not modelled	98.9	18	Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain containing 2; PDBTitle: crystal structure of protein from mouse mm.236127 PDB header: hydrolase
80	c3l8hC_	Alignment	not modelled	98.9	18	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 PDB header: hydrolase
81	c3skyA_	Alignment	not modelled	98.8	23	Chain: A: PDB Molecule: copper-exporting p-type atpase b; PDBTitle: 2.1a crystal structure of the phosphate bound atp binding domain of2 archaeoglobus fulgidus copb PDB header: structural genomics, unknown function
82	c3iruA_	Alignment	not modelled	98.8	23	Chain: A: PDB Molecule: phosphonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phosphonoacetaldehyde hydrolase like protein from2 oleispira antarctica PDB header: hydrolase
83	c2pibA_	Alignment	not modelled	98.8	15	Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima PDB header: hydrolase
84	c2hi0B_	Alignment	not modelled	98.7	14	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 PDB header: hydrolase
85	d1u7pa_	Alignment	not modelled	98.7	19	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
86	c3m9lA_	Alignment	not modelled	98.7	24	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: crystal structure of probable had family hydrolase from pseudomonas2 fluorescens pf-5
87	c3rfuC_	Alignment	not modelled	98.6	19	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
88	d1y8aa1	Alignment	not modelled	98.6	14	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
89	d1wpga2	Alignment	not modelled	98.6	22	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
90	c2qltA_	Alignment	not modelled	98.6	20	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
91	d1swva_	Alignment	not modelled	98.5	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
92	c3j09A_	Alignment	not modelled	98.5	23	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa PDB header: hydrolase, metal transport
93	c3j08A_	Alignment	not modelled	98.5	24	Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
94	d1x42a1	Alignment	not modelled	98.4	13	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
95	d1qvia_	Alignment	not modelled	98.4	28	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
96	d1cr6a1	Alignment	not modelled	98.4	34	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
97	c3s6jC_	Alignment	not modelled	98.4	26	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
98	d1te2a_	Alignment	not modelled	98.3	23	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
99	d2b8ea1	Alignment	not modelled	98.3	28	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
100	c4jyrG_	Alignment	not modelled	98.3	29	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
101	d1xpa_	Alignment	not modelled	98.3	22	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
102	d2hdoa1	Alignment	not modelled	98.2	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like

103	c4umwA_	Alignment	not modelled	98.2	25	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
104	d2fpwa1	Alignment	not modelled	98.2	22	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
105	d2obba1	Alignment	not modelled	98.2	25	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
106	c5mrwF_	Alignment	not modelled	98.2	15	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
107	c3kc2A_	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
108	c2no5B_	Alignment	not modelled	98.2	22	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
109	c3qypB_	Alignment	not modelled	98.2	22	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
110	d2fdra1	Alignment	not modelled	98.2	33	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
111	c4ex7A_	Alignment	not modelled	98.2	33	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
112	d2hsza1	Alignment	not modelled	98.1	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
113	c2om6A_	Alignment	not modelled	98.1	16	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
114	c3b9ba_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
115	d2vkqa1	Alignment	not modelled	98.1	18	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
116	c3mc1A_	Alignment	not modelled	98.1	26	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
117	c3kzxA_	Alignment	not modelled	98.1	14	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
118	c3dv9A_	Alignment	not modelled	98.1	19	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
119	c3d6jA_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
120	d2ah5a1	Alignment	not modelled	98.0	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like