Email	mdejesus@rockefeller.edu
Description	RVBD3813c_(-)_4278572_4279393
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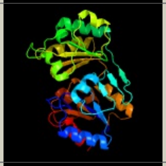
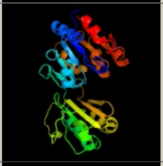
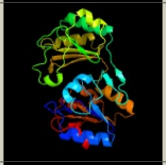
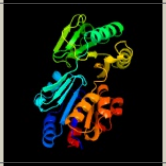
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dnpA_	Alignment		100.0	24	**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
2	c3niwA_	Alignment		100.0	25	**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
3	c4zexA_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pfhad1; **PDBTitle:** crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
4	d1nrwa_	Alignment		100.0	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
5	c3fzqA_	Alignment		100.0	16	**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
6	c3pgvB_	Alignment		100.0	24	**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
7	d1rlma_	Alignment		100.0	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
8	c3daoB_	Alignment		100.0	18	**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
9	c4qjbB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
10	d1nf2a_	Alignment		100.0	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
11	c2qyhD_	Alignment		100.0	26	**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

12	d2b30a1	Alignment		100.0	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
13	c3l7yA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1108c; **PDBTitle:** the crystal structure of smu.1108c from streptococcus mutans ua159
14	d2rbka1	Alignment		100.0	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
15	d1rkqa_	Alignment		100.0	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
16	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
17	c3r4cA_	Alignment		100.0	25	**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
18	d1wr8a_	Alignment		100.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
19	d1s2oa1	Alignment		100.0	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
20	d1l6ra_	Alignment		100.0	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
21	c3zupB_	Alignment	not modelled	100.0	21	**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.
22	c3mpoD_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
23	c4bndB_	Alignment	not modelled	100.0	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alpha-phosphoglucomutase; **PDBTitle:** structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
24	c2i55C_	Alignment	not modelled	100.0	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
25	c1xviA_	Alignment	not modelled	100.0	17	**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
26	d1xvia_	Alignment	not modelled	100.0	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
27	d2amya1	Alignment	not modelled	100.0	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
						PDB header:isomerase

28	c5ue7A_	Alignment	not modelled	100.0	14	**Chain:** A: **PDB Molecule:**phosphomannomutase; **PDBTitle:** crystal structure of the phosphomannomutase pmm1 from candida2 albicans, apoenzyme state
29	c5dxlA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-6-phosphate phosphatase; **PDBTitle:** structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
30	c5gvxA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-phosphate phosphatase; **PDBTitle:** structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
31	d1wzca1	Alignment	not modelled	100.0	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
32	c6cj0A_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trehalose phosphatase; **PDBTitle:** chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
33	d2fuea1	Alignment	not modelled	100.0	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
34	d1u02a_	Alignment	not modelled	100.0	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
35	c5dxiB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trehalose-6-phosphate phosphatase; **PDBTitle:** structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
36	c3n28A_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase; **PDBTitle:** crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
37	c3mmzA_	Alignment	not modelled	99.9	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
38	d1k1ea_	Alignment	not modelled	99.9	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
39	c3e8mD_	Alignment	not modelled	99.9	28	**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
40	c3p96A_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
41	c4umfC_	Alignment	not modelled	99.9	31	**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
42	c2r8zC_	Alignment	not modelled	99.9	35	**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
43	c3ewiB_	Alignment	not modelled	99.9	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
44	c4hgnB_	Alignment	not modelled	99.9	32	**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
45	c5dx9A_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-6-phosphate phosphatase; **PDBTitle:** structure of trehalose-6-phosphate phosphatase from cryptococcus2 neoformans
46	c3mn1B_	Alignment	not modelled	99.9	31	**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
47	c3n1uA_	Alignment	not modelled	99.9	34	**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
48	c3n07B_	Alignment	not modelled	99.9	34	**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
49	c4navB_	Alignment	not modelled	99.9	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein xcc279; **PDBTitle:** crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
50	c2p9jH_	Alignment	not modelled	99.9	24	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
51	c4ezeB_	Alignment	not modelled	99.9	16	**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)
52	d1j97a_	Alignment	not modelled	99.8	18	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: Phosphoserine phosphatase
53	d1rkua_	Alignment	not modelled	99.8	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
54	c3fvvA_	Alignment	not modelled	99.8	18	**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
55	c2iyeC_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b
56	d1wpga2	Alignment	not modelled	99.7	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
57	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
58	c3m1yA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
59	c2cftA_	Alignment	not modelled	99.7	15	**PDB header:**phosphatase **Chain:** A: **PDB Molecule:**pyridoxal phosphate phosphatase; **PDBTitle:** crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
60	c5mrwF_	Alignment	not modelled	99.7	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**potassium-transporting atpase atp-binding subunit; **PDBTitle:** structure of the kdpfabc complex
61	c5husA_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trehalose synthase regulatory protein; **PDBTitle:** structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain
62	d1nnla_	Alignment	not modelled	99.6	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
63	c3rfuC_	Alignment	not modelled	99.6	29	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
64	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
65	c3skyA_	Alignment	not modelled	99.6	29	**PDB header:**hydrolase **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
66	c4umwA_	Alignment	not modelled	99.6	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
67	d1yv9a1	Alignment	not modelled	99.6	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
68	c3j08A_	Alignment	not modelled	99.6	32	**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
69	c1mhsA_	Alignment	not modelled	99.6	21	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
70	c3b9bA_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
71	c3j09A_	Alignment	not modelled	99.6	30	**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
72	d1wvia_	Alignment	not modelled	99.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
73	c3kd3A_	Alignment	not modelled	99.5	16	**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
74	c2zxeA_	Alignment	not modelled	99.5	28	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
75	d1y8aa1	Alignment	not modelled	99.5	31	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**AF1437-like
76	d1ydfa1	Alignment	not modelled	99.5	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
77	c3ixzA_	Alignment	not modelled	99.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
						PDB header:hydrolase/transport protein

78	c3b8eC_	Alignment	not modelled	99.5	22	**Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
79	d1ys9a1	Alignment	not modelled	99.5	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
80	c6a69A_	Alignment	not modelled	99.4	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**plasma membrane calcium-transporting atpase 1; **PDBTitle:** cryo-em structure of a p-type atpase
81	d2b8ea1	Alignment	not modelled	99.4	35	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
82	c3b8cB_	Alignment	not modelled	99.4	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
83	c1zjjA_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ph1952; **PDBTitle:** crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
84	d2c4na1	Alignment	not modelled	99.3	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
85	c4ig4A_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable nppase; **PDBTitle:** crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
86	d1vjra_	Alignment	not modelled	99.2	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
87	c4b6jA_	Alignment	not modelled	99.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase; **PDBTitle:** crystal structure of phosphoserine phosphatase from t.2 onnurineus
88	c2b8eB_	Alignment	not modelled	99.2	34	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain
89	d2feaa1	Alignment	not modelled	99.2	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**MtnX-like
90	c6roiA_	Alignment	not modelled	99.2	16	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**probable phospholipid-transporting atpase drs2; **PDBTitle:** cryo-em structure of the partially activated drs2p-cdc50p
91	c3qgmC_	Alignment	not modelled	99.2	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**p-nitrophenyl phosphatase (pho2); **PDBTitle:** p-nitrophenyl phosphatase from archaeoglobus fulgidus
92	c2x4dA_	Alignment	not modelled	99.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholysine phosphohistidine inorganic pyrophosphate **PDBTitle:** crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
93	d1zs9a1	Alignment	not modelled	98.9	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
94	d1u7pa_	Alignment	not modelled	98.9	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
95	c2pibA_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphorylated carbohydrates phosphatase tm_1254; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
96	d2gmwa1	Alignment	not modelled	98.8	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
97	c4uavA_	Alignment	not modelled	98.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain-containing **PDBTitle:** crystal structure of cbby (at3g48420) from arabidobsis thaliana
98	c3esqA_	Alignment	not modelled	98.7	19	**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
99	c3l8hC_	Alignment	not modelled	98.7	23	**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
100	c3iruA_	Alignment	not modelled	98.6	14	**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
101	c2ho4A_	Alignment	not modelled	98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain containing 2; **PDBTitle:** crystal structure of protein from mouse mm.236127
102	d2hcfa1	Alignment	not modelled	98.6	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like

103	d2o2xa1	Alignment	not modelled	98.6	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
104	d2fdra1	Alignment	not modelled	98.5	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
105	d1xpja_	Alignment	not modelled	98.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
106	c3kzxA_	Alignment	not modelled	98.5	18	**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
107	d2obba1	Alignment	not modelled	98.5	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
108	c3mc1A_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted phosphatase, had family; **PDBTitle:** crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
109	c2hi0B_	Alignment	not modelled	98.4	14	**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
110	c4jyrG_	Alignment	not modelled	98.4	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
111	d1ltqa1	Alignment	not modelled	98.4	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
112	c4gibA_	Alignment	not modelled	98.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
113	d2hsza1	Alignment	not modelled	98.4	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
114	d2fpwa1	Alignment	not modelled	98.4	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
115	d1swva_	Alignment	not modelled	98.4	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
116	c2w11B_	Alignment	not modelled	98.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2-haloalkanoic acid dehalogenase; **PDBTitle:** structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
117	d1x42a1	Alignment	not modelled	98.4	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
118	d1te2a_	Alignment	not modelled	98.3	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
119	c3m9lA_	Alignment	not modelled	98.3	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
120	d1cr6a1	Alignment	not modelled	98.3	33	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like