
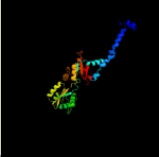
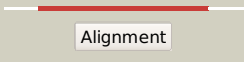
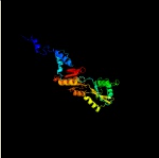
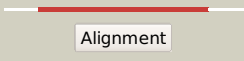
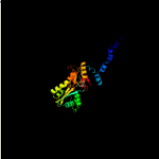
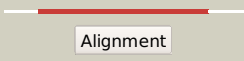
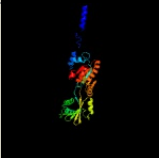
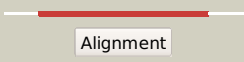
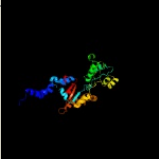
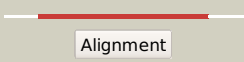

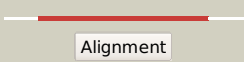

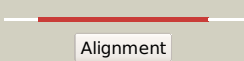
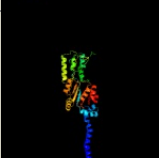
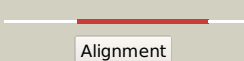

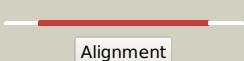
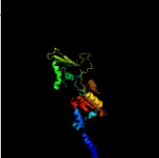
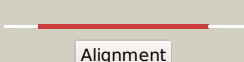
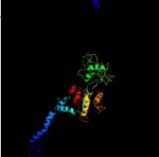


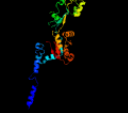








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0505c_(serB1)_595467_596588
Date	Fri Jul 26 01:50:05 BST 2019
Unique Job ID	b5451bfc435f3a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3rfuC_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> copper efflux atpase; <b>PDBTitle:</b> crystal structure of a copper-transporting pib-type atpase
2	<a href="#">c3j09A_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
3	<a href="#">c3j08A_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
4	<a href="#">c4umwA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
5	<a href="#">c5mrwF_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> potassium-transporting atpase atp-binding subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
6	<a href="#">c3n28A_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase; <b>PDBTitle:</b> crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
7	<a href="#">c3p96A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase serb; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
8	<a href="#">c1mhsA_</a>	 Alignment		100.0	18	<b>PDB header:</b> membrane protein, proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> plasma membrane atpase; <b>PDBTitle:</b> model of neurospora crassa proton atpase
9	<a href="#">c3fvvA_</a>	 Alignment		99.9	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
10	<a href="#">c3b9bA_</a>	 Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
11	<a href="#">c3b8cB_</a>	 Alignment		99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase 2, plasma membrane-type; <b>PDBTitle:</b> crystal structure of a plasma membrane proton pump

12	<a href="#">c2zzeA</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> na, k-atpase alpha subunit; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
13	<a href="#">c2iyeC</a>	Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> copper-transporting atpase; <b>PDBTitle:</b> structure of catalytic cpx-atpase domain copb-b
14	<a href="#">c3b8eC</a>	Alignment		99.9	15	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
15	<a href="#">c6a69A</a>	Alignment		99.9	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> plasma membrane calcium-transporting atpase 1; <b>PDBTitle:</b> cryo-em structure of a p-type atpase
16	<a href="#">c3ixzA</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> potassium-transporting atpase alpha; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
17	<a href="#">c2b8eB</a>	Alignment		99.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> cation-transporting atpase; <b>PDBTitle:</b> copa atp binding domain
18	<a href="#">c3skyA</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase b; <b>PDBTitle:</b> 2.1a crystal structure of the phosphate bound atp binding domain of2 archaeoglobus fulgidus copb
19	<a href="#">c4ezeB</a>	Alignment		99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of had family hydrolase t0658 from salmonella2 enterica subsp. enterica serovar typhi (target efi-501419)
20	<a href="#">c3m1yA</a>	Alignment		99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase (serb); <b>PDBTitle:</b> crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
21	<a href="#">d1j97a</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
22	<a href="#">c6roiA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> probable phospholipid-transporting atpase drs2; <b>PDBTitle:</b> cryo-em structure of the partially activated drs2p-cdc50p
23	<a href="#">d1nnla</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
24	<a href="#">c4umfC</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; <b>PDBTitle:</b> 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
25	<a href="#">c3mmzA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative had family hydrolase; <b>PDBTitle:</b> crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
26	<a href="#">c4gxtA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> a conserved functionally unknown protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
27	<a href="#">c2r8zC</a>	Alignment	not modelled	99.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
28	<a href="#">c3mn1B</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable yrbi family phosphatase;

28	<a href="#">c3m11B</a>	Alignment	not modelled	99.6	17	<b>PDBTitle:</b> crystal structure of probable yrbI family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
29	<a href="#">d1k1ea</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase YrbI
30	<a href="#">d1y8aa1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> AF1437-like
31	<a href="#">c3n1uA</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, had superfamily, subfamily iii a; <b>PDBTitle:</b> structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
32	<a href="#">c3n07B</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
33	<a href="#">d2feaa1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> MtnX-like
34	<a href="#">d1s2oa1</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
35	<a href="#">c4b6jA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase from t.2 onnurineus
36	<a href="#">c4navB</a>	Alignment	not modelled	99.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein xcc279; <b>PDBTitle:</b> crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
37	<a href="#">c4as2D</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
38	<a href="#">c3kd3A</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphohydrolase-like protein; <b>PDBTitle:</b> crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
39	<a href="#">c4hgnB</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
40	<a href="#">c3e8mD</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate cytidylyltransferase; <b>PDBTitle:</b> 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
41	<a href="#">c2p9jH</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> hypothetical protein aq2171; <b>PDBTitle:</b> crystal structure of aq2171 from aquifex aeolicus
42	<a href="#">d1rkua</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Homoserine kinase ThrH
43	<a href="#">c3fzqA</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
44	<a href="#">d2b8ea1</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
45	<a href="#">c3ewiB</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acylneuraminate cytidylyltransferase; <b>PDBTitle:</b> structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
46	<a href="#">d1wr8a</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
47	<a href="#">c3niwA</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
48	<a href="#">c2qyhD</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical conserved protein, gk1056; <b>PDBTitle:</b> crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
49	<a href="#">d1wpga2</a>	Alignment	not modelled	99.4	28	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
50	<a href="#">d2rbka1</a>	Alignment	not modelled	99.3	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
51	<a href="#">c3pgvB</a>	Alignment	not modelled	99.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
52	<a href="#">c4qjbB</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of the sugar phosphatase pfhd1 from plasmodium2 falciparum
53	<a href="#">d1nrwa</a>	Alignment	not modelled	99.2	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like

						<b>Family:</b> Predicted hydrolases Cof
54	<a href="#">d1l6ra_</a>	Alignment	not modelled	99.2	30	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
55	<a href="#">d2b30a1</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
56	<a href="#">c3dnpA_</a>	Alignment	not modelled	99.2	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stress response protein yhax; <b>PDBTitle:</b> crystal structure of stress response protein yhax from bacillus2 subtilis
57	<a href="#">c3r4cA_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
58	<a href="#">d2vkqa1</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
59	<a href="#">c4zexA_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pfhad1; <b>PDBTitle:</b> crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
60	<a href="#">d1rkqa_</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
61	<a href="#">d1zs9a1</a>	Alignment	not modelled	99.1	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
62	<a href="#">c3l7yA_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1108c; <b>PDBTitle:</b> the crystal structure of smu.1108c from streptococcus mutans ua159
63	<a href="#">c3gygA_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon putative hydrolase ntdb; <b>PDBTitle:</b> crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
64	<a href="#">c3iruA_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phoshoacetaldehyde hydrolase like protein; <b>PDBTitle:</b> crystal structure of phoshoacetaldehyde hydrolase like protein from2 oleispira antarctica
65	<a href="#">d1rlma_</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
66	<a href="#">d1xvia_</a>	Alignment	not modelled	98.9	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
67	<a href="#">c1xviA_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
68	<a href="#">c3daoB_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphate; <b>PDBTitle:</b> crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
69	<a href="#">d1wzca1</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
70	<a href="#">c3mpoD_</a>	Alignment	not modelled	98.9	39	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted hydrolase of the had superfamily; <b>PDBTitle:</b> the crystal structure of a hydrolase from lactobacillus brevis
71	<a href="#">d1nf2a_</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
72	<a href="#">d1swva_</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
73	<a href="#">c2pibA_</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylated carbohydrates phosphatase tm_1254; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
74	<a href="#">c1y8aA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1437; <b>PDBTitle:</b> structure of gene product af1437 from archaeoglobus fulgidus
75	<a href="#">d1zrna_</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
76	<a href="#">c3d6jA_</a>	Alignment	not modelled	98.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
77	<a href="#">d1u7pa_</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1

78	<a href="#">d1zd3a1</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
79	<a href="#">c3s6jC</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> the crystal structure of a hydrolase from pseudomonas syringae
80	<a href="#">c3mc1A</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted phosphatase, had family; <b>PDBTitle:</b> crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
81	<a href="#">c3cnhA</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase family protein; <b>PDBTitle:</b> crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
82	<a href="#">d2bdua1</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
83	<a href="#">c3um9A</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase, type ii; <b>PDBTitle:</b> crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530
84	<a href="#">d1te2a</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
85	<a href="#">d2hsza1</a>	Alignment	not modelled	98.7	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
86	<a href="#">c2ympB</a>	Alignment	not modelled	98.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-haloacid dehalogenase; <b>PDBTitle:</b> chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
87	<a href="#">d2go7a1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
88	<a href="#">d1cr6a1</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
89	<a href="#">c2om6A</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable phosphoserine phosphatase; <b>PDBTitle:</b> hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
90	<a href="#">c4uasA</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein cbby; <b>PDBTitle:</b> crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
91	<a href="#">c3umbA</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of the l-2-haloacid dehalogenase rsc1362
92	<a href="#">c3zupB</a>	Alignment	not modelled	98.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
93	<a href="#">c4ex7A</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alnb; <b>PDBTitle:</b> crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
94	<a href="#">c4nwiB</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 7-methylguanosine phosphate-specific 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of cytosolic 5'-nucleotidase iiib (cn-iiib) bound to2 cytidine
95	<a href="#">c5gvxA</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-phosphate phosphatase; <b>PDBTitle:</b> structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
96	<a href="#">c2hoqA</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative had-hydrolase ph1655; <b>PDBTitle:</b> crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
97	<a href="#">c2no5B</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> (s)-2-haloacid dehalogenase iva; <b>PDBTitle:</b> crystal structure analysis of a dehalogenase with intermediate complex
98	<a href="#">d1qq5a</a>	Alignment	not modelled	98.5	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
99	<a href="#">c4bndB</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-phosphoglucomutase; <b>PDBTitle:</b> structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
100	<a href="#">c6cj0A</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose phosphatase; <b>PDBTitle:</b> chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
101	<a href="#">c5dxlA</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
102	<a href="#">c4uw9A</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> the crystal structural of archaeal beta-phosphoglucomutase2 from hyper-thermophilic pyrococcus sp.

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103	<a href="#">c3m9IA</a>	Alignment	not modelled	98.5	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> crystal structure of probable had family hydrolase from pseudomonas2 fluorescens pf-5
104	<a href="#">c3nuqA</a>	Alignment	not modelled	98.5	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotide phosphatase; <b>PDBTitle:</b> structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
105	<a href="#">c3i28A</a>	Alignment	not modelled	98.5	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase 2; <b>PDBTitle:</b> crystal structure of soluble epoxide hydrolase
106	<a href="#">c3i5kA</a>	Alignment	not modelled	98.4	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain-containing <b>PDBTitle:</b> the crystal structure of human haloacid dehalogenase-like hydrolase2 domain containing 1a (hdhd1a)
107	<a href="#">c6f2xA</a>	Alignment	not modelled	98.4	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine kinase a; <b>PDBTitle:</b> structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
108	<a href="#">c2pkeA</a>	Alignment	not modelled	98.4	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like family hydrolase; <b>PDBTitle:</b> crystal structure of haloacid dehalogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
109	<a href="#">d2fuea1</a>	Alignment	not modelled	98.4	15 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
110	<a href="#">c3dv9A</a>	Alignment	not modelled	98.4	10 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> putative beta-phosphoglucomutase from bacteroides vulgatus.
111	<a href="#">c2i55C</a>	Alignment	not modelled	98.4	9 <b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
112	<a href="#">c3qypB</a>	Alignment	not modelled	98.3	11 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> inorganic pyrophosphatase; <b>PDBTitle:</b> crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
113	<a href="#">c4eekA</a>	Alignment	not modelled	98.3	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase-related protein; <b>PDBTitle:</b> crystal structure of had family hydrolase dr_1622 from deinococcus2 radiodurans r1 (target efi-501256) with bound phosphate and sodium
114	<a href="#">c4uavA</a>	Alignment	not modelled	98.3	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain-containing <b>PDBTitle:</b> crystal structure of cbby (at3g48420) from arabidopsis thaliana
115	<a href="#">d2fdra1</a>	Alignment	not modelled	98.3	11 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
116	<a href="#">c2hx1D</a>	Alignment	not modelled	98.3	10 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted sugar phosphatases of the had superfamily; <b>PDBTitle:</b> crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
117	<a href="#">c3qnmA</a>	Alignment	not modelled	98.3	16 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> haloalkane dehalogenase family member from bacteroides2 thetaiotaomicron of unknown function
118	<a href="#">c3ddhA</a>	Alignment	not modelled	98.3	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative haloacid dehalogenase-like family hydrolase; <b>PDBTitle:</b> the structure of a putative haloacid dehalogenase-like family2 hydrolase from bacteroides thetaiotaomicron vpi-5482
119	<a href="#">d2fi1a1</a>	Alignment	not modelled	98.3	13 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
120	<a href="#">d2b0ca1</a>	Alignment	not modelled	98.3	10 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like