
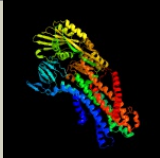



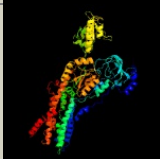

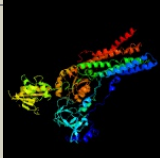

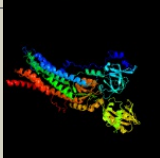





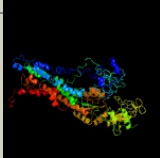

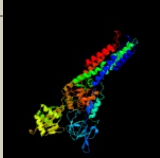









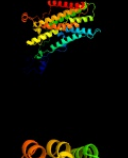


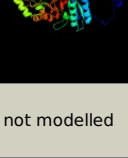


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1030\_(kdpB)\_1153728\_1155857  
 Date Wed Jul 31 22:05:10 BST 2019  
 Unique Job ID 4990d173720620fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mrwF_</a>	 Alignment		100.0	62	<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
2	<a href="#">c2zxeA_</a>	 Alignment		100.0	21	<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
3	<a href="#">c3ixzA_</a>	 Alignment		100.0	22	<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
4	<a href="#">c3b8eC_</a>	 Alignment		100.0	21	<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
5	<a href="#">c3b9bA_</a>	 Alignment		100.0	23	<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
6	<a href="#">c1mhsA_</a>	 Alignment		100.0	22	<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
7	<a href="#">c6a69A_</a>	 Alignment		100.0	21	<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
8	<a href="#">c3b8cB_</a>	 Alignment		100.0	22	<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
9	<a href="#">c3rfuC_</a>	 Alignment		100.0	26	<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
10	<a href="#">c6roiA_</a>	 Alignment		100.0	17	<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
11	<a href="#">c4umwA_</a>	 Alignment		100.0	24	<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

12	<a href="#">c3j09A_</a>	Alignment		100.0	26	<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
13	<a href="#">c3j08A_</a>	Alignment		100.0	27	<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
14	<a href="#">c3skyA_</a>	Alignment		100.0	32	<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 of 2 archaeoglobus fulgidus copb
15	<a href="#">c2b8eB_</a>	Alignment		100.0	30	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> cation-transporting atpase; <b>PDBTitle:</b> copa atp binding domain
16	<a href="#">c2iyeC_</a>	Alignment		100.0	23	<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
17	<a href="#">d1wpga4</a>	Alignment		100.0	25	<b>Fold:</b> Calcium ATPase, transmembrane domain M <b>Superfamily:</b> Calcium ATPase, transmembrane domain M <b>Family:</b> Calcium ATPase, transmembrane domain M
18	<a href="#">d1wpga2</a>	Alignment		100.0	35	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
19	<a href="#">d2b8ea1</a>	Alignment		100.0	35	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
20	<a href="#">c3p96A_</a>	Alignment		100.0	14	<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
21	<a href="#">d1y8aa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> AF1437-like
22	<a href="#">c3n28A_</a>	Alignment	not modelled	99.9	13	<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
23	<a href="#">c2hc8A_</a>	Alignment	not modelled	99.9	35	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> cation-transporting atpase, p-type; <b>PDBTitle:</b> structure of the a. fulgidus copa a-domain
24	<a href="#">c4ezeB_</a>	Alignment	not modelled	99.9	15	<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)
25	<a href="#">c2kja_</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the actuator domain of the copper-2 transporting atpase atp7a
26	<a href="#">d1wpga1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Calcium ATPase, transduction domain A <b>Family:</b> Calcium ATPase, transduction domain A
27	<a href="#">d1mo7a_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Superfamily:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Family:</b> Metal cation-transporting ATPase, ATP-binding domain N
28	<a href="#">c3gwiA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> magnesium-transporting atpase, p-type 1; <b>PDBTitle:</b> crystal structure of mg-atpase nucleotide binding domain

29	<a href="#">d1q3ia_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Superfamily:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Family:</b> Metal cation-transporting ATPase, ATP-binding domain N
30	<a href="#">d1wpga3</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Superfamily:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Family:</b> Metal cation-transporting ATPase, ATP-binding domain N
31	<a href="#">c4qjbB_</a>	Alignment	not modelled	99.6	20	<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 pfhad1 from plasmodium2 falciparum
32	<a href="#">c3n07B_</a>	Alignment	not modelled	99.6	11	<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="#">c4umfC_</a>	Alignment	not modelled	99.6	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
34	<a href="#">c2p9jH_</a>	Alignment	not modelled	99.5	14	<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
35	<a href="#">c2r8zC_</a>	Alignment	not modelled	99.5	14	<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
36	<a href="#">c3mmzA_</a>	Alignment	not modelled	99.5	16	<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
37	<a href="#">c3mn1B_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable yrbi family phosphatase; <b>PDBTitle:</b> crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
38	<a href="#">d1k1ea_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase Yrbl
39	<a href="#">c3l7yA_</a>	Alignment	not modelled	99.5	19	<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
40	<a href="#">c3ewiB_</a>	Alignment	not modelled	99.5	11	<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
41	<a href="#">c4navB_</a>	Alignment	not modelled	99.5	18	<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
42	<a href="#">c4hgnB_</a>	Alignment	not modelled	99.4	12	<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
43	<a href="#">c3n1uA_</a>	Alignment	not modelled	99.4	15	<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
44	<a href="#">c3e8mD_</a>	Alignment	not modelled	99.4	16	<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
45	<a href="#">d1wr8a_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
46	<a href="#">d1rkqa_</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
47	<a href="#">d1l6ra_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
48	<a href="#">c3m1yA_</a>	Alignment	not modelled	99.3	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
49	<a href="#">c3daoB_</a>	Alignment	not modelled	99.3	27	<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
50	<a href="#">d1j97a_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
51	<a href="#">d2a29a1</a>	Alignment	not modelled	99.3	56	<b>Fold:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Superfamily:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Family:</b> Metal cation-transporting ATPase, ATP-binding domain N
52	<a href="#">c4zexA_</a>	Alignment	not modelled	99.2	22	<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
						<b>Fold:</b> HAD-like

53	<a href="#">d2b30a1</a>	Alignment	not modelled	99.2	21	<b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
54	<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
55	<a href="#">d1rlma</a>	Alignment	not modelled	99.1	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
56	<a href="#">c3r4cA</a>	Alignment	not modelled	99.1	30	<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
57	<a href="#">d1rkua</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Homoserine kinase ThrH
58	<a href="#">c2kmvA</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form
59	<a href="#">d1nnla</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
60	<a href="#">c2koyA</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
61	<a href="#">c2qyhD</a>	Alignment	not modelled	99.1	22	<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
62	<a href="#">c3fzqA</a>	Alignment	not modelled	99.0	24	<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
63	<a href="#">c3dnpA</a>	Alignment	not modelled	99.0	25	<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
64	<a href="#">c3pgvB</a>	Alignment	not modelled	99.0	25	<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
65	<a href="#">d2feaa1</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> MtnX-like
66	<a href="#">d2rbka1</a>	Alignment	not modelled	98.9	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
67	<a href="#">c3niwA</a>	Alignment	not modelled	98.9	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
68	<a href="#">d1nf2a</a>	Alignment	not modelled	98.8	28	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
69	<a href="#">c3fvvA</a>	Alignment	not modelled	98.7	18	<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
70	<a href="#">c4b6jA</a>	Alignment	not modelled	98.6	21	<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
71	<a href="#">c3kd3A</a>	Alignment	not modelled	98.6	14	<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
72	<a href="#">c3gygA</a>	Alignment	not modelled	98.6	17	<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
73	<a href="#">d1s2oa1</a>	Alignment	not modelled	98.6	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
74	<a href="#">c2arfA</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> wilson disease atpase; <b>PDBTitle:</b> solution structure of the wilson atpase n-domain in the2 presence of atp
75	<a href="#">d1xvia</a>	Alignment	not modelled	98.3	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
76	<a href="#">c1xviA</a>	Alignment	not modelled	98.3	25	<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
77	<a href="#">d1wzca1</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof <b>PDB header:</b> hydrolase

78	<a href="#">c5gvxA</a>	Alignment	not modelled	98.3	25	<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
79	<a href="#">c2i55C</a>	Alignment	not modelled	98.2	23	<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
80	<a href="#">d2vkqa1</a>	Alignment	not modelled	98.2	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
81	<a href="#">c5lbkA</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase paa2, chloroplastic; <b>PDBTitle:</b> crystal structure of the n-domain of hma8, a copper-transporting p-2 type atpase
82	<a href="#">d1qyia</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein MW1667 (SA1546)
83	<a href="#">c3zupB</a>	Alignment	not modelled	98.1	31	<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.
84	<a href="#">d1zs9a1</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
85	<a href="#">c3iruA</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonoacetaldehyde hydrolase like protein; <b>PDBTitle:</b> crystal structure of phosonoacetaldehyde hydrolase like protein from2 oleispira antarctica
86	<a href="#">c5dxlA</a>	Alignment	not modelled	98.0	18	<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
87	<a href="#">c4bndB</a>	Alignment	not modelled	98.0	16	<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
88	<a href="#">c5lbdB</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> copper-transporting atpase paa1, chloroplastic; <b>PDBTitle:</b> crystal structure of the n-domain of hma6, a copper-transporting p-2 type atpase
89	<a href="#">d1swva</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
90	<a href="#">c6cj0A</a>	Alignment	not modelled	97.8	26	<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
91	<a href="#">c5ue7A</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> crystal structure of the phosphomannomutase pmm1 from candida2 albicans, apoenzyme state
92	<a href="#">c2voyB</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
93	<a href="#">c2voyH</a>	Alignment	not modelled	97.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
94	<a href="#">c4ex7A</a>	Alignment	not modelled	97.7	23	<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
95	<a href="#">d2fuea1</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
96	<a href="#">c1y8aA</a>	Alignment	not modelled	97.7	21	<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
97	<a href="#">d2b8ea2</a>	Alignment	not modelled	97.7	20	<b>Fold:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Superfamily:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Family:</b> Metal cation-transporting ATPase, ATP-binding domain N
98	<a href="#">d1u02a</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Trehalose-phosphatase
99	<a href="#">c3s6jC</a>	Alignment	not modelled	97.7	19	<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
100	<a href="#">c3mc1A</a>	Alignment	not modelled	97.7	11	<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
101	<a href="#">c3mpoD</a>	Alignment	not modelled	97.6	27	<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

102	<a href="#">d2amya1</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
103	<a href="#">d2bdua1</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
104	<a href="#">c3m9IA</a>	Alignment	not modelled	97.4	18	<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
105	<a href="#">c2voyK</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
106	<a href="#">c2pibA</a>	Alignment	not modelled	97.3	22	<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
107	<a href="#">c2odaB</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pspto_2114; <b>PDBTitle:</b> crystal structure of pspto_2114
108	<a href="#">c3pdwA</a>	Alignment	not modelled	97.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hydrolase yutf; <b>PDBTitle:</b> crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
109	<a href="#">d2hsza1</a>	Alignment	not modelled	97.2	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
110	<a href="#">c2yy6B</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglycolate phosphatase; <b>PDBTitle:</b> crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
111	<a href="#">c4eekA</a>	Alignment	not modelled	97.2	13	<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
112	<a href="#">c3d6jA</a>	Alignment	not modelled	97.1	25	<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
113	<a href="#">c4nwiB</a>	Alignment	not modelled	97.1	16	<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
114	<a href="#">c3qypB</a>	Alignment	not modelled	97.0	13	<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
115	<a href="#">c2hx1D</a>	Alignment	not modelled	97.0	23	<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
116	<a href="#">c3ib6B</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
117	<a href="#">c2hi0B</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoglycolate phosphatase; <b>PDBTitle:</b> crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
118	<a href="#">d2gmwa1</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
119	<a href="#">d1u7pa</a>	Alignment	not modelled	96.9	7	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1
120	<a href="#">c6f2xA</a>	Alignment	not modelled	96.9	16	<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)