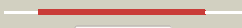



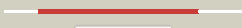














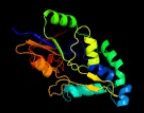








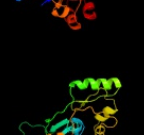

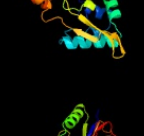


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3661 (-) _4099825_4100688
Date	Fri Aug 9 18:20:35 BST 2019
Unique Job ID	8eb39713e3086c83

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3fvvA_</a>	 Alignment		100.0	25	<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
2	<a href="#">c3p96A_</a>	 Alignment		99.9	23	<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
3	<a href="#">d1j97a_</a>	 Alignment		99.9	23	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
4	<a href="#">c4ezeB_</a>	 Alignment		99.9	17	<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)
5	<a href="#">c3m1yA_</a>	 Alignment		99.9	16	<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
6	<a href="#">c3n28A_</a>	 Alignment		99.8	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="#">d1nnla_</a>	 Alignment		99.8	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
8	<a href="#">d1s2oa1</a>	 Alignment		99.8	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
9	<a href="#">c4gxtA_</a>	 Alignment		99.8	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
10	<a href="#">d2feaa1</a>	 Alignment		99.8	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> MtnX-like
11	<a href="#">c3kd3A_</a>	 Alignment		99.8	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

12	<a href="#">c3dnpA</a>	Alignment		99.8	11	<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
13	<a href="#">c3gygA</a>	Alignment		99.8	12	<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
14	<a href="#">d1nrwa</a>	Alignment		99.7	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
15	<a href="#">c4b6jA</a>	Alignment		99.7	14	<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
16	<a href="#">d1wzca1</a>	Alignment		99.7	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
17	<a href="#">c3pgvB</a>	Alignment		99.7	18	<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
18	<a href="#">c3niwA</a>	Alignment		99.7	16	<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
19	<a href="#">d1rkua</a>	Alignment		99.7	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Homoserine kinase ThrH
20	<a href="#">c4as2D</a>	Alignment		99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
21	<a href="#">c2qyhD</a>	Alignment	not modelled	99.7	16	<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
22	<a href="#">d1xvia</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
23	<a href="#">c1xviA</a>	Alignment	not modelled	99.7	15	<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
24	<a href="#">c4zexA</a>	Alignment	not modelled	99.7	15	<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
25	<a href="#">c3mn1B</a>	Alignment	not modelled	99.7	25	<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
26	<a href="#">c4hgnB</a>	Alignment	not modelled	99.7	19	<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
27	<a href="#">c4umfC</a>	Alignment	not modelled	99.7	24	<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 <b>PDB header:</b> hydrolase

28	<a href="#">c3fqzA_</a>	Alignment	not modelled	99.7	12	<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
29	<a href="#">c3ewiB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acylneuraminate cytidyltransferase; <b>PDBTitle:</b> structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
30	<a href="#">d1rlma_</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
31	<a href="#">c3mmzA_</a>	Alignment	not modelled	99.7	24	<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
32	<a href="#">d2rbka1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
33	<a href="#">d1k1ea_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase Yrbl
34	<a href="#">c3r4cA_</a>	Alignment	not modelled	99.6	14	<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
35	<a href="#">c2r8zC_</a>	Alignment	not modelled	99.6	21	<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="#">c3zupB_</a>	Alignment	not modelled	99.6	22	<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.
37	<a href="#">d1nf2a_</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
38	<a href="#">c3e8mD_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate cytidyltransferase; <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
39	<a href="#">d2b30a1</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
40	<a href="#">c3n1uA_</a>	Alignment	not modelled	99.6	21	<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
41	<a href="#">c5gvxA_</a>	Alignment	not modelled	99.6	18	<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
42	<a href="#">c3daoB_</a>	Alignment	not modelled	99.6	10	<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
43	<a href="#">c2p9jH_</a>	Alignment	not modelled	99.6	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
44	<a href="#">c4qjbB_</a>	Alignment	not modelled	99.6	14	<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
45	<a href="#">c6cj0A_</a>	Alignment	not modelled	99.6	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
46	<a href="#">d1l6ra_</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
47	<a href="#">c4bndB_</a>	Alignment	not modelled	99.6	13	<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
48	<a href="#">c3l7yA_</a>	Alignment	not modelled	99.6	13	<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
49	<a href="#">d1rkqa_</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
50	<a href="#">d1zs9a1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
51	<a href="#">d1wr8a_</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
52	<a href="#">c3iruA_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phoshonoacetaldehyde hydrolase like protein;

						<b>PDBTitle:</b> crystal structure of phosphonoacetaldehyde hydrolase like protein from <i>2 oleispira antarctica</i>
53	<a href="#">c4navB_</a>	Alignment	not modelled	99.5	22	<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 <i>xanthomonas2 campestris</i> , target efi-508608
54	<a href="#">c3mpoD_</a>	Alignment	not modelled	99.5	12	<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 <i>lactobacillus brevis</i>
55	<a href="#">d1swva_</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
56	<a href="#">d1y8aa1</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> AF1437-like
57	<a href="#">d2fuea1</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
58	<a href="#">c2piBA_</a>	Alignment	not modelled	99.5	11	<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 from <i>2 thermotoga maritima</i>
59	<a href="#">c2i55C_</a>	Alignment	not modelled	99.4	13	<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 from <i>2 leishmania mexicana</i>
60	<a href="#">d1zd3a1</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
61	<a href="#">c5dxIA_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of <i>aspergillus fumigatus</i> trehalose-6-phosphate phosphatase2 crystal form 1
62	<a href="#">c5ue7A_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> crystal structure of the phosphomannomutase pmm1 from <i>candida2 albicans</i> , apoenzyme state
63	<a href="#">c3i28A_</a>	Alignment	not modelled	99.4	14	<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
64	<a href="#">c3s6jC_</a>	Alignment	not modelled	99.4	16	<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 <i>pseudomonas syringae</i>
65	<a href="#">c2cftA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal phosphate phosphatase; <b>PDBTitle:</b> crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
66	<a href="#">c3n07B_</a>	Alignment	not modelled	99.4	19	<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 <i>vibrio cholerae</i>
67	<a href="#">c2hx1D_</a>	Alignment	not modelled	99.4	12	<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 <i>cytophaga hutchinsonii</i> atcc 33406 at 2.10 a3 resolution
68	<a href="#">d2amya1</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
69	<a href="#">c3i5kA_</a>	Alignment	not modelled	99.4	12	<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)
70	<a href="#">d2go7a1</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
71	<a href="#">c2om6A_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable phosphoserine phosphatase; <b>PDBTitle:</b> hypothetical protein (probable phosphoserine phosphatase) from <i>2 pyrococcus horikoshii</i> ot3
72	<a href="#">c3d6jA_</a>	Alignment	not modelled	99.3	12	<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 <i>bacteroides fragilis</i>
73	<a href="#">c2ympB_</a>	Alignment	not modelled	99.3	11	<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 <i>rhodobacteraceae</i> family bacterium
74	<a href="#">d2b0ca1</a>	Alignment	not modelled	99.3	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
75	<a href="#">d1te2a_</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
76	<a href="#">d2vkqa1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)

77	<a href="#">d1zrna_</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
78	<a href="#">c3cnnA_</a>	Alignment	not modelled	99.3	13	<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
79	<a href="#">d1u02a_</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Trehalose-phosphatase
80	<a href="#">c3um9A_</a>	Alignment	not modelled	99.3	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
81	<a href="#">c3nuqA_</a>	Alignment	not modelled	99.3	13	<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
82	<a href="#">d2hsza1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
83	<a href="#">c4ex7A_</a>	Alignment	not modelled	99.3	14	<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
84	<a href="#">c4eekA_</a>	Alignment	not modelled	99.3	15	<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
85	<a href="#">d1yv9a1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
86	<a href="#">c4uasA_</a>	Alignment	not modelled	99.3	21	<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
87	<a href="#">d1wvia_</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
88	<a href="#">c3mc1A_</a>	Alignment	not modelled	99.3	14	<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
89	<a href="#">c5dxiB_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
90	<a href="#">d1cr6a1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
91	<a href="#">c4uw9A_</a>	Alignment	not modelled	99.2	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. strain st 04
92	<a href="#">d1ydfa1</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
93	<a href="#">c3umbA_</a>	Alignment	not modelled	99.2	13	<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
94	<a href="#">c3m91A_</a>	Alignment	not modelled	99.2	16	<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
95	<a href="#">c2pkeA_</a>	Alignment	not modelled	99.2	18	<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
96	<a href="#">c3dv9A_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> putative beta-phosphoglucomutase from bacteroides vulgatus.
97	<a href="#">d2fdra1</a>	Alignment	not modelled	99.2	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
98	<a href="#">d1u7pa_</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1
99	<a href="#">d1qq5a_</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
100	<a href="#">c6f2xA_</a>	Alignment	not modelled	99.2	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)
101	<a href="#">c4uavA_</a>	Alignment	not modelled	99.2	21	<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
102	<a href="#">c2no5B_</a>	Alignment	not modelled	99.2	12 <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
103	<a href="#">c3qypB_</a>	Alignment	not modelled	99.2	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
104	<a href="#">c2yy6B_</a>	Alignment	not modelled	99.2	16 <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
105	<a href="#">c1cr6A_</a>	Alignment	not modelled	99.2	15 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
106	<a href="#">c2hoqA_</a>	Alignment	not modelled	99.2	13 <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
107	<a href="#">c3pdwA_</a>	Alignment	not modelled	99.1	11 <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
108	<a href="#">c3nasA_</a>	Alignment	not modelled	99.1	15 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
109	<a href="#">c3qgmC_</a>	Alignment	not modelled	99.1	14 <b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> p-nitrophenyl phosphatase (pho2); <b>PDBTitle:</b> p-nitrophenyl phosphatase from archaeoglobus fulgidus
110	<a href="#">d1o08a_</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
111	<a href="#">c2x4dA_</a>	Alignment	not modelled	99.1	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholysine phosphohistidine inorganic pyrophosphate <b>PDBTitle:</b> crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
112	<a href="#">c3qnmA_</a>	Alignment	not modelled	99.1	13 <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
113	<a href="#">d2c4na1</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
114	<a href="#">c3ddhA_</a>	Alignment	not modelled	99.1	12 <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
115	<a href="#">c4g9bA_</a>	Alignment	not modelled	99.1	14 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> crystal structure of beta-phosphoglucomutase homolog from escherichia2 coli, target efi-501172, with bound mg, open lid
116	<a href="#">d2fi1a1</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
117	<a href="#">d2hdoa1</a>	Alignment	not modelled	99.1	9 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
118	<a href="#">d1ys9a1</a>	Alignment	not modelled	99.1	14 <b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
119	<a href="#">c2qltA_</a>	Alignment	not modelled	99.1	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> (dl)-glycerol-3-phosphatase 1; <b>PDBTitle:</b> crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
120	<a href="#">c3e58A_</a>	Alignment	not modelled	99.1	9 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-phosphoglucomutase; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus