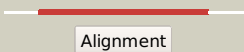

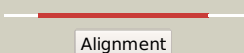

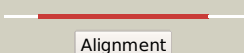

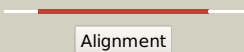


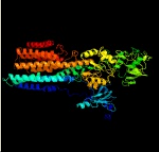


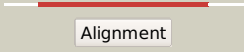

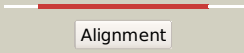





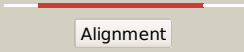
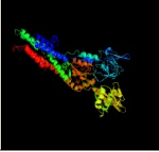


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1997_(ctpF)_2240167_2242884
Date	Mon Aug 5 13:25:10 BST 2019
Unique Job ID	a981ec9c830f4993

Detailed template information

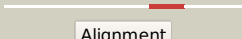
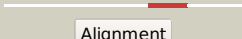
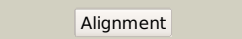
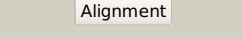
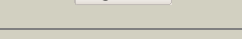
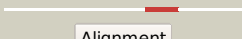

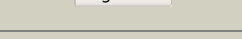

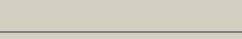
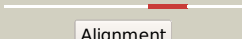
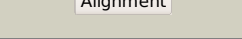





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b9bA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
2	c2zxeA_	 Alignment		100.0	33	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: na, k-atpase alpha subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
3	c3ixzA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
4	c3b8eC_	 Alignment		100.0	33	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
5	c6a69A_	 Alignment		100.0	29	PDB header: structural protein Chain: A: PDB Molecule: plasma membrane calcium-transporting atpase 1; PDBTitle: cryo-em structure of a p-type atpase
6	c1mhsA_	 Alignment		100.0	25	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
7	c3b8cB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
8	c6roiA_	 Alignment		100.0	17	PDB header: lipid transport Chain: A: PDB Molecule: probable phospholipid-transporting atpase drs2; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p
9	c5mrwF_	 Alignment		100.0	24	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
10	c4umwA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
11	c3rfuC_	 Alignment		100.0	25	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase

12	c3j08A_	Alignment		100.0	29	PDB header: hydrolase, metal transport Chain: A; PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
13	c3j09A_	Alignment		100.0	28	PDB header: hydrolase, metal transport Chain: A; PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
14	d1wpga4	Alignment		100.0	40	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
15	c3skyA_	Alignment		100.0	33	PDB header: hydrolase Chain: A; PDB Molecule: copper-exporting p-type atpase b; PDBTitle: 2.1a crystal structure of the phosphate bound atp binding domain of2 archaeoglobus fulgidus copb
16	c2b8eB_	Alignment		100.0	36	PDB header: membrane protein Chain: B; PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
17	c2iyeC_	Alignment		100.0	23	PDB header: hydrolase Chain: C; PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
18	d1wpga2	Alignment		100.0	48	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
19	d1mo7a_	Alignment		100.0	26	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
20	d2b8ea1	Alignment		99.9	48	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
21	d1y8aa1	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
22	c3p96A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
23	d1wpga3	Alignment	not modelled	99.9	21	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
24	d1q3ia_	Alignment	not modelled	99.9	24	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
25	d1wpga1	Alignment	not modelled	99.9	41	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
26	c3n28A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
27	c2hc8A_	Alignment	not modelled	99.9	33	PDB header: transport protein Chain: A; PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
28	c2kijA_	Alignment	not modelled	99.8	32	PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the actuator domain of the copper-2 transporting atpase atp7a PDB header: hydrolase

29	c4ezeB_	Alignment	not modelled	99.8	12	Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family hydrolase t0658 from salmonella2 enterica subsp. enterica serovar typhi (target efi-501419)
30	c3gwiA_	Alignment	not modelled	99.8	25	PDB header: hydrolase Chain: A: PDB Molecule: magnesium-transporting atpase, p-type 1; PDBTitle: crystal structure of mg-atpase nucleotide binding domain
31	c4qjbB_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
32	c4umfC_	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; PDBTitle: crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
33	c3n07B_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: B: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
34	c2r8zC_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
35	c2p9jH_	Alignment	not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
36	c3mn1B_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: B: PDB Molecule: probable yrbi family phosphatase; PDBTitle: crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
37	c4navB_	Alignment	not modelled	99.4	23	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
38	c3mmzA_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
39	c3l7yA_	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
40	d1k1ea_	Alignment	not modelled	99.4	22	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi
41	d1wr8a_	Alignment	not modelled	99.3	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
42	d1rkqa_	Alignment	not modelled	99.3	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
43	c3ewiB_	Alignment	not modelled	99.3	18	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidylyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
44	c4hgnB_	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: B: PDB Molecule: 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate PDBTitle: crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
45	d1l6ra_	Alignment	not modelled	99.3	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
46	c3e8mD_	Alignment	not modelled	99.2	20	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidylyltransferase; PDBTitle: structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
47	c4zexA_	Alignment	not modelled	99.2	18	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
48	c3n1uA_	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, had superfamily, subfamily iii a; PDBTitle: structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
49	c3daoB_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
50	c3m1yA_	Alignment	not modelled	99.1	28	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
51	d1nrwa_	Alignment	not modelled	99.1	23	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
52	d1j97a_	Alignment	not modelled	99.1	24	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
53	d1rlma_	Alignment	not modelled	99.1	21	Fold: HAD-like Superfamily: HAD-like

						Family: Predicted hydrolases Cof
54	c3dnpA	Alignment	not modelled	99.1	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stress response protein yhax; PDBTitle: crystal structure of stress response protein yhax from bacillus2 subtilis
55	c2qyhD	Alignment	not modelled	99.0	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical conserved protein, gk1056; PDBTitle: crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
56	d2b30a1	Alignment	not modelled	99.0	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
57	c3fzqA	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
58	c3r4cA	Alignment	not modelled	99.0	30	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like hydrolase; PDBTitle: divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
59	c3pgvB	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
60	c3niwA	Alignment	not modelled	98.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
61	d1nlna	Alignment	not modelled	98.9	19	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
62	d1rkua	Alignment	not modelled	98.9	14	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
63	d2rbka1	Alignment	not modelled	98.9	26	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
64	d1nf2a	Alignment	not modelled	98.8	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
65	d2feaa1	Alignment	not modelled	98.7	18	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
66	c3gygA	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: ntd biosynthesis operon putative hydrolase ntdb; PDBTitle: crystal structure of yhjK (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
67	d1s2oa1	Alignment	not modelled	98.5	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
68	c4b6jA	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
69	c3fvvA	Alignment	not modelled	98.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
70	c3kd3A	Alignment	not modelled	98.4	10	PDB header: unknown function Chain: A: PDB Molecule: phosphoserine phosphohydrolase-like protein; PDBTitle: crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
71	d1xvia	Alignment	not modelled	98.3	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
72	c1xviA	Alignment	not modelled	98.3	22	PDB header: hydrolase Chain: A: PDB Molecule: putative mannosyl-3-phosphoglycerate phosphatase; PDBTitle: crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
73	d1wzca1	Alignment	not modelled	98.2	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
74	c2i55C	Alignment	not modelled	98.2	19	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
75	c3zupB	Alignment	not modelled	98.0	21	PDB header: hydrolase Chain: B: PDB Molecule: mannosyl-3-phosphoglycerate phosphatase; PDBTitle: the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
76	d2vkqa1	Alignment	not modelled	98.0	13	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
77	c5gvxA	Alignment	not modelled	97.9	25	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-phosphate phosphatase; PDBTitle: structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis

78	c1y8aA	Alignment	not modelled	97.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
79	d1zs9a1	Alignment	not modelled	97.9	17	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
80	c6cj0A	Alignment	not modelled	97.9	19	PDB header: lyase Chain: A: PDB Molecule: trehalose phosphatase; PDBTitle: chromosomal trehalose-6-phosphate phosphatase from <i>p. aeruginosa</i>
81	c2koyA	Alignment	not modelled	97.9	14	PDB header: metal transport Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
82	c2voyB	Alignment	not modelled	97.9	31	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
83	c3iruA	Alignment	not modelled	97.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phosphonoacetaldehyde hydrolase like protein from2 oleispira antarctica
84	c4bndB	Alignment	not modelled	97.8	19	PDB header: isomerase Chain: B: PDB Molecule: alpha-phosphoglucomutase; PDBTitle: structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
85	c2kmvA	Alignment	not modelled	97.8	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form
86	d1qyia	Alignment	not modelled	97.7	22	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
87	d2a29a1	Alignment	not modelled	97.7	17	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
88	c5dxIA	Alignment	not modelled	97.7	18	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
89	d1swva	Alignment	not modelled	97.6	23	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
90	c2voyH	Alignment	not modelled	97.6	53	PDB header: hydrolase Chain: H: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
91	d2bdua1	Alignment	not modelled	97.5	13	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
92	c3mpoD	Alignment	not modelled	97.5	27	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
93	d1u02a	Alignment	not modelled	97.5	15	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
94	c5ue7A	Alignment	not modelled	97.4	14	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: crystal structure of the phosphomannomutase pmm1 from candida2 albicans, apoenzyme state
95	c3mc1A	Alignment	not modelled	97.4	13	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
96	d2fuea1	Alignment	not modelled	97.3	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
97	d2amya1	Alignment	not modelled	97.3	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
98	c2pibA	Alignment	not modelled	97.3	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
99	c4ex7A	Alignment	not modelled	97.2	29	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
100	c3s6jC	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
101	c3pdwA	Alignment	not modelled	97.2	20	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
102	c2odaB	Alignment	not modelled	97.2	20	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114

103	c2hx1D_	 Alignment	not modelled	97.1	12	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had superfamily; PDBTitle: crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
104	c3m9IA_	 Alignment	not modelled	97.1	20	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: crystal structure of probable had family hydrolase from pseudomonas2 fluorescens pf-5
105	c4nwiB_	 Alignment	not modelled	96.9	15	PDB header: hydrolase Chain: B: PDB Molecule: 7-methylguanosine phosphate-specific 5'-nucleotidase; PDBTitle: crystal structure of cytosolic 5'-nucleotidase iiib (cn-iiib) bound to2 cytidine
106	c2hi0B_	 Alignment	not modelled	96.9	14	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphoglycolate phosphatase; PDBTitle: crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
107	c2yy6B_	 Alignment	not modelled	96.8	16	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
108	c2cftA_	 Alignment	not modelled	96.8	24	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
109	d1u7pa_	 Alignment	not modelled	96.8	13	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
110	c3qypB_	 Alignment	not modelled	96.8	14	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
111	c5dxiB_	 Alignment	not modelled	96.7	22	PDB header: hydrolase Chain: B: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
112	c3ib6B_	 Alignment	not modelled	96.6	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
113	c4gxtA_	 Alignment	not modelled	96.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
114	d2ah5a1	 Alignment	not modelled	96.4	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
115	c2voyK_	 Alignment	not modelled	96.4	32	PDB header: hydrolase Chain: K: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
116	d2hsza1	 Alignment	not modelled	96.4	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
117	d2gmwa1	 Alignment	not modelled	96.4	21	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
118	c2qltA_	 Alignment	not modelled	96.4	13	PDB header: hydrolase Chain: A: PDB Molecule: (dl)-glycerol-3-phosphatase 1; PDBTitle: crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
119	c3esqA_	 Alignment	not modelled	96.4	21	PDB header: hydrolase Chain: A: PDB Molecule: d,d-heptose 1,7-bisphosphate phosphatase; PDBTitle: crystal structure of calcium-bound d,d-heptose 1.7-bisphosphate2 phosphatase from e. coli
120	c3um9A_	 Alignment	not modelled	96.3	13	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530