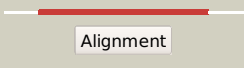

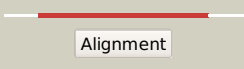

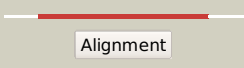

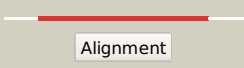

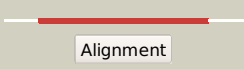

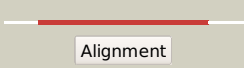

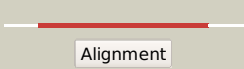

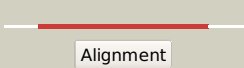

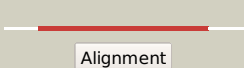

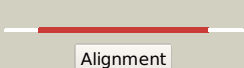

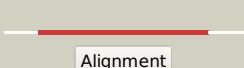



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1469_(ctpD)_1656969_1658942
 Date Fri Aug 2 13:30:05 BST 2019
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Detailed template information

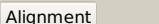
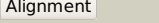



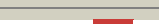
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1	c3rfuC_	 Alignment		100.0	29	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
2	c3j08A_	 Alignment		100.0	31	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
3	c3j09A_	 Alignment		100.0	31	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
4	c4umwA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
5	c5mrwF_	 Alignment		100.0	23	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
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	c2zxeA_	 Alignment		100.0	26	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
8	c3ixzA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
9	c3b9bA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
10	c3b8eC_	 Alignment		100.0	25	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
11	c6a69A_	 Alignment		100.0	21	PDB header: structural protein Chain: A: PDB Molecule: plasma membrane calcium-transporting atpase 1; PDBTitle: cryo-em structure of a p-type atpase

12	c3b8cB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
13	c6roiA_	Alignment		100.0	21	PDB header: lipid transport Chain: A: PDB Molecule: probable phospholipid-transporting atpase drs2; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p
14	c3skyA_	Alignment		100.0	37	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 of f2 archaeoglobus fulgidus copb
15	c2b8eB_	Alignment		100.0	37	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
16	c2iyeC_	Alignment		100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
17	c3p96A_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
18	d1wpga2	Alignment		100.0	27	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
19	c3n28A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
20	d2b8ea1	Alignment		99.9	38	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
21	d1y8aa1	Alignment	not modelled	99.9	23	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
22	c2hc8A_	Alignment	not modelled	99.9	49	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
23	c2kijA_	Alignment	not modelled	99.9	39	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
24	d1wpga1	Alignment	not modelled	99.8	32	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
25	c2kmvA_	Alignment	not modelled	99.8	22	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
26	c4ezeB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family hydrolase t0658 from salmonella2 enterica subsp. enterica serovar typhi (target efi-501419)
27	c2koyA_	Alignment	not modelled	99.7	31	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
28	c2arfA_	Alignment	not modelled	99.6	34	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp

29	c2r8zC	Alignment	not modelled	99.6	29	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
30	c3mmzA	Alignment	not modelled	99.6	24	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
31	d2a29a1	Alignment	not modelled	99.6	23	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
32	c5lbkA	Alignment	not modelled	99.6	28	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase paa2, chloroplastic; PDBTitle: crystal structure of the n-domain of hma8, a copper-transporting p-2 type atpase
33	c3l7yA	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
34	d1k1ea	Alignment	not modelled	99.5	27	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi
35	c3n07B	Alignment	not modelled	99.5	18	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
36	c4umfC	Alignment	not modelled	99.5	17	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
37	c2p9jH	Alignment	not modelled	99.5	12	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
38	c4qjbB	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
39	c5lbdB	Alignment	not modelled	99.5	29	PDB header: hydrolase Chain: B: PDB Molecule: copper-transporting atpase paa1, chloroplastic; PDBTitle: crystal structure of the n-domain of hma6, a copper-transporting p-2 type atpase
40	c3mn1B	Alignment	not modelled	99.4	20	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
41	c3e8mD	Alignment	not modelled	99.4	15	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidyltransferase; 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
42	d2b30a1	Alignment	not modelled	99.4	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
43	c3ewiB	Alignment	not modelled	99.4	8	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
44	d2b8ea2	Alignment	not modelled	99.4	33	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
45	c4hgnB	Alignment	not modelled	99.3	15	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
46	c4navB	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
47	c3n1uA	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, had superfamily, subfamily iii a; PDBTitle: structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
48	d1rkqa	Alignment	not modelled	99.2	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
49	d1nnla	Alignment	not modelled	99.2	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
50	d1wpga4	Alignment	not modelled	99.2	16	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
51	d1wr8a	Alignment	not modelled	99.2	24	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
52	c3m1yA	Alignment	not modelled	99.2	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori

53	d1l6ra_	Alignment	not modelled	99.2	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
54	c3daoB_	Alignment	not modelled	99.1	22	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
55	d1j97a_	Alignment	not modelled	99.1	17	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
56	c4zexA_	Alignment	not modelled	99.1	23	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
57	d1nrwa_	Alignment	not modelled	99.0	28	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
58	d1rkua_	Alignment	not modelled	99.0	18	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
59	d1rlma_	Alignment	not modelled	98.9	24	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
60	c3r4cA_	Alignment	not modelled	98.9	22	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
61	c3fzqA_	Alignment	not modelled	98.9	20	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
62	c3dnpA_	Alignment	not modelled	98.9	26	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
63	c2qyhD_	Alignment	not modelled	98.9	24	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
64	c3pgvB_	Alignment	not modelled	98.8	25	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
65	c3niwA_	Alignment	not modelled	98.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
66	d2feaa1	Alignment	not modelled	98.8	18	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
67	d2rbka1	Alignment	not modelled	98.7	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
68	d1nf2a_	Alignment	not modelled	98.7	23	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
69	c3fvvA_	Alignment	not modelled	98.5	21	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	c3gyvA_	Alignment	not modelled	98.4	15	PDB header: hydrolase Chain: A: PDB Molecule: ntd biosynthesis operon putative hydrolase ntdb; PDBTitle: crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
71	d1s2oa1	Alignment	not modelled	98.3	26	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
72	c3kd3A_	Alignment	not modelled	98.3	14	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
73	c4b6jA_	Alignment	not modelled	98.3	23	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
74	d1wzca1	Alignment	not modelled	98.2	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
75	d1q3ia_	Alignment	not modelled	98.2	14	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
76	c5gvxA_	Alignment	not modelled	98.1	22	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-phosphate phosphatase; PDBTitle: structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
77	d1xvia_	Alignment	not modelled	98.0	26	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof PDB header: hydrolase

78	c1xviA_	Alignment	not modelled	98.0	26	Chain: A: PDB Molecule: putative mannosyl-3-phosphoglycerate phosphatase; PDBTitle: crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
79	d2vkqa1	Alignment	not modelled	97.9	16	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
80	c2i55C_	Alignment	not modelled	97.9	20	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
81	d1zs9a1	Alignment	not modelled	97.8	15	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
82	c4bndB_	Alignment	not modelled	97.8	20	PDB header: isomerase Chain: B: PDB Molecule: alpha-phosphoglucomutase; PDBTitle: structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
83	c1y8aA_	Alignment	not modelled	97.7	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
84	c5dxlA_	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
85	c3iruA_	Alignment	not modelled	97.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phosonoacetaldehyde hydrolase like protein from2 oleispira antarctica
86	c6cj0A_	Alignment	not modelled	97.6	24	PDB header: lyase Chain: A: PDB Molecule: trehalose phosphatase; PDBTitle: chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
87	c3zupB_	Alignment	not modelled	97.6	23	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.
88	d2fuea1	Alignment	not modelled	97.5	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
89	d1qvia_	Alignment	not modelled	97.5	17	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
90	d1swva_	Alignment	not modelled	97.4	17	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
91	c5ue7A_	Alignment	not modelled	97.4	18	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: crystal structure of the phosphomannomutase pmm1 from candida2 albicans, apoenzyme state
92	c3d6jA_	Alignment	not modelled	97.2	21	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
93	c3gwiA_	Alignment	not modelled	97.2	17	PDB header: hydrolase Chain: A: PDB Molecule: magnesium-transporting atpase, p-type 1; PDBTitle: crystal structure of mg-atpase nucleotide binding domain
94	d1u02a_	Alignment	not modelled	97.2	20	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
95	c3mc1A_	Alignment	not modelled	97.2	9	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
96	d2bdua1	Alignment	not modelled	97.2	17	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
97	c3mpoD_	Alignment	not modelled	97.2	33	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
98	c6f2xA_	Alignment	not modelled	97.2	17	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
99	d2ah5a1	Alignment	not modelled	97.1	22	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
100	c4eekA_	Alignment	not modelled	97.1	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-phosphoglucomutase-related protein; PDBTitle: crystal structure of had family hydrolase dr_1622 from deinococcus2 radiodurans r1 (target efi-501256) with bound phosphate and sodium
101	d2amya1	Alignment	not modelled	97.1	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
102	d1te2a_	Alignment	not modelled	97.0	22	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like

103	c3s6jC	 Alignment	not modelled	97.0	18	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
104	c2pibA	 Alignment	not modelled	96.9	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
105	c3ib6B	 Alignment	not modelled	96.9	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
106	c3sd7A	 Alignment	not modelled	96.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
107	c3m9lA	 Alignment	not modelled	96.7	18	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
108	c2odaB	 Alignment	not modelled	96.7	18	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
109	c2voyH	 Alignment	not modelled	96.6	13	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
110	d1u7pa	 Alignment	not modelled	96.6	11	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
111	d2hsza1	 Alignment	not modelled	96.5	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
112	d1mo7a	 Alignment	not modelled	96.5	14	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
113	c4nwiB	 Alignment	not modelled	96.5	21	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
114	c4gxtA	 Alignment	not modelled	96.4	16	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
115	c2qltA	 Alignment	not modelled	96.4	20	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
116	c3qypB	 Alignment	not modelled	96.4	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
117	d2gmwa1	 Alignment	not modelled	96.4	16	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
118	c4ex7A	 Alignment	not modelled	96.4	26	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
119	c3esqA	 Alignment	not modelled	96.2	16	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	c2pr7A	 Alignment	not modelled	96.2	17	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution