






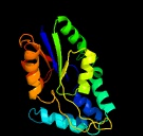




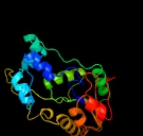
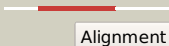

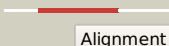







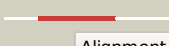

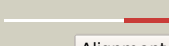






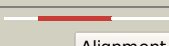
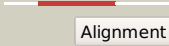



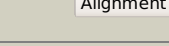



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2483c_(plsC)_2789290_2791032
Date	Wed Aug 7 12:50:11 BST 2019
Unique Job ID	d5d2d509835f27e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsC, from thermotoga maritima
2	c3fvvA_	 Alignment		100.0	25	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
3	c3p96A_	Alignment		99.9	23	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
4	c4gxtA_	Alignment		99.9	20	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
5	d1j97a_	Alignment		99.9	23	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
6	c3m1yA_	Alignment		99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
7	c4ezeB_	Alignment		99.9	19	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)
8	c3n28A_	Alignment		99.8	22	PDB header: hydrolase Chain: A; PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
9	c4as2D_	Alignment		99.8	22	PDB header: hydrolase Chain: D; PDB Molecule: phosphorylcholine phosphatase; PDBTitle: pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
10	d2feaa1	Alignment		99.8	12	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
11	d1nnla_	Alignment		99.7	19	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase

12	c4b6jA	 Alignment		99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
13	c3kd3A	 Alignment		99.6	17	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
14	d1s2oa1	 Alignment		99.6	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
15	d1rkua	 Alignment		99.6	19	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
16	c4umfC	 Alignment		99.6	22	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
17	c4hgnB	 Alignment		99.6	22	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
18	c5f34A	 Alignment		99.6	17	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
19	c3mmzA	 Alignment		99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
20	c3mn1B	 Alignment		99.5	22	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
21	c2r8zC	 Alignment	not modelled	99.5	17	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
22	d2vkqa1	 Alignment	not modelled	99.5	15	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
23	d1k1ea	 Alignment	not modelled	99.5	16	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi
24	c3n1uA	 Alignment	not modelled	99.5	22	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
25	c3niwA	 Alignment	not modelled	99.5	31	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
26	c2qyhD	 Alignment	not modelled	99.5	33	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
27	c3fzqA	 Alignment	not modelled	99.5	23	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
28	c2p9jH	 Alignment	not modelled	99.5	21	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus

29	c3ewiB	Alignment	not modelled	99.4	21	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
30	c3e8mD	Alignment	not modelled	99.4	18	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
31	c3dnpA	Alignment	not modelled	99.4	23	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
32	d1nrwa	Alignment	not modelled	99.4	32	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
33	c3pgvB	Alignment	not modelled	99.4	30	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
34	c3gygA	Alignment	not modelled	99.4	19	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
35	c4navB	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
36	d2rbka1	Alignment	not modelled	99.4	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
37	c4zexA	Alignment	not modelled	99.4	25	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
38	d1y8aa1	Alignment	not modelled	99.3	16	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
39	d1wr8a	Alignment	not modelled	99.3	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
40	c5knkB	Alignment	not modelled	99.3	14	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
41	d1l6ra	Alignment	not modelled	99.3	31	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
42	d2bdua1	Alignment	not modelled	99.3	18	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
43	c5gvxA	Alignment	not modelled	99.3	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
44	d1zs9a1	Alignment	not modelled	99.3	11	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
45	d1rlma	Alignment	not modelled	99.3	28	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
46	c4qjbB	Alignment	not modelled	99.3	32	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
47	d1wzca1	Alignment	not modelled	99.3	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
48	c1xviA	Alignment	not modelled	99.2	27	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
49	d1xvia	Alignment	not modelled	99.2	27	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
50	c3r4cA	Alignment	not modelled	99.2	31	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
51	c3n07B	Alignment	not modelled	99.2	16	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
52	c3iruA	Alignment	not modelled	99.2	10	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
						PDB header: hydrolase

53	c3daoB_	Alignment	not modelled	99.2	23	Chain: B: PDB Molecule: putative pnosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
54	d1rkqa_	Alignment	not modelled	99.2	29	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
55	d2b30a1	Alignment	not modelled	99.2	24	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
56	d1nf2a_	Alignment	not modelled	99.2	33	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
57	c5dxlA_	Alignment	not modelled	99.1	22	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
58	c2pibA_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
59	c3l5kA_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: the crystal structure of human haloacid dehalogenase-like hydrolase2 domain containing 1a (hdhd1a)
60	c3zupB_	Alignment	not modelled	99.1	37	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.
61	d1iuqa_	Alignment	not modelled	99.1	23	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
62	d1swva_	Alignment	not modelled	99.1	11	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
63	c4nwiB_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: B: PDB Molecule: 7-methylguanosine phosphate-specific 5'-nucleotidase; PDBTitle: crystal structure of cytosolic 5'-nucleotidase iiii (cn-iiii) bound to2 cytidine
64	c3d6jA_	Alignment	not modelled	99.1	10	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
65	c3l7yA_	Alignment	not modelled	99.0	24	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
66	d1zrna_	Alignment	not modelled	99.0	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
67	d2hsza1	Alignment	not modelled	99.0	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
68	d2go7a1	Alignment	not modelled	99.0	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
69	c3mc1A_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
70	c6cj0A_	Alignment	not modelled	99.0	28	PDB header: lyase Chain: A: PDB Molecule: trehalose phosphatase; PDBTitle: chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
71	c3s6jC_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
72	d1u02a_	Alignment	not modelled	99.0	24	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
73	c4bndB_	Alignment	not modelled	99.0	21	PDB header: isomerase Chain: B: PDB Molecule: alpha-phosphoglucomutase; PDBTitle: structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
74	d1u7pa_	Alignment	not modelled	99.0	22	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
75	c1y8aA_	Alignment	not modelled	98.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
76	c3nuqA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
77	c3um9A_	Alignment	not modelled	98.9	12	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase, type ii; PDBTitle: crystal structure of the defluorinating I-2-haloacid

						dehalogenase2 bpro0530
78	c5mrwF_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
79	c3cnhA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase family protein; PDBTitle: crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
80	c4uasA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
81	c2hoqA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
82	c2ympB_	Alignment	not modelled	98.9	10	PDB header: hydrolase Chain: B: PDB Molecule: l-haloacid dehalogenase; PDBTitle: chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
83	d2fuea1	Alignment	not modelled	98.9	27	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
84	d1te2a_	Alignment	not modelled	98.9	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
85	c4uw9A_	Alignment	not modelled	98.9	14	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structural of archaeal beta-phosphoglucomutase2 from hyper-thermophilic pyrococcus sp. strain st 04
86	c2om6A_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosphatase (ph0253) from2 pyrococcus horikoshii ot3
87	c4ex7A_	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
88	c5dxiB_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: B: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
89	c3mpoD_	Alignment	not modelled	98.9	33	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
90	c3m9IA_	Alignment	not modelled	98.8	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
91	d1zd3a1	Alignment	not modelled	98.8	14	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
92	c3umbA_	Alignment	not modelled	98.8	15	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase rsc1362
93	c4eekA_	Alignment	not modelled	98.8	17	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
94	c2no5B_	Alignment	not modelled	98.8	15	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
95	c3i28A_	Alignment	not modelled	98.8	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
96	d1cr6a1	Alignment	not modelled	98.8	15	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
97	c3dv9A_	Alignment	not modelled	98.8	10	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
98	d1qq5a_	Alignment	not modelled	98.8	13	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
99	c3qnmA_	Alignment	not modelled	98.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: haloalkane dehalogenase family member from bacteroides2 thetaiotaomicron of unknown function
100	d2amya1	Alignment	not modelled	98.8	26	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
101	c2pkeA_	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like family hydrolase; PDBTitle: crystal structure of haloacid dehalogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
						PDB header: isomerase

102	c3nasA	Alignment	not modelled	98.7	14	Chain: A; PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
103	c2qltA	Alignment	not modelled	98.7	14	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
104	d2fdra1	Alignment	not modelled	98.7	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
105	c3rfuC	Alignment	not modelled	98.7	17	PDB header: hydrolase, membrane protein Chain: C; PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
106	c6f2xA	Alignment	not modelled	98.7	14	PDB header: transferase Chain: A; PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
107	c3qypB	Alignment	not modelled	98.7	9	PDB header: hydrolase Chain: B; PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
108	d2b0ca1	Alignment	not modelled	98.7	15	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
109	d2ah5a1	Alignment	not modelled	98.7	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
110	c3e58A	Alignment	not modelled	98.6	11	PDB header: isomerase Chain: A; PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
111	c4uavA	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: A; PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidobis thaliana
112	d2b8ea1	Alignment	not modelled	98.6	15	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
113	c2yy6B	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: B; PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
114	d2hdoa1	Alignment	not modelled	98.6	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
115	d2fi1a1	Alignment	not modelled	98.6	15	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
116	d1wpga2	Alignment	not modelled	98.6	14	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
117	d2hcfa1	Alignment	not modelled	98.6	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
118	c3umcC	Alignment	not modelled	98.5	13	PDB header: hydrolase Chain: C; PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase pa0810
119	c2p11A	Alignment	not modelled	98.5	16	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bx_e_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
120	c3dghA	Alignment	not modelled	98.5	10	PDB header: hydrolase Chain: A; PDB Molecule: putative haloacid dehalogenase-like family hydrolase; PDBTitle: the structure of a putative haloacid dehalogenase-like family2 hydrolase from bacteroides thetaiotaomicron vpi-5482