

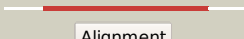

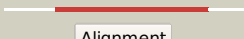







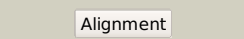

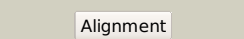



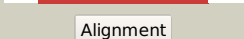



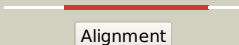








Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3042c_serB2_3401944_3403173
 Date Thu Aug 8 16:20:21 BST 2019
 Unique Job ID 6e5445d1f5a0ce35

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p96A_	 Alignment		100.0	85	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
2	c3n28A_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
3	c4ezeB_	 Alignment		100.0	29	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)
4	c3b9bA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
5	c2zxeA_	 Alignment		100.0	14	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
6	c3b8eC_	 Alignment		100.0	13	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
7	c1mhsA_	 Alignment		100.0	18	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
8	c3ixzA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
9	c3rfuC_	 Alignment		100.0	17	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
10	c3j09A_	 Alignment		100.0	20	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
11	c6a69A_	 Alignment		100.0	15	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	18	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
13	c5mrwF_	 Alignment		100.0	15	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
14	d1j97a_	 Alignment		100.0	39	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
15	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
16	c3j08A_	 Alignment		100.0	23	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
17	c4umwA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
18	c3m1yA_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
19	d1y8aa1	 Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
20	c3skyA_	 Alignment		100.0	22	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
21	c2b8eB_	 Alignment	not modelled	100.0	24	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
22	d1wpga2	 Alignment	not modelled	100.0	19	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
23	c2iyeC_	 Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
24	c3dnpA_	 Alignment	not modelled	100.0	19	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
25	c2qyhD_	 Alignment	not modelled	99.9	22	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
26	c3fzqA_	 Alignment	not modelled	99.9	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
27	c4qjbB_	 Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
28	d1nrwa_	 Alignment	not modelled	99.9	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof

29	d1nnla_	Alignment	not modelled	99.9	25	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
30	d1l6ra_	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
31	c3r4cA_	Alignment	not modelled	99.9	25	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
32	d1rkqa_	Alignment	not modelled	99.9	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
33	d2rbka1	Alignment	not modelled	99.9	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
34	c4zexA_	Alignment	not modelled	99.9	14	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
35	c3pgvB_	Alignment	not modelled	99.9	19	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
36	c3niwA_	Alignment	not modelled	99.9	22	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
37	c3gygA_	Alignment	not modelled	99.9	17	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
38	d1nf2a_	Alignment	not modelled	99.9	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
39	d2b30a1	Alignment	not modelled	99.9	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
40	d2b8ea1	Alignment	not modelled	99.9	32	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
41	c2r8zC_	Alignment	not modelled	99.9	25	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
42	c3daoB_	Alignment	not modelled	99.9	20	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
43	c3fvvA_	Alignment	not modelled	99.9	26	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
44	d1wr8a_	Alignment	not modelled	99.9	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
45	d1rlma_	Alignment	not modelled	99.9	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
46	c3l7yA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
47	c4umfC_	Alignment	not modelled	99.9	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
48	d1s2oa1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
49	c3mn1B_	Alignment	not modelled	99.9	25	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
50	c4hgnB_	Alignment	not modelled	99.9	21	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
51	c3n07B_	Alignment	not modelled	99.9	20	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	d1k1ea_	Alignment	not modelled	99.9	24	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi

53	d1rkua_	Alignment	not modelled	99.9	27	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
54	c3mmzA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
55	c3ewiB_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
56	c3e8mD_	Alignment	not modelled	99.9	23	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
57	c3kd3A_	Alignment	not modelled	99.9	20	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
58	c4b6jA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of phosphoserine phosphatase from t.2 onnurineus
59	c4navB_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
60	c3n1uA_	Alignment	not modelled	99.9	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
61	d2feaa1	Alignment	not modelled	99.8	15	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
62	c2p9jH_	Alignment	not modelled	99.8	21	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
63	c3zupB_	Alignment	not modelled	99.8	18	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.
64	c2nyiB_	Alignment	not modelled	99.8	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
65	d1wzca1	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
66	c5gvxA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-phosphate phosphatase; PDBTitle: structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
67	c1u8sB_	Alignment	not modelled	99.8	14	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
68	c5dxlA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
69	c4bndB_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: B: PDB Molecule: alpha-phosphoglucomutase; PDBTitle: structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
70	c3mpoD_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
71	d1xvia_	Alignment	not modelled	99.8	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
72	c1xviA_	Alignment	not modelled	99.8	19	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	c2i55C_	Alignment	not modelled	99.7	13	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
74	c6cj0A_	Alignment	not modelled	99.7	17	PDB header: lyase Chain: A: PDB Molecule: trehalose phosphatase; PDBTitle: chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
75	d1u02a_	Alignment	not modelled	99.7	15	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
76	d2amya1	Alignment	not modelled	99.7	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
77	c5ue7A_	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: crystal structure of the phosphomannomutase pmm1

						from candida2 albicans, apoenzyme state
78	d2fuea1	Alignment	not modelled	99.7	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
79	c5dxiB	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: B: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
80	c2hx1D	Alignment	not modelled	99.6	15	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
81	c3iruA	Alignment	not modelled	99.6	14	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
82	d1zs9a1	Alignment	not modelled	99.6	13	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
83	c3pdwA	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
84	d2vkqa1	Alignment	not modelled	99.6	16	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
85	c2cftA	Alignment	not modelled	99.6	19	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
86	d1swva	Alignment	not modelled	99.5	18	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
87	c2pibA	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
88	d1wvia	Alignment	not modelled	99.5	23	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
89	d1yv9a1	Alignment	not modelled	99.5	24	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
90	d1u8sa1	Alignment	not modelled	99.5	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
91	c3m9IA	Alignment	not modelled	99.5	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
92	c6f2xA	Alignment	not modelled	99.5	20	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
93	d2hcfa1	Alignment	not modelled	99.5	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
94	c3s6jC	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
95	d1ydfa1	Alignment	not modelled	99.4	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
96	c3mc1A	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
97	d1te2a	Alignment	not modelled	99.4	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
98	c1y8aA	Alignment	not modelled	99.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
99	c3d6jA	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
100	d2hsza1	Alignment	not modelled	99.4	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
101	d1u7pa	Alignment	not modelled	99.4	23	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
102	c2yy6B	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase

						from aquifex2 aeolicus vf5
103	d1vjra_	Alignment	not modelled	99.4	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
104	c4ex7A_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: alnb; PDBTitle: crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
105	c4uavA_	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of cbby (at3g48420) from arabidopsis thaliana
106	d2c4na1	Alignment	not modelled	99.4	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
107	d2ah5a1	Alignment	not modelled	99.3	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
108	c4eekA_	Alignment	not modelled	99.3	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
109	c3qgmC_	Alignment	not modelled	99.3	21	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
110	c2x4dA_	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
111	d2go7a1	Alignment	not modelled	99.3	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
112	d2bdua1	Alignment	not modelled	99.3	19	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
113	d1zpa1	Alignment	not modelled	99.3	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
114	c4uasA_	Alignment	not modelled	99.3	23	PDB header: hydrolase Chain: A: PDB Molecule: protein cbby; PDBTitle: crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
115	c3dv9A_	Alignment	not modelled	99.3	17	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
116	d1zd3a1	Alignment	not modelled	99.3	15	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
117	d1ys9a1	Alignment	not modelled	99.3	18	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
118	c3umbA_	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: dehalogenase-like hydrolase; PDBTitle: crystal structure of the l-2-haloacid dehalogenase rsc1362
119	c2hi0B_	Alignment	not modelled	99.3	18	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
120	d2fdra1	Alignment	not modelled	99.3	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like