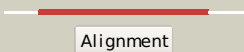

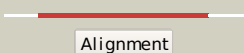


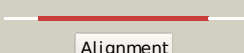



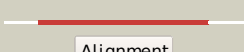

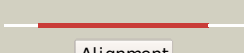

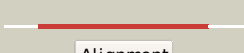















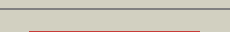
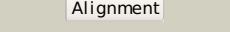
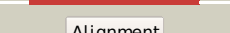




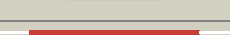

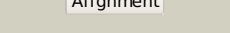
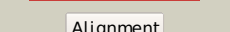
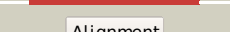


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u02a_	 Alignment		100.0	23	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
2	c3dnpA_	 Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stress response protein yhax; PDBTitle: crystal structure of stress response protein yhax from bacillus2 subtilis
3	d1nrwa_	 Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
4	c3fzqA_	 Alignment		100.0	13	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
5	c3gygA_	 Alignment		100.0	12	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
6	c3niwA_	 Alignment		100.0	17	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
7	c2qyhD_	 Alignment		100.0	18	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
8	c3pgvB_	 Alignment		100.0	17	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
9	d2rbka1	 Alignment		100.0	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
10	c3daoB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphatse; PDBTitle: crystal structure of a putative phosphatse (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
11	d1rlma_	 Alignment		100.0	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof

12	dlnf2a_	Alignment		100.0	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
13	dls2oa1	Alignment		100.0	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
14	c3r4cA_	Alignment		100.0	15	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
15	d2b30a1	Alignment		100.0	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
16	c3l7yA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
17	d2amyA1	Alignment		100.0	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
18	c2i55C_	Alignment		100.0	18	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
19	c1xviA_	Alignment		100.0	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
20	d1xvia_	Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
21	d1wr8a_	Alignment	not modelled	100.0	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
22	c3mpoD_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
23	d2fuea1	Alignment	not modelled	100.0	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
24	d1rkqa_	Alignment	not modelled	100.0	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
25	d1wzca1	Alignment	not modelled	99.9	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
26	d1l6ra_	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
27	c2r8zC_	Alignment	not modelled	99.8	22	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
28	d1k1ea_	Alignment	not modelled	99.8	22	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbi

29	c2cftA	 Alignment	not modelled	99.8	15	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
30	c3mmzA	 Alignment	not modelled	99.8	22	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	c3e8mD	 Alignment	not modelled	99.8	16	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
32	c3ewiB	 Alignment	not modelled	99.8	21	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
33	c3mn1B	 Alignment	not modelled	99.8	26	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
34	c3n1uA	 Alignment	not modelled	99.8	23	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
35	c3n07B	 Alignment	not modelled	99.7	21	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	c2p9jH	 Alignment	not modelled	99.7	21	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
37	c2hx1D	 Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had PDBTitle: crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
38	c3p96A	 Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
39	d1wvia	 Alignment	not modelled	99.7	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
40	d1yv9a1	 Alignment	not modelled	99.7	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
41	c3n28A	 Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
42	c3pdwA	 Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
43	d1ydfa1	 Alignment	not modelled	99.6	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
44	d1rkua	 Alignment	not modelled	99.6	10	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
45	d1j97a	 Alignment	not modelled	99.6	22	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
46	d1ys9a1	 Alignment	not modelled	99.5	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
47	c3kd3A	 Alignment	not modelled	99.5	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
48	c3qgmC	 Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
49	c3m1yA	 Alignment	not modelled	99.5	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
50	c3fvvA	 Alignment	not modelled	99.5	14	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
51	d1vjra	 Alignment	not modelled	99.4	11	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
52	c1zjjA	 Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
53	d2c4na1	 Alignment	not modelled	99.3	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
		 Alignment				Fold: HAD-like

54	d1nnla_	Alignment	not modelled	99.3	21	Superfamily: HAD-like Family: Phosphoserine phosphatase
55	c3l8hC_	Alignment	not modelled	99.3	21	PDB header: hydrolase Chain: C: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of d,d-heptose 1.7-bisphosphate phosphatase from b.2 bronchiseptica complexed with magnesium and phosphate
56	d1u7pa_	Alignment	not modelled	99.2	20	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
57	c3iruA_	Alignment	not modelled	99.2	17	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
58	c2iyeC_	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
59	d2o2xa1	Alignment	not modelled	99.1	18	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
60	d2feaa1	Alignment	not modelled	99.1	13	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
61	d2gmwa1	Alignment	not modelled	99.1	16	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
62	c2ho4A_	Alignment	not modelled	99.1	18	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain PDBTitle: crystal structure of protein from mouse mm.236127
63	c3esqA_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: d,d-heptose 1,7-bisphosphate phosphatase; PDBTitle: crystal structure of calcium-bound d,d-heptose 1.7-2 bisphosphate phosphatase from e. coli
64	c3dv9A_	Alignment	not modelled	99.0	19	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucosmutase; PDBTitle: putative beta-phosphoglucosmutase from bacteroides vulgatus.
65	c3s6jC_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
66	d1zs9a1	Alignment	not modelled	99.0	21	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
67	c3m9lA_	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: crystal structure of probable had family hydrolase from2 pseudomonas fluorescens pf-5
68	c2hi0B_	Alignment	not modelled	98.9	12	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
69	d2fdra1	Alignment	not modelled	98.9	12	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosmutase-like
70	c2pibA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucosmutase from2 thermotoga maritima
71	d2go7a1	Alignment	not modelled	98.9	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosmutase-like
72	c2odaB_	Alignment	not modelled	98.8	25	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
73	c2yy6B_	Alignment	not modelled	98.8	23	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
74	d2hsza1	Alignment	not modelled	98.8	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosmutase-like
75	c3mc1A_	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
76	d1swva_	Alignment	not modelled	98.8	14	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
77	d2ah5a1	Alignment	not modelled	98.8	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosmutase-like
78	c1cr6A_	Alignment	not modelled	98.7	18	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor

79	c3d6jA	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
80	c2pkeA	Alignment	not modelled	98.7	9	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
81	d1cr6a1	Alignment	not modelled	98.7	23	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
82	d2hcfa1	Alignment	not modelled	98.7	12	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosaminidase-like
83	c3qnmA	Alignment	not modelled	98.6	18	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
84	d1qq5a	Alignment	not modelled	98.6	24	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
85	d1wpga2	Alignment	not modelled	98.6	20	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
86	d1x42a1	Alignment	not modelled	98.6	13	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
87	d2fpwa1	Alignment	not modelled	98.6	18	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
88	c3j08A	Alignment	not modelled	98.6	16	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
89	c2om6A	Alignment	not modelled	98.6	13	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosphatase) from2 pyrococcus horikoshii ot3
90	d1y8aa1	Alignment	not modelled	98.5	14	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
91	c3nuqA	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
92	c3l5kA	Alignment	not modelled	98.5	23	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain- PDBTitle: the crystal structure of human haloacid dehalogenase-like2 hydrolase domain containing 1a (hdhd1a)
93	c3nasA	Alignment	not modelled	98.5	12	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucosaminidase; PDBTitle: the crystal structure of beta-phosphoglucosaminidase from bacillus2 subtilis
94	c3kzxA	Alignment	not modelled	98.5	13	PDB header: hydrolase Chain: A: PDB Molecule: had-superfamily hydrolase, subfamily ia, variant 1; PDBTitle: crystal structure of a had-superfamily hydrolase from ehrlichia2 chaffeensis at 1.9a resolution
95	c3e58A	Alignment	not modelled	98.5	9	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucosaminidase; PDBTitle: crystal structure of putative beta-phosphoglucosaminidase from2 streptococcus thermophilus
96	d2b8ea1	Alignment	not modelled	98.4	29	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
97	d1te2a	Alignment	not modelled	98.4	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosaminidase-like
98	d1zrna	Alignment	not modelled	98.4	23	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
99	c3kc2A	Alignment	not modelled	98.4	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
100	d1o08a	Alignment	not modelled	98.4	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosaminidase-like
101	c3rfuC	Alignment	not modelled	98.4	25	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting piib-type atpase
102	c3j09A	Alignment	not modelled	98.3	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
103	c3ib6B	Alignment	not modelled	98.3	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
						PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase2

104	c2hoqA_	Alignment	not modelled	98.3	24	Chain: A; PDB Molecule: putative nad-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
105	d2hdoa1	Alignment	not modelled	98.3	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
106	c2qltA_	Alignment	not modelled	98.3	16	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
107	d2gfha1	Alignment	not modelled	98.2	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
108	d1xpja_	Alignment	not modelled	98.2	19	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
109	c3k1zA_	Alignment	not modelled	98.2	12	PDB header: hydrolase Chain: A; PDB Molecule: haloacid dehalogenase-like hydrolase domain-containing PDBTitle: crystal structure of human haloacid dehalogenase-like hydrolase domain2 containing 3 (hdhd3)
110	c2zxeA_	Alignment	not modelled	98.1	13	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
111	c3sd7A_	Alignment	not modelled	98.1	16	PDB header: hydrolase Chain: A; PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
112	c3ddhA_	Alignment	not modelled	98.1	11	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
113	c3b9bA_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
114	d2obba1	Alignment	not modelled	98.0	27	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
115	c2b8eB_	Alignment	not modelled	98.0	23	PDB header: membrane protein Chain: B; PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
116	c3cnhA_	Alignment	not modelled	97.9	10	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
117	c2w11B_	Alignment	not modelled	97.9	11	PDB header: hydrolase Chain: B; PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
118	d1ltqa1	Alignment	not modelled	97.9	25	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
119	c1mhsA_	Alignment	not modelled	97.9	12	PDB header: membrane protein, proton transport Chain: A; PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
120	d2fila1	Alignment	not modelled	97.9	12	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like