



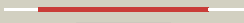



















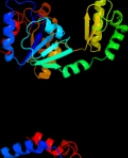





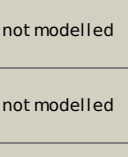


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dnpA_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stress response protein yhax; PDBTitle: crystal structure of stress response protein yhax from bacillus2 subtilis
2	c3niwA_	 Alignment		100.0	21	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
3	d1nrwa_	 Alignment		100.0	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
4	d1nf2a_	 Alignment		100.0	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
5	c3pgvB_	 Alignment		100.0	34	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
6	d1rlma_	 Alignment		100.0	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
7	c3fzqA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
8	c2qyhD_	 Alignment		100.0	21	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
9	c3daoB_	 Alignment		100.0	20	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
10	d2rbka1	 Alignment		100.0	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
11	d2b30a1	 Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof

12	dlrkqa_	Alignment		100.0	24	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
13	c3r4cA_	Alignment		100.0	21	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
14	c3gygA_	Alignment		100.0	14	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
15	c3l7yA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
16	c3mpoD_	Alignment		100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: predicted hydrolase of the had superfamily; PDBTitle: the crystal structure of a hydrolase from lactobacillus brevis
17	dlS2oa1	Alignment		100.0	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
18	dlwr8a_	Alignment		100.0	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
19	dl16ra_	Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
20	c2i55C_	Alignment		100.0	19	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
21	dlwzca1	Alignment	not modelled	100.0	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
22	dlxvia_	Alignment	not modelled	100.0	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
23	clxviA_	Alignment	not modelled	100.0	16	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
24	dlu02a_	Alignment	not modelled	100.0	17	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
25	d2amya1	Alignment	not modelled	100.0	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
26	d2fuea1	Alignment	not modelled	100.0	18	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
27	dlk1ea_	Alignment	not modelled	99.9	29	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
28	c3e8mD_	Alignment	not modelled	99.9	27	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

29	c3mmzA_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
30	c3n1uA_	Alignment	not modelled	99.9	32	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
31	c3mn1B_	Alignment	not modelled	99.9	28	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
32	c2r8zC_	Alignment	not modelled	99.9	20	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
33	c3ewiB_	Alignment	not modelled	99.9	28	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
34	c3n07B_	Alignment	not modelled	99.9	24	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
35	c2p9jH_	Alignment	not modelled	99.9	21	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
36	c3p96A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
37	c3n28A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
38	d1j97a_	Alignment	not modelled	99.8	27	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
39	c2hx1D_	Alignment	not modelled	99.8	12	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
40	d1rkua_	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
41	c2cftA_	Alignment	not modelled	99.8	13	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
42	c3m1yA_	Alignment	not modelled	99.8	33	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
43	c3fvvA_	Alignment	not modelled	99.8	13	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	d1yv9a1	Alignment	not modelled	99.7	13	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
45	c3pdwA_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
46	d1nnla_	Alignment	not modelled	99.6	21	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
47	d1wvia_	Alignment	not modelled	99.6	12	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
48	c3kd3A_	Alignment	not modelled	99.6	18	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
49	d1ydfa1	Alignment	not modelled	99.6	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
50	d1ys9a1	Alignment	not modelled	99.6	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
51	d1y8aa1	Alignment	not modelled	99.5	15	Fold: HAD-like Superfamily: HAD-like Family: AF1437-like
52	d2c4na1	Alignment	not modelled	99.4	12	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
53	d1wpga2	Alignment	not modelled	99.4	16	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
						PDB header: hydrolase

54	c1zjjA	Alignment	not modelled	99.4	14	Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
55	c2iyeC	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
56	c3qgmC	Alignment	not modelled	99.3	13	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
57	d2feaa1	Alignment	not modelled	99.3	14	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
58	d1vjra	Alignment	not modelled	99.2	14	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
59	d1zs9a1	Alignment	not modelled	99.2	16	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
60	c3rfuC	Alignment	not modelled	99.1	20	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
61	c3b9bA	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
62	c3j08A	Alignment	not modelled	99.0	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
63	c3l8hC	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: C: PDB Molecule: putative haloacid dehalogenase-like PDBTitle: crystal structure of d,d-heptose 1,7-bisphosphate phosphatase from b.2 bronchiseptica complexed with magnesium and phosphate
64	c3j09A	Alignment	not modelled	99.0	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
65	c1mhsA	Alignment	not modelled	99.0	22	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
66	c2zxeA	Alignment	not modelled	99.0	21	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
67	d2b8ea1	Alignment	not modelled	98.9	31	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
68	d2gmwa1	Alignment	not modelled	98.9	18	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
69	c3mc1A	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
70	d1u7pa	Alignment	not modelled	98.9	27	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
71	c3esqA	Alignment	not modelled	98.9	18	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
72	c2pibA	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
73	c3b8eC	Alignment	not modelled	98.9	15	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
74	c3b8cB	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
75	d1cr6a1	Alignment	not modelled	98.8	22	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
76	c3ixZA	Alignment	not modelled	98.8	12	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
77	c3iruA	Alignment	not modelled	98.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phoshonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phoshonoacetaldehyde hydrolase like protein from2 oleispira antarctica
78	c3m9lA	Alignment	not modelled	98.8	21	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 PDB header: hydrolase

79	c1cr6A_	Alignment	not modelled	98.7	18	Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
80	c2ho4A_	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain PDBTitle: crystal structure of protein from mouse mm.236127
81	c3d6jA_	Alignment	not modelled	98.7	27	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
82	d1xpja_	Alignment	not modelled	98.7	17	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
83	d2o2xa1	Alignment	not modelled	98.7	22	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
84	d2obba1	Alignment	not modelled	98.6	22	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
85	d1zd3a1	Alignment	not modelled	98.6	19	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
86	c2b8eB_	Alignment	not modelled	98.6	28	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
87	c3dv9A_	Alignment	not modelled	98.6	20	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
88	d2hsza1	Alignment	not modelled	98.6	31	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
89	d2fpwa1	Alignment	not modelled	98.6	20	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
90	d1qq5a_	Alignment	not modelled	98.5	19	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
91	d1o08a_	Alignment	not modelled	98.5	9	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
92	c3kzxA_	Alignment	not modelled	98.4	14	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
93	d2fdra1	Alignment	not modelled	98.4	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
94	c2hi0B_	Alignment	not modelled	98.4	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
95	d1swva_	Alignment	not modelled	98.4	26	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
96	c3nuqA_	Alignment	not modelled	98.4	27	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
97	c3s6jC_	Alignment	not modelled	98.4	26	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
98	c3nasA_	Alignment	not modelled	98.4	27	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
99	d1te2a_	Alignment	not modelled	98.4	23	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
100	d1x42a1	Alignment	not modelled	98.4	12	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
101	c3ddhA_	Alignment	not modelled	98.4	32	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
102	d2fi1a1	Alignment	not modelled	98.4	22	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
103	c2hoqA_	Alignment	not modelled	98.4	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
104	d2hcfal	Alignment	not modelled	98.3	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like

105	c2yy6B_	Alignment	not modelled	98.3	32	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
106	dlzrna_	Alignment	not modelled	98.2	22	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
107	d2go7a1	Alignment	not modelled	98.2	28	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
108	d2vkqa1	Alignment	not modelled	98.2	28	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
109	d1ltqa1	Alignment	not modelled	98.1	19	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
110	d2ah5a1	Alignment	not modelled	98.1	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
111	c2w11B_	Alignment	not modelled	98.0	13	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfobolus2 tokodaii
112	c3e58A_	Alignment	not modelled	98.0	16	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucumutase; PDBTitle: crystal structure of putative beta-phosphoglucumutase from2 streptococcus thermophilus
113	c3cnhA_	Alignment	not modelled	98.0	16	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
114	c3l5kA_	Alignment	not modelled	98.0	22	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)
115	c2om6A_	Alignment	not modelled	98.0	12	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
116	d2hdoa1	Alignment	not modelled	98.0	22	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
117	c2i6xA_	Alignment	not modelled	98.0	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the structure of a predicted had-like family hydrolase from2 porphyromonas gingivalis.
118	c3qnmA_	Alignment	not modelled	98.0	13	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
119	c2pkeA_	Alignment	not modelled	97.9	11	PDB header: hydrolase Chain: A: PDB Molecule: haloacid delahogenase-like family hydrolase; PDBTitle: crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
120	c3ib6B_	Alignment	not modelled	97.8	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b