



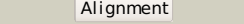

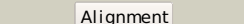


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d6jA_	 Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
2	c3dv9A_	 Alignment		99.9	20	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
3	d1te2a_	 Alignment		99.9	23	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
4	d2fdra1	 Alignment		99.9	23	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
5	d2hdoa1	 Alignment		99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
6	c3iruA_	 Alignment		99.9	20	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
7	c2piB_A_	 Alignment		99.9	29	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
8	d1o08a_	 Alignment		99.9	23	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
9	d2go7a1	 Alignment		99.9	14	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
10	d2hsza1	 Alignment		99.9	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
11	c3e58A_	 Alignment		99.9	23	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucomutase; PDBTitle: crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus

12	d1swva_	Alignment		99.9	21	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
13	d2ah5a1	Alignment		99.9	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosucrose hydrolase-like
14	c3mc1A_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
15	c3s6jC_	Alignment		99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
16	d2fi1a1	Alignment		99.9	21	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
17	c3nuqA_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
18	c3l5ka_	Alignment		99.9	28	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)
19	c2hi0B_	Alignment		99.9	22	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
20	c3nasA_	Alignment		99.9	27	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucosucrose hydrolase; PDBTitle: the crystal structure of beta-phosphoglucosucrose hydrolase from bacillus2 subtilis
21	c2yy6B_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
22	c2pkeA_	Alignment	not modelled	99.9	14	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
23	c2qltA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: (dl)-glycerol-3-phosphatase 1; PDBTitle: crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
24	c3qnmA_	Alignment	not modelled	99.9	15	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
25	c3cnhA_	Alignment	not modelled	99.9	20	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
26	d2gfha1	Alignment	not modelled	99.9	22	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosucrose hydrolase-like
27	c3sd7A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
						Fold: HAD-like

28	d2g80a1	Alignment	not modelled	99.9	15	Superfamily: HAD-like Family: Enolase-phosphatase E1
29	d1zs9a1	Alignment	not modelled	99.9	13	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
30	c2g80C	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: C: PDB Molecule: protein utr4; PDBTitle: crystal structure of utr4 protein (unknown transcript 4 protein)2 (yel038w) from saccharomyces cerevisiae at 2.28 a resolution
31	c3kzxA	Alignment	not modelled	99.9	19	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
32	c2om6A	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
33	c2no5B	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
34	c2i6xA	Alignment	not modelled	99.8	12	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.
35	c3ed5A	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yfnb; PDBTitle: the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
36	c2hogA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
37	c3m9lA	Alignment	not modelled	99.8	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
38	c3ddhA	Alignment	not modelled	99.8	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
39	d1qq5a	Alignment	not modelled	99.8	21	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
40	d1x42a1	Alignment	not modelled	99.8	19	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
41	d1zd3a1	Alignment	not modelled	99.8	13	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
42	d1zrna	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
43	c3k1zA	Alignment	not modelled	99.8	19	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)
44	c3pdwA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
45	c2w11B	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfobolus2 tokodaii
46	d2hcfa1	Alignment	not modelled	99.8	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
47	d2b0ca1	Alignment	not modelled	99.8	14	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
48	d2o2xa1	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
49	c1cr6A	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
50	c3qgmC	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
51	d1u7pa	Alignment	not modelled	99.7	18	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
52	d1wvia	Alignment	not modelled	99.7	17	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
						Fold: HAD-like

53	d2c4na1	Alignment	not modelled	99.7	14	Superfamily: HAD-like Family: NagD-like
54	d1cr6a1	Alignment	not modelled	99.7	17	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
55	c2ho4A	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain PDBTitle: crystal structure of protein from mouse mm.236127
56	d1vjra	Alignment	not modelled	99.7	11	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
57	d2gmwa1	Alignment	not modelled	99.7	21	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
58	d1ys9a1	Alignment	not modelled	99.7	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
59	c3l8hC	Alignment	not modelled	99.7	23	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
60	c2p11A	Alignment	not modelled	99.7	13	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
61	c3esqA	Alignment	not modelled	99.7	19	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
62	d1ydfa1	Alignment	not modelled	99.7	13	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
63	c2cftA	Alignment	not modelled	99.7	19	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
64	c2x4dB	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine2 inorganic pyrophosphate phosphatase lhpp
65	d1yv9a1	Alignment	not modelled	99.7	15	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
66	c3kd3A	Alignment	not modelled	99.6	9	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
67	d1j97a	Alignment	not modelled	99.6	15	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
68	c2zg6A	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein st2620; PDBTitle: crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfobolus tokodaii
69	c3m1yA	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
70	c2hx1D	Alignment	not modelled	99.6	15	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
71	d2fpwa1	Alignment	not modelled	99.6	13	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
72	d2feaa1	Alignment	not modelled	99.6	12	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
73	d1rkua	Alignment	not modelled	99.5	10	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH
74	c2odaB	Alignment	not modelled	99.5	16	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
75	d1nnla	Alignment	not modelled	99.5	13	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
76	c1zjjA	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
77	c2pr7A	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032

					kitasato at 1.44 a resolution
78	d1qyia_	Alignment	not modelled	99.4	22 Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
79	c3ib6B_	Alignment	not modelled	99.4	17 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
80	c3fvvA_	Alignment	not modelled	99.2	16 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
81	d1l6ra_	Alignment	not modelled	99.2	8 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
82	c3e8mD_	Alignment	not modelled	99.1	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
83	c3p96A_	Alignment	not modelled	99.1	16 PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
84	d1k1ea_	Alignment	not modelled	99.1	23 Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
85	c3mn1B_	Alignment	not modelled	99.1	19 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
86	d1wr8a_	Alignment	not modelled	99.0	13 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
87	c2i7dB_	Alignment	not modelled	99.0	13 PDB header: hydrolase Chain: B: PDB Molecule: 5'(3')-deoxyribonucleotidase, cytosolic type; PDBTitle: structure of human cytosolic deoxyribonucleotidase in2 complex with deoxyuridine, alf4 and mg2+
88	c3kc2A_	Alignment	not modelled	99.0	15 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
89	c3ewiB_	Alignment	not modelled	99.0	13 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
90	c2r8zC_	Alignment	not modelled	98.9	23 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
91	c3n28A_	Alignment	not modelled	98.9	16 PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
92	c2p9jH_	Alignment	not modelled	98.9	22 PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
93	c3mmzA_	Alignment	not modelled	98.9	15 PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
94	c3n1uA_	Alignment	not modelled	98.8	13 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
95	c3n07B_	Alignment	not modelled	98.8	14 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
96	c2qyhD_	Alignment	not modelled	98.8	15 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
97	d1q92a_	Alignment	not modelled	98.8	10 Fold: HAD-like Superfamily: HAD-like Family: 5'(3')-deoxyribonucleotidase (dNT-2)
98	d1s2oa1	Alignment	not modelled	98.7	16 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
99	d1nf2a_	Alignment	not modelled	98.7	16 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
100	d2b30a1	Alignment	not modelled	98.6	16 Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
101	c3niwA_	Alignment	not modelled	98.6	12 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
102	c3fzqA_	Alignment	not modelled	98.6	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
103	c3r4cA_	Alignment	not modelled	98.6	17	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
104	c3zvmA_	Alignment	not modelled	98.6	19	PDB header: hydrolase/transferase/dna Chain: A: PDB Molecule: bifunctional polynucleotide phosphatase/kinase; PDBTitle: the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
105	d1wzca1	Alignment	not modelled	98.6	11	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
106	d2rbka1	Alignment	not modelled	98.6	16	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
107	d1nrwa_	Alignment	not modelled	98.6	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
108	c3dnpA_	Alignment	not modelled	98.5	14	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
109	c1xviA_	Alignment	not modelled	98.5	9	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
110	d1xvia_	Alignment	not modelled	98.5	9	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
111	c3l7yA_	Alignment	not modelled	98.4	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
112	d1rlma_	Alignment	not modelled	98.4	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
113	d1vj5a1	Alignment	not modelled	98.4	18	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
114	d1rkqa_	Alignment	not modelled	98.4	15	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
115	c3gygA_	Alignment	not modelled	98.4	10	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
116	c3pgvB_	Alignment	not modelled	98.3	13	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
117	c1vj5B_	Alignment	not modelled	98.2	17	PDB header: transferase Chain: B: PDB Molecule: 5' polynucleotide kinase-3' phosphatase catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
118	c3daoB_	Alignment	not modelled	98.2	13	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
119	d1z5ga1	Alignment	not modelled	98.2	14	Fold: HAD-like Superfamily: HAD-like Family: Class B acid phosphatase, AphA
120	d1ltqa1	Alignment	not modelled	98.1	15	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase