




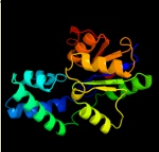

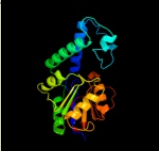



























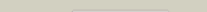








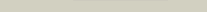
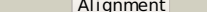

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iruA_	 Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phoshonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phoshonoacetaldehyde hydrolase like protein from2 oleispira antarctica
2	c2qltA_	 Alignment		100.0	31	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
3	c3d6jA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
4	d1te2a_	 Alignment		100.0	21	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
5	c3dv9A_	 Alignment		100.0	30	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: putative beta-phosphoglucomutase from bacteroides vulgatus.
6	d1swva_	 Alignment		100.0	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
7	c3nuqA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
8	c3mc1A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
9	c3s6jC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
10	d2hsza1	 Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
11	c2yy6B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5

12	d2ah5a1	Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
13	c3qnmA	Alignment		100.0	14	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
14	d2hdoa1	Alignment		100.0	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
15	d2go7a1	Alignment		100.0	19	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
16	c3l5kA	Alignment		100.0	27	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)
17	c3e58A	Alignment		100.0	16	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucumutase; PDBTitle: crystal structure of putative beta-phosphoglucumutase from2 streptococcus thermophilus
18	c2hi0B	Alignment		100.0	17	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
19	c2no5B	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
20	d2fdra1	Alignment		99.9	23	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
21	c2om6A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
22	c2pibA	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucumutase from2 thermotoga maritima
23	c3m9lA	Alignment	not modelled	99.9	24	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
24	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
25	c2hoqA	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
26	dlzrna	Alignment	not modelled	99.9	19	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
27	dlzs9a1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
28	d2fila1	Alignment	not modelled	99.9	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like

29	d1x42a1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
30	d2gfhA1	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
31	c3ed5A	Alignment	not modelled	99.9	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
32	d1o08a	Alignment	not modelled	99.9	25	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
33	d1qq5a	Alignment	not modelled	99.9	22	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
34	c2w11B	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfobolus2 tokodaii
35	c3ddhA	Alignment	not modelled	99.9	16	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
36	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
37	c3k1zA	Alignment	not modelled	99.9	20	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)
38	c3nasA	Alignment	not modelled	99.9	22	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucumutase; PDBTitle: the crystal structure of beta-phosphoglucumutase from bacillus2 subtilis
39	c2pkeA	Alignment	not modelled	99.9	16	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
40	d2g80a1	Alignment	not modelled	99.9	16	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
41	d2hcfA1	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucumutase-like
42	c2g80C	Alignment	not modelled	99.9	14	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
43	d1zd3a1	Alignment	not modelled	99.9	19	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
44	c3l8hC	Alignment	not modelled	99.9	22	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
45	d2gmwa1	Alignment	not modelled	99.9	22	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
46	c2p11A	Alignment	not modelled	99.9	18	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
47	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
48	c3esqA	Alignment	not modelled	99.9	22	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
49	d2c4na1	Alignment	not modelled	99.9	18	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
50	d1u7pa	Alignment	not modelled	99.8	19	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
51	d2o2xa1	Alignment	not modelled	99.8	21	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
52	c3kd3A	Alignment	not modelled	99.8	14	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
53	c2zg6A	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein st2620; PDBTitle: crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfobus tokodai
54	c2ho4A	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain PDBTitle: crystal structure of protein from mouse mm.236127
55	c3pdwA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
56	c2i6xA	Alignment	not modelled	99.8	13	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.
57	c1cr6A	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
58	c3m1yA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
59	d2b0ca1	Alignment	not modelled	99.8	15	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
60	d1cr6a1	Alignment	not modelled	99.8	22	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
61	d1vjra	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
62	d1wvia	Alignment	not modelled	99.8	22	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
63	c3qgmC	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
64	c2x4dB	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine2 inorganic pyrophosphate phosphatase lhpp
65	d1ys9a1	Alignment	not modelled	99.8	22	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
66	d1nnla	Alignment	not modelled	99.8	12	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
67	d1qvia	Alignment	not modelled	99.8	23	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
68	d1j97a	Alignment	not modelled	99.8	18	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
69	d2fpwa1	Alignment	not modelled	99.8	17	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
70	d2feaa1	Alignment	not modelled	99.8	11	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
71	c2odaB	Alignment	not modelled	99.8	26	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
72	d1ydfa1	Alignment	not modelled	99.8	18	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
73	d1yv9a1	Alignment	not modelled	99.7	20	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
74	c3ib6B	Alignment	not modelled	99.7	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
75	c2cftA	Alignment	not modelled	99.7	21	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
76	c1zjjA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
77	c2hx1D	Alignment	not modelled	99.6	18	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
78	d1rkua	Alignment	not modelled	99.6	14	Fold: HAD-like Superfamily: HAD-like

						Family: Homoserine kinase ThrH
79	c2pr7A_	Alignment	not modelled	99.6	20	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
80	d1q92a_	Alignment	not modelled	99.5	17	Fold: HAD-like Superfamily: HAD-like Family: 5'(3')-deoxyribonucleotidase (dNT-2)
81	c2i7dB_	Alignment	not modelled	99.5	15	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+
82	c3kc2A_	Alignment	not modelled	99.5	30	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
83	c3mn1B_	Alignment	not modelled	99.4	18	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
84	c3p96A_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
85	d1k1ea_	Alignment	not modelled	99.4	24	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
86	c3e8mD_	Alignment	not modelled	99.4	19	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
87	c3n07B_	Alignment	not modelled	99.4	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
88	c2r8zC_	Alignment	not modelled	99.3	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
89	c3fvvA_	Alignment	not modelled	99.3	21	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
90	c3n1uA_	Alignment	not modelled	99.3	24	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
91	c3n28A_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
92	d1wr8a_	Alignment	not modelled	99.2	29	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
93	c2p9jH_	Alignment	not modelled	99.2	19	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
94	c3mmzA_	Alignment	not modelled	99.2	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
95	c3ewiB_	Alignment	not modelled	99.1	17	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
96	d1l6ra_	Alignment	not modelled	99.1	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
97	c3niwA_	Alignment	not modelled	99.0	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
98	d1rkqa_	Alignment	not modelled	98.9	24	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
99	d2vkqa1	Alignment	not modelled	98.9	15	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
100	c3zvmA_	Alignment	not modelled	98.9	31	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
101	d1yj5a1	Alignment	not modelled	98.8	27	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
102	c2qyhD_	Alignment	not modelled	98.7	27	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

103	c3fzqA_	 Alignment	not modelled	98.7	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
104	c3daoB_	 Alignment	not modelled	98.7	22	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
105	d1z5ga1	 Alignment	not modelled	98.7	18	Fold: HAD-like Superfamily: HAD-like Family: Class B acid phosphatase, AphA
106	d1ltqa1	 Alignment	not modelled	98.6	17	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
107	c3dnpA_	 Alignment	not modelled	98.6	25	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
108	d2rbka1	 Alignment	not modelled	98.6	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
109	d1s2oa1	 Alignment	not modelled	98.6	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
110	c1yj5B_	 Alignment	not modelled	98.6	25	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
111	d2b30a1	 Alignment	not modelled	98.5	21	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
112	c3gygA_	 Alignment	not modelled	98.5	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
113	c3pgvB_	 Alignment	not modelled	98.5	31	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
114	d2bdua1	 Alignment	not modelled	98.5	14	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
115	d1rlma_	 Alignment	not modelled	98.5	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
116	c3l7yA_	 Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
117	d2b82a1	 Alignment	not modelled	98.4	16	Fold: HAD-like Superfamily: HAD-like Family: Class B acid phosphatase, AphA
118	d1nf2a_	 Alignment	not modelled	98.4	13	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
119	c3bwvB_	 Alignment	not modelled	98.3	20	PDB header: hydrolase Chain: B: PDB Molecule: putative 5'(3')-deoxyribonucleotidase; PDBTitle: crystal structure of deoxyribonucleotidase-like protein (np_764060.1)2 from staphylococcus epidermidis atcc 12228 at 1.55 a resolution
120	d1nrwa_	 Alignment	not modelled	98.3	17	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof