Phyre^2

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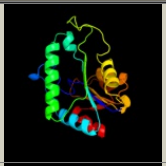
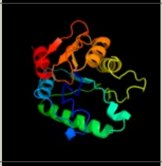
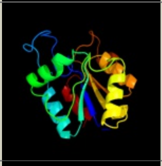
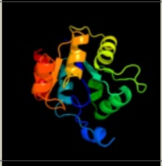
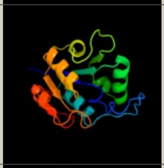
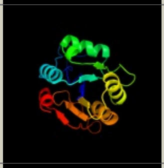
Description	P63228
Date	Thu Jan 5 12:07:58 GMT 2012
Unique Job ID	edfd7adbc8d276ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gmwa1	Alignment		100.0	100	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
2	c3esqA_	Alignment		100.0	100	**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
3	d2o2xa1	Alignment		100.0	34	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
4	c3l8hC_	Alignment		100.0	29	**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
5	c3iruA_	Alignment		100.0	23	**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
6	d1swva_	Alignment		100.0	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
7	c3dv9A_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** putative beta-phosphoglucomutase from bacteroides vulgatus.
8	d2hsza1	Alignment		100.0	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
9	c2odaB_	Alignment		100.0	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**hypothetical protein pspto_2114; **PDBTitle:** crystal structure of pspto_2114
10	c3mc1A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted phosphatase, had family; **PDBTitle:** crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
11	c3s6jC_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas syringae

12	c3d6jA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
13	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
14	c3nuqA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nucleotide phosphatase; **PDBTitle:** structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
15	d1te2a_	Alignment		100.0	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
16	d2fdra1	Alignment		99.9	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
17	d2ah5a1	Alignment		99.9	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
18	c2yy6B_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphoglycolate phosphatase; **PDBTitle:** crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
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	d1zs9a1	Alignment		99.9	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
21	d1zrna_	Alignment	not modelled	99.9	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
22	c3m9lA_	Alignment	not modelled	99.9	22	**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
23	d2gfha1	Alignment	not modelled	99.9	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
24	c2pibA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphorylated carbohydrates phosphatase tm_1254; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
25	c2ho4A_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain **PDBTitle:** crystal structure of protein from mouse mm.236127
26	d2fpwa1	Alignment	not modelled	99.9	29	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
27	c2hoqA_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had-hydrolase ph1655; **PDBTitle:** crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
28	c2om6A_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable phosphoserine phosphatase; **PDBTitle:** hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3

29	d1qq5a_	Alignment	not modelled	99.9	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
30	c3e58A_	Alignment	not modelled	99.9	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative beta-phosphoglucomutase; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
31	d2go7a1	Alignment	not modelled	99.9	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
32	c1cr6A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
33	d2hdoa1	Alignment	not modelled	99.9	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
34	c3sd7A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphatase; **PDBTitle:** 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
35	c2w11B_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2-haloalkanoic acid dehalogenase; **PDBTitle:** structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
36	d2hcfa1	Alignment	not modelled	99.9	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
37	d1x42a1	Alignment	not modelled	99.9	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
38	c3ib6B_	Alignment	not modelled	99.9	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
39	c3qnmA_	Alignment	not modelled	99.9	16	**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
40	d1vjra_	Alignment	not modelled	99.9	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
41	d1cr6a1	Alignment	not modelled	99.9	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
42	c3pdwA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized hydrolase yutf; **PDBTitle:** crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
43	c2qltA_	Alignment	not modelled	99.9	21	**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
44	c3qgmC_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**p-nitrophenyl phosphatase (pho2); **PDBTitle:** p-nitrophenyl phosphatase from archaeoglobus fulgidus
45	d1u7pa_	Alignment	not modelled	99.9	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
46	d1ys9a1	Alignment	not modelled	99.9	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
47	c3ddhA_	Alignment	not modelled	99.9	24	**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
48	c3l5kA_	Alignment	not modelled	99.9	21	**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)
49	d2c4na1	Alignment	not modelled	99.9	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
50	c2x4dB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phospholysine phosphohistidine inorganic pyrophosphate **PDBTitle:** crystal structure of human phospholysine phosphohistidine2 inorganic pyrophosphate phosphatase lhpp
51	c2cftA_	Alignment	not modelled	99.9	29	**PDB header:**phosphatase **Chain:** A: **PDB Molecule:**pyridoxal phosphate phosphatase; **PDBTitle:** crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
52	c2pkeA_	Alignment	not modelled	99.9	22	**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
53	d2g80a1	Alignment	not modelled	99.9	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
						Fold:HAD-like

54	d1zd3a1	Alignment	not modelled	99.9	21	**Superfamily:**HAD-like **Family:**YihX-like
55	d1qyia_	Alignment	not modelled	99.9	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
56	d1wvia_	Alignment	not modelled	99.9	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
57	c3cnhA_	Alignment	not modelled	99.9	14	**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
58	c3kd3A_	Alignment	not modelled	99.9	17	**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
59	d1o08a_	Alignment	not modelled	99.9	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
60	d1yv9a1	Alignment	not modelled	99.9	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
61	d1ydfa1	Alignment	not modelled	99.9	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
62	c3k1zA_	Alignment	not modelled	99.9	23	**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)
63	c2g80C_	Alignment	not modelled	99.9	11	**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
64	c3ed5A_	Alignment	not modelled	99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yfnb; **PDBTitle:** the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
65	c2i6xA_	Alignment	not modelled	99.9	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.
66	c3nasA_	Alignment	not modelled	99.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
67	c1zjjA_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ph1952; **PDBTitle:** crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
68	c3kzxA_	Alignment	not modelled	99.8	24	**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
69	c2p11A_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bxe_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
70	d1yj5a1	Alignment	not modelled	99.8	27	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
71	c3kc2A_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
72	d1nnla_	Alignment	not modelled	99.8	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
73	c2hx1D_	Alignment	not modelled	99.8	17	**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
74	d2fi1a1	Alignment	not modelled	99.8	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
75	d1j97a_	Alignment	not modelled	99.8	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
76	c3zvmA_	Alignment	not modelled	99.8	28	**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
77	d2feaa1	Alignment	not modelled	99.8	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**MtnX-like
78	d2b0ca1	Alignment	not modelled	99.8	15	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: YihX-like
79	c3m1yA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
80	c1yj5B_	Alignment	not modelled	99.8	27	**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
81	c2zg6A_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein st2620; **PDBTitle:** crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfolobus tokodaii
82	c2pr7A_	Alignment	not modelled	99.7	17	**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
83	d1rkua_	Alignment	not modelled	99.6	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
84	c3mn1B_	Alignment	not modelled	99.6	17	**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
85	d1k1ea_	Alignment	not modelled	99.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
86	d1wr8a_	Alignment	not modelled	99.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
87	c3e8mD_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acylneuraminate cytidylyltransferase; **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
88	d1l6ra_	Alignment	not modelled	99.5	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
89	c3n07B_	Alignment	not modelled	99.5	17	**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
90	c2r8zC_	Alignment	not modelled	99.5	18	**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	c3n1uA_	Alignment	not modelled	99.5	19	**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
92	c3ewiB_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
93	c2p9jH_	Alignment	not modelled	99.5	17	**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	99.4	16	**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	c3p96A_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
96	d1q92a_	Alignment	not modelled	99.3	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**5'(3')-deoxyribonucleotidase (dNT-2)
97	c2qyhD_	Alignment	not modelled	99.3	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
98	c2i7dB_	Alignment	not modelled	99.3	14	**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+
99	c3n28A_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase; **PDBTitle:** crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
100	c3fzqA_	Alignment	not modelled	99.2	16	**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
101	c3niwA_	Alignment	not modelled	99.2	15	**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	d1rkqa_	Alignment	not modelled	99.1	25	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: Predicted hydrolases Cof
103	d2b30a1	Alignment	not modelled	99.1	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
104	c3r4cA_	Alignment	not modelled	99.1	20	**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
105	c3dnpA_	Alignment	not modelled	99.1	18	**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
106	c3daoB_	Alignment	not modelled	99.1	18	**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
107	c3l7yA_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1108c; **PDBTitle:** the crystal structure of smu.1108c from streptococcus mutans ua159
108	d1rlma_	Alignment	not modelled	99.1	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
109	d1nf2a_	Alignment	not modelled	99.0	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
110	d2rbka1	Alignment	not modelled	99.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
111	d1wzca1	Alignment	not modelled	99.0	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
112	d1xpja_	Alignment	not modelled	98.9	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
113	c3fvvA_	Alignment	not modelled	98.9	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
114	d1nrwa_	Alignment	not modelled	98.9	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
115	c2iyeC_	Alignment	not modelled	98.9	30	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b
116	d1xvia_	Alignment	not modelled	98.8	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
117	c1xviA_	Alignment	not modelled	98.8	12	**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
118	c3pgvB_	Alignment	not modelled	98.8	18	**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
119	c3gygA_	Alignment	not modelled	98.8	16	**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
120	d1z5ga1	Alignment	not modelled	98.7	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Class B acid phosphatase, AphA