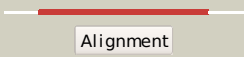

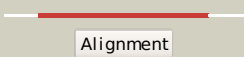

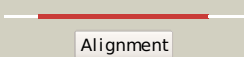

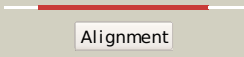

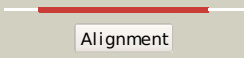

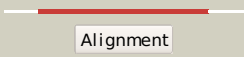

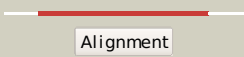

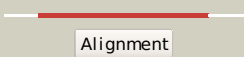

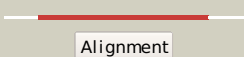

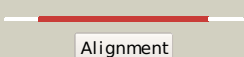

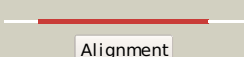

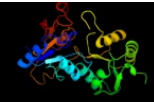










# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AF24
Date	Thu Jan 5 11:24:57 GMT 2012
Unique Job ID	db3a9b9076d868eb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2c4na1</a>	 Alignment		100.0	100	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
2	<a href="#">dlwvia_</a>	 Alignment		100.0	30	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
3	<a href="#">dlys9a1</a>	 Alignment		100.0	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
4	<a href="#">dlydfa1</a>	 Alignment		100.0	30	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
5	<a href="#">dlyv9a1</a>	 Alignment		100.0	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
6	<a href="#">c3pdwA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hydrolase yutf; <b>PDBTitle:</b> crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
7	<a href="#">d1vjra_</a>	 Alignment		100.0	29	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
8	<a href="#">c3qgmC_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> p-nitrophenyl phosphatase (pho2); <b>PDBTitle:</b> p-nitrophenyl phosphatase from archaeoglobus fulgidus
9	<a href="#">c1zija_</a>	 Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1952; <b>PDBTitle:</b> crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
10	<a href="#">c2cftA_</a>	 Alignment		100.0	29	<b>PDB header:</b> phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal phosphate phosphatase; <b>PDBTitle:</b> crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
11	<a href="#">c2ho4A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain <b>PDBTitle:</b> crystal structure of protein from mouse mm.236127

12	<a href="#">c2hx1D</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted sugar phosphatases of the had <b>PDBTitle:</b> crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
13	<a href="#">c3iruA</a>	Alignment		100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonoacetaldehyde hydrolase like protein; <b>PDBTitle:</b> crystal structure of phosphonoacetaldehyde hydrolase like protein from2 oleispira antarctica
14	<a href="#">c3kc2A</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ykr070w; <b>PDBTitle:</b> crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
15	<a href="#">c3dv9A</a>	Alignment		100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucumutase; <b>PDBTitle:</b> putative beta-phosphoglucumutase from bacteroides vulgatus.
16	<a href="#">c3d6jA</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
17	<a href="#">d2hsza1</a>	Alignment		100.0	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucumutase-like
18	<a href="#">d1swva</a>	Alignment		100.0	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
19	<a href="#">c3qnmA</a>	Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> haloalkane dehalogenase family member from bacteroides2 thetaiotaomicron of unknown function
20	<a href="#">c2hi0B</a>	Alignment		99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoglycolate phosphatase; <b>PDBTitle:</b> crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
21	<a href="#">c3mc1A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted phosphatase, had family; <b>PDBTitle:</b> crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
22	<a href="#">d1te2a</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucumutase-like
23	<a href="#">d1qq5a</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
24	<a href="#">c3nuqA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotide phosphatase; <b>PDBTitle:</b> structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
25	<a href="#">c3s6jC</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> the crystal structure of a hydrolase from pseudomonas syringae
26	<a href="#">d1zs9a1</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
27	<a href="#">c2hoqA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative had-hydrolase ph1655; <b>PDBTitle:</b> crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
28	<a href="#">d2fdra1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucumutase-like
						<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phospholysine phosphohistidine

29	<a href="#">c2x4dB_</a>	Alignment	not modelled	99.9	20	inorganic pyrophosphate <b>PDBTitle:</b> crystal structure of human phospholysine phosphohistidine2 inorganic pyrophosphate phosphatase lhpp
30	<a href="#">d2gfha1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
31	<a href="#">d2hdoa1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
32	<a href="#">d2ah5a1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
33	<a href="#">d1zrna_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
34	<a href="#">c2yy6B_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglycolate phosphatase; <b>PDBTitle:</b> crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
35	<a href="#">c3e58A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-phosphoglucomutase; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
36	<a href="#">d1x42a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
37	<a href="#">c2om6A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable phosphoserine phosphatase; <b>PDBTitle:</b> hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
38	<a href="#">c2qlta_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> (dl)-glycerol-3-phosphatase 1; <b>PDBTitle:</b> crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
39	<a href="#">c3sd7A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphatase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
40	<a href="#">c3ed5A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yfnb; <b>PDBTitle:</b> the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
41	<a href="#">d2hcfa1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
42	<a href="#">c2no5B_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> (s)-2-haloacid dehalogenase iva; <b>PDBTitle:</b> crystal structure analysis of a dehalogenase with intermediate complex
43	<a href="#">c2pibA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylated carbohydrates phosphatase tm_1254; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
44	<a href="#">c3k1zA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain-containing <b>PDBTitle:</b> crystal structure of human haloacid dehalogenase-like hydrolase domain2 containing 3 (hdhd3)
45	<a href="#">c2pkeA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like family hydrolase; <b>PDBTitle:</b> crystal structure of haloacid dehalogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
46	<a href="#">c3ddhA_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative haloacid dehalogenase-like family hydrolase; <b>PDBTitle:</b> the structure of a putative haloacid dehalogenase-like family2 hydrolase from bacteroides thetaiotaomicron vpi-5482
47	<a href="#">c3l5kA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain- <b>PDBTitle:</b> the crystal structure of human haloacid dehalogenase-like2 hydrolase domain containing 1a (hdhd1a)
48	<a href="#">c3cnhA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase family protein; <b>PDBTitle:</b> crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
49	<a href="#">d2go7a1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
50	<a href="#">d2gmwa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
51	<a href="#">c3l8hC_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of d,d-heptose 1,7-bisphosphate phosphatase from b.2 bronchiseptica complexed with magnesium and phosphate
52	<a href="#">c3esqA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d,d-heptose 1,7-bisphosphate phosphatase; <b>PDBTitle:</b> crystal structure of calcium-bound d,d-heptose 1,7-2 bisphosphate phosphatase from e. coli

53	<a href="#">d1qyia_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein MW1667 (SA1546)
54	<a href="#">d1o08a_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucumutase-like
55	<a href="#">c3kd3A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphohydrolase-like protein; <b>PDBTitle:</b> crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
56	<a href="#">c3m9lA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> crystal structure of probable had family hydrolase from2 pseudomonas fluorescens pf-5
57	<a href="#">c2w11B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-haloalkanoic acid dehalogenase; <b>PDBTitle:</b> structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
58	<a href="#">d2g80a1</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
59	<a href="#">c2g80C_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protein utr4; <b>PDBTitle:</b> crystal structure of utr4 protein (unknown transcript 4 protein)2 (ye1038w) from saccharomyces cerevisiae at 2.28 a resolution
60	<a href="#">c2p11A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bxg_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
61	<a href="#">d1zd3a1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
62	<a href="#">d2o2xa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
63	<a href="#">d2fi1a1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
64	<a href="#">c2i6xA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> the structure of a predicted had-like family hydrolase from2 porphyromonas gingivalis.
65	<a href="#">c3kzxA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> had-superfamily hydrolase, subfamily ia, variant 1; <b>PDBTitle:</b> crystal structure of a had-superfamily hydrolase from ehrlichia2 chaffeensis at 1.9a resolution
66	<a href="#">c3nasA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucumutase; <b>PDBTitle:</b> the crystal structure of beta-phosphoglucumutase from bacillus2 subtilis
67	<a href="#">d1cr6a1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
68	<a href="#">c1cr6A_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
69	<a href="#">c3m1yA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase (serb); <b>PDBTitle:</b> crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
70	<a href="#">d2b0ca1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
71	<a href="#">d1u7pa_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1
72	<a href="#">d1nnla_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
73	<a href="#">c3ib6B_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
74	<a href="#">c2odaB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pspto_2114; <b>PDBTitle:</b> crystal structure of pspto_2114
75	<a href="#">c2zg6A_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein st2620; <b>PDBTitle:</b> crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfolobus tokodaii
76	<a href="#">c2qyhD_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical conserved protein, gk1056; <b>PDBTitle:</b> crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
77	<a href="#">d1wr8a_</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
						<b>Fold:</b> HAD-like

78	<a href="#">dlrkqa_</a>	Alignment	not modelled	99.7	14	<b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
79	<a href="#">c3fzqA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
80	<a href="#">dlj97a_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
81	<a href="#">c3r4cA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
82	<a href="#">c2pr7A_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase/epoxide hydrolase family; <b>PDBTitle:</b> crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
83	<a href="#">dl16ra_</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
84	<a href="#">c3niwA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
85	<a href="#">dlrkua_</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Homoserine kinase ThrH
86	<a href="#">d2fpwa1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
87	<a href="#">c3dnpA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stress response protein yhax; <b>PDBTitle:</b> crystal structure of stress response protein yhax from bacillus2 subtilis
88	<a href="#">d2feaa1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> MtnX-like
89	<a href="#">d2rbka1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
90	<a href="#">dlnrwa_</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
91	<a href="#">c3daoB_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphatse; <b>PDBTitle:</b> crystal structure of a putative phosphatse (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
92	<a href="#">c3l7yA_</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1108c; <b>PDBTitle:</b> the crystal structure of smu.1108c from streptococcus mutans ua159
93	<a href="#">d2b30a1</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
94	<a href="#">dlrlma_</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
95	<a href="#">dlwzca1</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
96	<a href="#">dls2oa1</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
97	<a href="#">clxviA_</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
98	<a href="#">dlxvia_</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
99	<a href="#">c3pgvB_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
100	<a href="#">dlnf2a_</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
101	<a href="#">c3p96A_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase serb; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
102	<a href="#">dlk1ea_</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase Yrbl
						<b>PDB header:</b> hydrolase



103	<a href="#">c3gygA_</a>	Alignment	not modelled	99.4	11	<b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon putative hydrolase ntdb; <b>PDBTitle:</b> crystal structure of yhjK (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
104	<a href="#">c3mn1B_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable yrbi family phosphatase; <b>PDBTitle:</b> crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
105	<a href="#">c3fvvA_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
106	<a href="#">c3n07B_</a>	Alignment	not modelled	99.4	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
107	<a href="#">c3n28A_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase; <b>PDBTitle:</b> crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
108	<a href="#">c3e8mD_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate cytidyltransferase; <b>PDBTitle:</b> 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
109	<a href="#">c2r8zC_</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
110	<a href="#">c2p9jH_</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> hypothetical protein aq2171; <b>PDBTitle:</b> crystal structure of aq2171 from aquifex aeolicus
111	<a href="#">c3n1uA_</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, had superfamily, subfamily iii a; <b>PDBTitle:</b> structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
112	<a href="#">c3ewiB_</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acylneuraminate cytidyltransferase; <b>PDBTitle:</b> structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
113	<a href="#">c3mmzA_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative had family hydrolase; <b>PDBTitle:</b> crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
114	<a href="#">c2i55C_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
115	<a href="#">c3mpoD_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted hydrolase of the had superfamily; <b>PDBTitle:</b> the crystal structure of a hydrolase from lactobacillus brevis
116	<a href="#">d2amya1</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
117	<a href="#">d1u02a_</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Trehalose-phosphatase
118	<a href="#">d2fuea1</a>	Alignment	not modelled	98.9	9	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
119	<a href="#">d1yj5a1</a>	Alignment	not modelled	98.8	34	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> phosphatase domain of polynucleotide kinase
120	<a href="#">c2iyeC_</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> copper-transporting atpase; <b>PDBTitle:</b> structure of catalytic cpx-atpase domain copb-b