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1	<a href="#">c3pgvB_</a>	 Alignment		100.0	82	<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
2	<a href="#">c3niwA_</a>	 Alignment		100.0	22	<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
3	<a href="#">c3dnpA_</a>	 Alignment		100.0	20	<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
4	<a href="#">d1nrwa_</a>	 Alignment		100.0	27	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
5	<a href="#">d1nf2a_</a>	 Alignment		100.0	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
6	<a href="#">d1rlma_</a>	 Alignment		100.0	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
7	<a href="#">c3fzqA_</a>	 Alignment		100.0	16	<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
8	<a href="#">c2qyhD_</a>	 Alignment		100.0	24	<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
9	<a href="#">c3daoB_</a>	 Alignment		100.0	18	<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
10	<a href="#">d1rkqa_</a>	 Alignment		100.0	27	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
11	<a href="#">d2rbka1</a>	 Alignment		100.0	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof

12	<a href="#">c3r4cA_</a>	Alignment		100.0	23	<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
13	<a href="#">c3l7yA_</a>	Alignment		100.0	19	<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
14	<a href="#">d2b30a1</a>	Alignment		100.0	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
15	<a href="#">c3gygA_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <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
16	<a href="#">c3mpoD_</a>	Alignment		100.0	23	<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
17	<a href="#">d1s2oa1</a>	Alignment		100.0	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
18	<a href="#">d1l6ra_</a>	Alignment		100.0	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
19	<a href="#">d1wr8a_</a>	Alignment		100.0	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
20	<a href="#">d1xvia_</a>	Alignment		100.0	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
21	<a href="#">c1xviA_</a>	Alignment	not modelled	100.0	17	<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
22	<a href="#">d1wzca1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
23	<a href="#">c2i55C_</a>	Alignment	not modelled	100.0	18	<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
24	<a href="#">d1u02a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Trehalose-phosphatase
25	<a href="#">d2amya1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
26	<a href="#">d2fuea1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
27	<a href="#">d1k1ea_</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase Yrbl
28	<a href="#">c3mmzA_</a>	Alignment	not modelled	99.9	27	<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 <b>PDB header:</b> transferase

29	<a href="#">c3e8mD</a>	Alignment	not modelled	99.9	29	<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
30	<a href="#">c3mn1B</a>	Alignment	not modelled	99.9	27	<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
31	<a href="#">c2r8zC</a>	Alignment	not modelled	99.9	26	<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
32	<a href="#">c3n1uA</a>	Alignment	not modelled	99.9	30	<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
33	<a href="#">c3ewiB</a>	Alignment	not modelled	99.9	24	<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
34	<a href="#">c3n07B</a>	Alignment	not modelled	99.9	27	<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
35	<a href="#">c2p9jH</a>	Alignment	not modelled	99.9	19	<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
36	<a href="#">c3p96A</a>	Alignment	not modelled	99.9	20	<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
37	<a href="#">c3n28A</a>	Alignment	not modelled	99.9	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
38	<a href="#">c2hx1D</a>	Alignment	not modelled	99.8	14	<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
39	<a href="#">d1j97a</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
40	<a href="#">c2cftA</a>	Alignment	not modelled	99.8	16	<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
41	<a href="#">c3fvvA</a>	Alignment	not modelled	99.8	16	<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
42	<a href="#">d1rkua</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Homoserine kinase ThrH
43	<a href="#">c3m1yA</a>	Alignment	not modelled	99.8	17	<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
44	<a href="#">d1yv9a1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
45	<a href="#">c3pdwA</a>	Alignment	not modelled	99.7	18	<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
46	<a href="#">d1wvia</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
47	<a href="#">d1ydfa1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
48	<a href="#">d1nnla</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
49	<a href="#">d1ys9a1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
50	<a href="#">c3kd3A</a>	Alignment	not modelled	99.6	24	<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
51	<a href="#">c1zjjA</a>	Alignment	not modelled	99.6	17	<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
52	<a href="#">c3qgmC</a>	Alignment	not modelled	99.5	14	<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
53	<a href="#">d2c4na1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
						<b>Fold:</b> HAD-like

54	<a href="#">d1vjra_</a>	Alignment	not modelled	99.5	15	<b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
55	<a href="#">d1y8aa1</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> AF1437-like
56	<a href="#">d1wpga2</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
57	<a href="#">c2iyeC_</a>	Alignment	not modelled	99.4	23	<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
58	<a href="#">d2feaa1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> MtnX-like
59	<a href="#">d1zs9a1</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
60	<a href="#">c3rfuC_</a>	Alignment	not modelled	99.2	27	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> copper efflux atpase; <b>PDBTitle:</b> crystal structure of a copper-transporting pib-type atpase
61	<a href="#">d2gmwa1</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
62	<a href="#">d1u7pa_</a>	Alignment	not modelled	99.1	23	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1
63	<a href="#">c3l8hC_</a>	Alignment	not modelled	99.1	19	<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
64	<a href="#">c3mc1A_</a>	Alignment	not modelled	99.1	29	<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
65	<a href="#">c3b9bA_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
66	<a href="#">c3esqA_</a>	Alignment	not modelled	99.1	20	<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
67	<a href="#">c2pibA_</a>	Alignment	not modelled	99.1	12	<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-phosphoglucutase from2 thermotoga maritima
68	<a href="#">c3iruA_</a>	Alignment	not modelled	99.1	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phoshonoacetaldehyde hydrolase like protein; <b>PDBTitle:</b> crystal structure of phoshonoacetaldehyde hydrolase like protein from2 oleispira antarctica
69	<a href="#">c2ho4A_</a>	Alignment	not modelled	99.0	17	<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
70	<a href="#">c2zzeA_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> na, k-atpase alpha subunit; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
71	<a href="#">c3j08A_</a>	Alignment	not modelled	99.0	29	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
72	<a href="#">c1cr6A_</a>	Alignment	not modelled	99.0	16	<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
73	<a href="#">c1mhsA_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> membrane protein, proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> plasma membrane atpase; <b>PDBTitle:</b> model of neurospora crassa proton atpase
74	<a href="#">c3j09A_</a>	Alignment	not modelled	99.0	31	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
75	<a href="#">d1cr6a1</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
76	<a href="#">d2o2xa1</a>	Alignment	not modelled	98.9	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
77	<a href="#">c3d6jA_</a>	Alignment	not modelled	98.9	28	<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
78	<a href="#">d2fdra1</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucutase-like
						<b>Fold:</b> HAD-like

79	<a href="#">d1o08a_</a>	Alignment	not modelled	98.9	17	<b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosucrose-like
80	<a href="#">d2b8ea1</a>	Alignment	not modelled	98.9	34	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
81	<a href="#">c3b8cB_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase 2, plasma membrane-type; <b>PDBTitle:</b> crystal structure of a plasma membrane proton pump
82	<a href="#">c3m91A_</a>	Alignment	not modelled	98.9	28	<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
83	<a href="#">c3b8eC_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
84	<a href="#">c3ixzA_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> potassium-transporting atpase alpha; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
85	<a href="#">c3kc2A_</a>	Alignment	not modelled	98.9	15	<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
86	<a href="#">d1x42a1</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
87	<a href="#">c2hoqA_</a>	Alignment	not modelled	98.9	14	<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
88	<a href="#">c3dv9A_</a>	Alignment	not modelled	98.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucosucrose; <b>PDBTitle:</b> putative beta-phosphoglucosucrose from bacteroides vulgatus.
89	<a href="#">c2hi0B_</a>	Alignment	not modelled	98.8	17	<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
90	<a href="#">d2hcfa1</a>	Alignment	not modelled	98.7	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosucrose-like
91	<a href="#">d1swva_</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
92	<a href="#">d1qq5a_</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
93	<a href="#">d1xpja_</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein VC0232
94	<a href="#">d2fpwa1</a>	Alignment	not modelled	98.7	26	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
95	<a href="#">d1zd3a1</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
96	<a href="#">d2hsza1</a>	Alignment	not modelled	98.7	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosucrose-like
97	<a href="#">d2ah5a1</a>	Alignment	not modelled	98.6	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosucrose-like
98	<a href="#">c3cnhA_</a>	Alignment	not modelled	98.6	12	<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
99	<a href="#">c3kzxA_</a>	Alignment	not modelled	98.6	14	<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
100	<a href="#">c3s6jC_</a>	Alignment	not modelled	98.6	15	<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
101	<a href="#">c3nuqA_</a>	Alignment	not modelled	98.6	11	<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
102	<a href="#">c2om6A_</a>	Alignment	not modelled	98.5	13	<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
103	<a href="#">d2obba1</a>	Alignment	not modelled	98.5	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
104	<a href="#">d1te2a_</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosucrose-like

105	<a href="#">c3qnmA</a>	Alignment	not modelled	98.5	11	<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
106	<a href="#">c2pkeA</a>	Alignment	not modelled	98.5	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
107	<a href="#">c2b8eB</a>	Alignment	not modelled	98.5	34	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> cation-transporting atpase; <b>PDBTitle:</b> copa atp binding domain
108	<a href="#">c3nasA</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucosyltransferase; <b>PDBTitle:</b> the crystal structure of beta-phosphoglucosyltransferase from bacillus2 subtilis
109	<a href="#">c3ddhA</a>	Alignment	not modelled	98.5	16	<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
110	<a href="#">d2go7a1</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosyltransferase-like
111	<a href="#">d2gfha1</a>	Alignment	not modelled	98.4	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosyltransferase-like
112	<a href="#">dlzrna</a>	Alignment	not modelled	98.4	26	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
113	<a href="#">c2yy6B</a>	Alignment	not modelled	98.4	19	<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
114	<a href="#">c2i6xA</a>	Alignment	not modelled	98.4	14	<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.
115	<a href="#">c3e58A</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-phosphoglucosyltransferase; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucosyltransferase from2 streptococcus thermophilus
116	<a href="#">c2g80C</a>	Alignment	not modelled	98.4	13	<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 (yel038w) from saccharomyces cerevisiae at 2.28 a resolution
117	<a href="#">d2hdoa1</a>	Alignment	not modelled	98.4	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucosyltransferase-like
118	<a href="#">c3k1zA</a>	Alignment	not modelled	98.4	14	<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)
119	<a href="#">d2f1a1</a>	Alignment	not modelled	98.3	26	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
120	<a href="#">c3sd7A</a>	Alignment	not modelled	98.3	13	<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