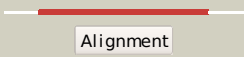

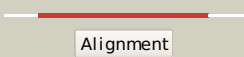

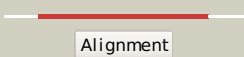

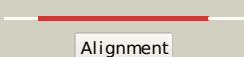

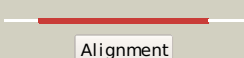

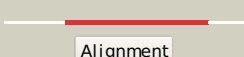

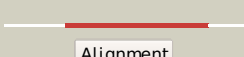

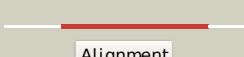

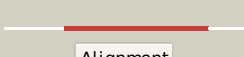

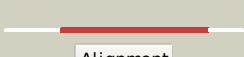





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlz5ga1	 Alignment		100.0	90	Fold: HAD-like Superfamily: HAD-like Family: Class B acid phosphatase, AphA
2	d2b82a1	 Alignment		100.0	100	Fold: HAD-like Superfamily: HAD-like Family: Class B acid phosphatase, AphA
3	c2i34B_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
4	c3pctA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: class c acid phosphatase; PDBTitle: structure of the class c acid phosphatase from pasteurilla multocida
5	c3et4A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: outer membrane protein p4, nadp phosphatase; PDBTitle: structure of recombinant haemophilus influenzae e(p4) acid phosphatase
6	d1ltqa1	 Alignment		99.7	17	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
7	c2ia5C_	 Alignment		99.1	18	PDB header: transferase Chain: C: PDB Molecule: polynucleotide kinase; PDBTitle: t4 polynucleotide kinase/phosphatase with bound sulfate and2 magnesium.
8	d1u7pa_	 Alignment		98.8	14	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
9	d1q92a_	 Alignment		98.8	14	Fold: HAD-like Superfamily: HAD-like Family: 5'(3')-deoxyribonucleotidase (dNT-2)
10	d2go7a1	 Alignment		98.7	18	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosyltransferase-like
11	c2i7dB_	 Alignment		98.7	18	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+

12	d1swva_	Alignment		98.7	18	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
13	c3s6jC_	Alignment		98.7	16	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the crystal structure of a hydrolase from pseudomonas syringae
14	c3iruA_	Alignment		98.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphonoacetaldehyde hydrolase like protein; PDBTitle: crystal structure of phosphonoacetaldehyde hydrolase like protein from2 oleispira antarctica
15	c3d6jA_	Alignment		98.6	15	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
16	c3l5kA_	Alignment		98.6	13	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 (hhdh1a)
17	d1zd3a1	Alignment		98.6	17	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
18	d1zrna_	Alignment		98.6	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
19	c2pkeA_	Alignment		98.6	19	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like family hydrolase; PDBTitle: crystal structure of haloacid dehalogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
20	c1cr6A_	Alignment		98.6	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
21	c3ddhA_	Alignment	not modelled	98.5	14	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
22	c2om6A_	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: probable phosphoserine phosphatase; PDBTitle: hypothetical protein (probable phosphoserine phosphatase) (ph0253) from2 pyrococcus horikoshii ot3
23	c3mc1A_	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted phosphatase, had family; PDBTitle: crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
24	c3ib6B_	Alignment	not modelled	98.5	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
25	d1nnla_	Alignment	not modelled	98.5	20	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
26	d1zs9a1	Alignment	not modelled	98.5	11	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
27	c2pibA_	Alignment	not modelled	98.5	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphorylated carbohydrates phosphatase tm_1254; PDBTitle: crystal structure of putative beta-phosphoglucosyltransferase from2 thermotoga maritima
28	c3m9lA_	Alignment	not modelled	98.5	18	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
29	d1cr6a1	Alignment	not modelled	98.4	12	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
30	c2qltA	Alignment	not modelled	98.4	17	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
31	d2fil1a1	Alignment	not modelled	98.4	16	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
32	d1te2a	Alignment	not modelled	98.3	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosutase-like
33	c3cnhA	Alignment	not modelled	98.3	17	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
34	d2fpwa1	Alignment	not modelled	98.3	18	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
35	c3l8hC	Alignment	not modelled	98.3	18	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
36	c3kc2A	Alignment	not modelled	98.3	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
37	d2gmwa1	Alignment	not modelled	98.3	16	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
38	c3nuqA	Alignment	not modelled	98.3	16	PDB header: hydrolase Chain: A: PDB Molecule: putative nucleotide phosphatase; PDBTitle: structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
39	d2feaa1	Alignment	not modelled	98.3	15	Fold: HAD-like Superfamily: HAD-like Family: MtnX-like
40	c3esqA	Alignment	not modelled	98.2	16	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
41	c2yy6B	Alignment	not modelled	98.2	13	PDB header: hydrolase Chain: B: PDB Molecule: phosphoglycolate phosphatase; PDBTitle: crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
42	c2r8zC	Alignment	not modelled	98.2	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
43	c3mn1B	Alignment	not modelled	98.2	20	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
44	d1k1ea	Alignment	not modelled	98.2	15	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
45	d2o2xa1	Alignment	not modelled	98.1	19	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
46	c3dv9A	Alignment	not modelled	98.1	13	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucosutase; PDBTitle: putative beta-phosphoglucosutase from bacteroides vulgatus.
47	c3n07B	Alignment	not modelled	98.1	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
48	c3bwvB	Alignment	not modelled	98.1	11	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
49	d2hsza1	Alignment	not modelled	98.1	16	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosutase-like
50	d2hdoo1	Alignment	not modelled	98.1	15	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucosutase-like
51	c3e58A	Alignment	not modelled	98.0	10	PDB header: isomerase Chain: A: PDB Molecule: putative beta-phosphoglucosutase; PDBTitle: crystal structure of putative beta-phosphoglucosutase from2 streptococcus thermophilus
52	c3sd7A	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
						Fold: HAD-like

53	d1ydfa1	Alignment	not modelled	98.0	33	Superfamily: HAD-like Family: NagD-like
54	c2w11B	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: B: PDB Molecule: 2-haloalkanoic acid dehalogenase; PDBTitle: structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
55	d1j97a	Alignment	not modelled	98.0	15	Fold: HAD-like Superfamily: HAD-like Family: Phosphoserine phosphatase
56	c2no5B	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: B: PDB Molecule: (s)-2-haloacid dehalogenase iva; PDBTitle: crystal structure analysis of a dehalogenase with intermediate complex
57	d2b0ca1	Alignment	not modelled	98.0	16	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
58	d2vkqa1	Alignment	not modelled	98.0	16	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
59	c3nasA	Alignment	not modelled	97.9	18	PDB header: isomerase Chain: A: PDB Molecule: beta-phosphoglucomutase; PDBTitle: the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
60	c2hi0B	Alignment	not modelled	97.9	21	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
61	c3e8mD	Alignment	not modelled	97.9	23	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
62	c2hoqA	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative had-hydrolase ph1655; PDBTitle: crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
63	d2obba1	Alignment	not modelled	97.9	14	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
64	c3kd3A	Alignment	not modelled	97.9	16	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
65	c3p96A	Alignment	not modelled	97.9	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
66	d1qq5a	Alignment	not modelled	97.9	15	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
67	c3k1zA	Alignment	not modelled	97.9	12	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)
68	c3kzxA	Alignment	not modelled	97.9	15	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	c3m1yA	Alignment	not modelled	97.9	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase (serb); PDBTitle: crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
70	d1ys9a1	Alignment	not modelled	97.9	29	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
71	c2i6xA	Alignment	not modelled	97.9	17	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.
72	d2ah5a1	Alignment	not modelled	97.8	21	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
73	d2hcfa1	Alignment	not modelled	97.8	20	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
74	d2fdra1	Alignment	not modelled	97.8	17	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
75	c3n1uA	Alignment	not modelled	97.8	12	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
76	d1x42a1	Alignment	not modelled	97.8	17	Fold: HAD-like Superfamily: HAD-like Family: HAD-related
77	c3qnmA	Alignment	not modelled	97.8	19	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

78	d2bdua1	Alignment	not modelled	97.7	20	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
79	c2p11A	Alignment	not modelled	97.7	11	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bxo_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
80	d1xpja	Alignment	not modelled	97.7	18	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
81	d1o08a	Alignment	not modelled	97.6	21	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
82	c2p9jH	Alignment	not modelled	97.6	16	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
83	c3ed5A	Alignment	not modelled	97.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yfnb; PDBTitle: the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
84	c2zg6A	Alignment	not modelled	97.5	14	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
85	c2ho4A	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase domain PDBTitle: crystal structure of protein from mouse mm.236127
86	c2cftA	Alignment	not modelled	97.4	25	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
87	c3mmzA	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
88	d2gfha1	Alignment	not modelled	97.3	13	Fold: HAD-like Superfamily: HAD-like Family: beta-Phosphoglucomutase-like
89	c2hx1D	Alignment	not modelled	97.3	16	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
90	d1l6ra	Alignment	not modelled	97.3	19	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
91	c2g80C	Alignment	not modelled	97.3	19	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
92	d1qyia	Alignment	not modelled	97.3	23	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
93	d2g80a1	Alignment	not modelled	97.2	18	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
94	c3ewiB	Alignment	not modelled	97.1	16	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
95	d1xvia	Alignment	not modelled	97.0	25	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
96	c1xviA	Alignment	not modelled	97.0	25	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
97	d1yv9a1	Alignment	not modelled	96.8	28	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
98	c2qyhD	Alignment	not modelled	96.8	33	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
99	c1zjiA	Alignment	not modelled	96.7	30	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ph1952; PDBTitle: crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
100	c3fvvA	Alignment	not modelled	96.6	22	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
101	c2b8eB	Alignment	not modelled	96.6	19	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
102	d1yj5a1	Alignment	not modelled	96.6	21	Fold: HAD-like Superfamily: HAD-like Family: phosphatase domain of polynucleotide kinase
103	d1rkua	Alignment	not modelled	96.6	17	Fold: HAD-like Superfamily: HAD-like Family: Homoserine kinase ThrH

104	c2pr7A_	Alignment	not modelled	96.5	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
105	c3zvmA_	Alignment	not modelled	96.5	24	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
106	d2c4na1	Alignment	not modelled	96.3	16	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
107	d1wvia_	Alignment	not modelled	96.3	25	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
108	d1vjra_	Alignment	not modelled	96.1	17	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
109	c1vj5B_	Alignment	not modelled	96.0	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
110	d2b8ea1	Alignment	not modelled	95.9	25	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
111	c3dnpA_	Alignment	not modelled	95.9	27	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
112	c3qgmC_	Alignment	not modelled	95.8	25	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
113	c3pdwA_	Alignment	not modelled	95.8	31	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized hydrolase yutf; PDBTitle: crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
114	c3n28A_	Alignment	not modelled	95.8	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase; PDBTitle: crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
115	d1wpga2	Alignment	not modelled	95.8	16	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
116	c2i55C_	Alignment	not modelled	95.7	22	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
117	c3fzqA_	Alignment	not modelled	95.6	30	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
118	c3j09A_	Alignment	not modelled	95.6	24	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
119	d1nrwa_	Alignment	not modelled	95.5	28	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
120	c3pgvB_	Alignment	not modelled	95.5	25	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