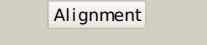
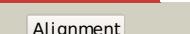
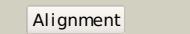
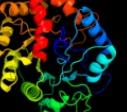
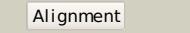
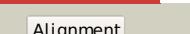


Phyre²

Email	i.a.kelley@imperial.ac.uk
Description	P45548
Date	Thu Jan 5 12:03:05 GMT 2012
Unique Job ID	97b88562bee92491

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bf6a_			100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
2	c3k2gA_			100.0	32	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
3	c3f4cA_			100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
4	c3rhgA_			100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
5	c2vc7A_			100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
6	c2zc1A_			100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
7	c3pnzD_			100.0	29	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
8	d2d2ja1			100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
9	d1i0da_			100.0	30	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
10	clpscA_			100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
11	c2xioA_			100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a

12	c2y1hA			100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
13	c3ipwA			100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba histolytica
14	c3e2vA			99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
15	c3msrA			99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
16	d1xwya1			99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
17	d1yixal			99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
18	d1j6oa			99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
19	d1zzma1			99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
20	c2gzxB			99.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative tatd related dnase; PDBTitle: crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
21	c3rcmA		not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
22	c2qahA		not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: 2-pyrone-4,6-dicarboxylic acid hydrolase; PDBTitle: crystal structure of the 2-pyrone-4,6-dicarboxylic acid2 hydrolase from spingomonas paucimobilis
23	d2ffia1		not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
24	c3irsB		not modelled	99.9	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bb4693; PDBTitle: crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica
25	c3gg7A		not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
26	d2dvta1		not modelled	99.9	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
27	c3ij6A		not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
28	d2gwga1		not modelled	99.9	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like

29	c3guwB	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af1765; PDBTitle: crystal structure of the tatd-like protein (af1765) from2 archaeoglobus fulgidus, northeast structural genomics3 consortium target gr121
30	c2wm1A	Alignment	not modelled	99.9	14	PDB header: lyase Chain: A: PDB Molecule: 2-amino-3-carboxymuconate-6-semialdehyde PDBTitle: the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis
31	c3cpA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted amidohydrolase, dihydroorotate family; PDBTitle: crystal structure of an uncharacterized amidohydrolase cac3332 from clostridium acetobutylicum
32	d2hbv1	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
33	d2f6ka1	Alignment	not modelled	99.8	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
34	c3nurA	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
35	d1xrt2	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
36	d1k1da2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
37	d1nfga2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
38	d1ynya2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
39	d1gkra2	Alignment	not modelled	99.6	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
40	c3pnua	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotate; PDBTitle: 2.4 angstrom crystal structure of dihydroorotate (pyrc) from2 campylobacter jejuni.
41	d3be7a2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
42	d2icsa2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
43	d1kcxa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
44	d2paja2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
45	d1onwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
46	d2qs8a2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
47	d2uz9a2	Alignment	not modelled	99.5	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
48	d2ftwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
49	c3jzeC	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotate; PDBTitle: 1.8 angstrom resolution crystal structure of dihydroorotate (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
50	d2eg6a1	Alignment	not modelled	99.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotate
51	d2i9ua2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
52	d2r8ca2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
53	c2qpxA	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted metal-dependent hydrolase of the tim-barrel fold; PDBTitle: crystal structure of putative metal-dependent hydrolase (yp_805737.1)2 from lactobacillus casei atcc 334 at 1.40 a resolution

54	d1gkpa2	Alignment	not modelled	99.4	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
55	d2fvka2	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
56	d2p9ba2	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
57	c1xrfA_	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution
58	d1p1ma2	Alignment	not modelled	99.3	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
59	c2pajA_	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
60	d21mra2	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
61	c2ogjB_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
62	c3e0IB_	Alignment	not modelled	99.2	10	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
63	d2bb0a2	Alignment	not modelled	99.1	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
64	c2vr2A_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
65	d2puza2	Alignment	not modelled	99.1	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
66	c3hpaB_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
67	c2vunC_	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of enamidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
68	d2ooda2	Alignment	not modelled	99.1	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
69	c3gnhA_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: A: PDB Molecule: l-lysine, l-arginine carboxypeptidase cc2672; PDBTitle: crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine.
70	c2aqoB_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
71	c3nqbB_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from arrobacterium tumefaciens2 (str. c 58)
72	c3dc8B_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
73	d2q09a2	Alignment	not modelled	99.1	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
74	c1p1mA_	Alignment	not modelled	99.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tm0936; PDBTitle: structure of thermotoga maritima amidohydrolase tm0936 bound to ni and methionine
75	c3itcA_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
76	c1nfgA_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
77	c3lsbA_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aurescens tc1 complexed with zinc and ametrin
78	c2ftwA_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
79	c2q09A_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxo-

						imidazolidin-4-yl)-propionic acid
80	c2bb0A	Alignment	not modelled	99.0	11	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
81	c2i9uA	Alignment	not modelled	99.0	12	PDB header: hydrolase Chain: A: PDB Molecule: cytosine/guanine deaminase related protein; PDBTitle: crystal structure of guanine deaminase from c. acetobutylicum with 2 bound guanine in the active site
82	c2gseC	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidine-like 2
83	c1gkpD	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
84	c3d6nA	Alignment	not modelled	99.0	15	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
85	c3lnpA	Alignment	not modelled	99.0	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase family protein olei01672_1_465; PDBTitle: crystal structure of amidohydrolase family protein2 olei01672_1_465 from oleispira antarctica
86	c1k1dF	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
87	c2icsA	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
88	c2imrA	Alignment	not modelled	98.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
89	c1gkra	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
90	c2fvmA	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine
91	c2gokA	Alignment	not modelled	98.9	12	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
92	d1o12a2	Alignment	not modelled	98.9	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
93	d1ra0a2	Alignment	not modelled	98.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
94	d4ubpc2	Alignment	not modelled	98.9	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha/beta-subunit of urease, catalytic domain
95	d1titu	Alignment	not modelled	98.9	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase
96	c3be7B	Alignment	not modelled	98.9	12	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
97	c3fdgA	Alignment	not modelled	98.8	12	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase ac. metallo peptidase. merops family m19; PDBTitle: the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
98	d1m7ja3	Alignment	not modelled	98.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
99	c2i5gB	Alignment	not modelled	98.8	14	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
100	c3hm7A	Alignment	not modelled	98.8	12	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
101	c2ragB	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus
102	c3mduA	Alignment	not modelled	98.7	18	PDB header: hydrolase Chain: A: PDB Molecule: n-formimino-l-glutamate iminohydrolase; PDBTitle: the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
103	c1r9yA	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
104	c2qwaA	All	not modelled	98.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydroorotase;

104	c2yv1M	Alignment	not modelled	98.7	14	PDBTitle: the structure of putative dihydroorotate from porphyromonas2 gingivalis. PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
105	c3oogC	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: C: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of a xaa-pro dipeptidase with bound methionine in the active site
106	c2qs8A	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: C: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
107	c2p50C	Alignment	not modelled	98.7	12	PDB header: hydrolase Chain: C: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
108	c3lu2B	Alignment	not modelled	98.7	11	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
109	c3b40A	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
110	c3mpgB	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotate; PDBTitle: dihydroorotate from bacillus anthracis
111	c2z00A	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotate; PDBTitle: crystal structure of dihydroorotate from thermus thermophilus
112	c3e74D	Alignment	not modelled	98.6	13	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at2 the metal center
113	c2qt3A	Alignment	not modelled	98.6	8	PDB header: hydrolase Chain: A: PDB Molecule: n-isopropylammelide isopropyl amidohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase atzc2 from pseudomonas sp. strain adp complexed with zn
114	c2r8cB	Alignment	not modelled	98.6	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
115	c3gr1B	Alignment	not modelled	98.5	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotate; PDBTitle: the crystal structure of a dihydroorotate from staphylococcus aureus
116	c2wjeA	Alignment	not modelled	98.5	14	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
117	c3feqB	Alignment	not modelled	98.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
118	c2p9bA	Alignment	not modelled	98.5	12	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
119	c2oodA	Alignment	not modelled	98.4	11	PDB header: hydrolase Chain: A: PDB Molecule: b1r3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
120	d1j5sa	Alignment	not modelled	98.3	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like