
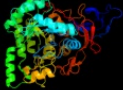
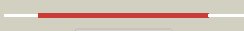





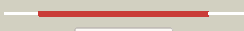















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gseC_	 Alignment		100.0	33	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
2	c1k1dF_	 Alignment		100.0	41	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
3	c1gkpD_	 Alignment		100.0	37	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
4	c2ftwA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
5	c1nfgA_	 Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
6	c2vr2A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
7	c3dc8B_	 Alignment		100.0	40	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
8	c1gkrA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
9	c2fvmA_	 Alignment		100.0	30	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
10	c3e74D_	 Alignment		100.0	31	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at2 the metal center
11	c3hm7A_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125

12	c2gwnA_	Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
13	c3mpgB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
14	c3griB_	Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
15	c3d6nA_	Alignment		100.0	24	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
16	c2z00A_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
17	c1xrfA_	Alignment		100.0	24	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
18	c3lnpA_	Alignment		100.0	16	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
19	c3hpaB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
20	c3lsbA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureusens tc1 complexed with zinc and ametrin
21	c1rjqA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
22	c3gipB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: n-acyl-d-glutamate deacylase; PDBTitle: crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.
23	c2pajA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
24	c1p1mA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tm0936; PDBTitle: structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine
25	c2aqoB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
26	c2bb0A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
27	c3e0lB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
28	c2qt3A_	Alignment	not modelled	100.0	14	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
29	c2vunC	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of amidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
30	c3nqbB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
31	c3la4A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
32	c2oodA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
33	c2i9uA	Alignment	not modelled	100.0	10	PDB header: hydrolase Chain: A: PDB Molecule: cytosine/guanine deaminase related protein; PDBTitle: crystal structure of guanine deaminase from c. acetobutylicum with2 bound guanine in the active site
34	c3gnhA	Alignment	not modelled	100.0	15	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.
35	c2p9bA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
36	c2q09A	Alignment	not modelled	100.0	19	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
37	c2gokA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
38	c2r8cB	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
39	c2vhlB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: the three-dimensional structure of the n-acetylglucosamine-2 6-phosphate deacetylase from bacillus subtilis
40	c1e9yB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
41	c3be7B	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
42	c3v7pA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase family protein; PDBTitle: crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratriptor sp. sb155-2
43	c2ubpC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
44	c3feqB	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
45	c1fwcC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5
46	c2qs8A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of a xaa-pro dipeptidase with bound2 methionine in the active site
47	c1r9yA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
48	c2p50C	Alignment	not modelled	100.0	14	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
49	c3ooqC	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
50	c3egjA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
51	d1k1da2	Alignment	not modelled	100.0	40	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
52	c3mduA	Alignment	not modelled	100.0	12	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
53	c2icsA	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
54	d1nfga2	Alignment	not modelled	100.0	38 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
55	c1o12B	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: B: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: crystal structure of n-acetylglucosamine-6-phosphate2 deacetylase (tm0814) from thermotoga maritima at 2.5 a3 resolution
56	d1ynya2	Alignment	not modelled	100.0	41 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
57	d2eg6a1	Alignment	not modelled	100.0	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
58	d1gkra2	Alignment	not modelled	100.0	29 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
59	c3pnuA	Alignment	not modelled	100.0	11 PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
60	d1gkpa2	Alignment	not modelled	100.0	35 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
61	c3jzeC	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
62	c3ighX	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
63	c2ogjB	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
64	c3etkA	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
65	c2imrA	Alignment	not modelled	100.0	13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
66	d1kcx2	Alignment	not modelled	100.0	31 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
67	d2fvka2	Alignment	not modelled	100.0	30 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
68	d2ftwa2	Alignment	not modelled	99.9	34 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
69	c3msrA	Alignment	not modelled	99.8	13 PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
70	d4ubpc2	Alignment	not modelled	99.8	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
71	d1nfga1	Alignment	not modelled	99.7	28 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
72	d1xrta2	Alignment	not modelled	99.7	23 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
73	d2uz9a2	Alignment	not modelled	99.7	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
74	d2p9ba2	Alignment	not modelled	99.7	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
75	d1ra0a2	Alignment	not modelled	99.7	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
76	d2ooda2	Alignment	not modelled	99.7	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
77	d1m7ja3	Alignment	not modelled	99.6	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
78	d1gkra1	Alignment	not modelled	99.6	23 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases

					Family: Hydantoinase (dihydropyrimidinase)
79	d2bb0a2	Alignment	not modelled	99.6	25 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
80	d2imra2	Alignment	not modelled	99.6	13 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
81	d1kcxa1	Alignment	not modelled	99.6	32 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
82	d2i9ua2	Alignment	not modelled	99.6	10 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
83	d2qs8a2	Alignment	not modelled	99.6	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
84	d1i0da_	Alignment	not modelled	99.6	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
85	d2puza2	Alignment	not modelled	99.6	24 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
86	d2paja2	Alignment	not modelled	99.6	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
87	d1gkpa1	Alignment	not modelled	99.5	34 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
88	d1e9yb1	Alignment	not modelled	99.5	23 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
89	d3be7a2	Alignment	not modelled	99.5	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
90	d1ynya1	Alignment	not modelled	99.5	39 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
91	d2q09a2	Alignment	not modelled	99.5	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
92	d1ejxc1	Alignment	not modelled	99.5	27 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
93	d2fvka1	Alignment	not modelled	99.5	26 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
94	d2r8ca2	Alignment	not modelled	99.5	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
95	d1k1da1	Alignment	not modelled	99.4	38 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
96	d1onwa2	Alignment	not modelled	99.4	12 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
97	c3ggmB_	Alignment	not modelled	99.4	22 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bt9727_2919; PDBTitle: crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
98	d1plma2	Alignment	not modelled	99.4	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
99	c1pscA_	Alignment	not modelled	99.4	16 PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
100	d1onwa1	Alignment	not modelled	99.4	14 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Isoaspartyl dipeptidase
101	d1yrra1	Alignment	not modelled	99.4	10 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
102	d2d2ja1	Alignment	not modelled	99.4	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
103	d1yrra2	Alignment	not modelled	99.4	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
104	d1un7a2	Alignment	not modelled	99.3	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
105	d2r8ca1	Alignment	not modelled	99.3	25 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
					Fold: Composite domain of metallo-dependent hydrolases

106	d2p9ba1	Alignment	not modelled	99.3	18	Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
107	d1xrtal	Alignment	not modelled	99.3	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
108	d2icsa2	Alignment	not modelled	99.3	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
109	d1o12a2	Alignment	not modelled	99.2	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
110	d2paja1	Alignment	not modelled	99.2	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
111	c3pnzD_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
112	d2ftwa1	Alignment	not modelled	99.1	37	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
113	d1bf6a_	Alignment	not modelled	99.0	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
114	d1plma1	Alignment	not modelled	98.9	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
115	c2vc7A_	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
116	c2zc1A_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
117	c3f4cA_	Alignment	not modelled	98.9	14	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 steartothermophilus strain 10, with glycerol bound
118	d1m7ja2	Alignment	not modelled	98.9	30	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
119	d1m7ja1	Alignment	not modelled	98.8	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
120	d3be7a1	Alignment	not modelled	98.8	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like