



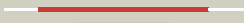

























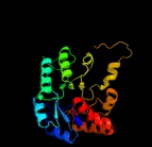


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlyxa1	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
2	dlj6oa_	 Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
3	dlxwya1	 Alignment		100.0	33	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
4	c3rcmA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
5	c2gzxB_	 Alignment		100.0	38	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.
6	c2xioA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyri bonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
7	dlzzma1	 Alignment		100.0	28	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
8	c3ipwA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
9	c2y1hA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyri bonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
10	c3e2vA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
11	c3gg7A_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans

12	d2ffia1	Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
13	c3irsB	Alignment		100.0	14	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
14	c2wm1A	Alignment		100.0	17	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
15	c3ij6A	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
16	d2f6ka1	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
17	d2gwga1	Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
18	c3guwB	Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_1765; PDBTitle: crystal structure of the tatd-like protein (af1765) from2 archaeoglobus fulgidus, northeast structural genomics3 consortium target gr121
19	d2hbva1	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
20	d2dvta1	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
21	c3cjpA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted amidohydrolase, dihydroorotase family; PDBTitle: crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
22	c2qahA	Alignment	not modelled	100.0	14	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 sphingomonas paucimobilis
23	c3nurA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
24	d1bf6a	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
25	c3f4cA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
26	c2vc7A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
27	d2d2ja1	Alignment	not modelled	99.9	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
28	c3pnzD	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria

					monocytogenes
29	d1i0da	Alignment	not modelled	99.9	19 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
30	c1pscA	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
31	c2zc1A	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
32	c3k2gA	Alignment	not modelled	99.8	16 PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
33	c3rhgA	Alignment	not modelled	99.8	17 PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
34	d1xrta2	Alignment	not modelled	99.8	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
35	c3msrA	Alignment	not modelled	99.6	13 PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
36	c2qpxA	Alignment	not modelled	99.6	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
37	c3pnuA	Alignment	not modelled	99.6	16 PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
38	d1nfga2	Alignment	not modelled	99.6	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
39	d1k1da2	Alignment	not modelled	99.6	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
40	d1ynya2	Alignment	not modelled	99.5	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
41	d1gkra2	Alignment	not modelled	99.5	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
42	c3nqbB	Alignment	not modelled	99.5	16 PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
43	d2ftwa2	Alignment	not modelled	99.5	17 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
44	c1xrfA	Alignment	not modelled	99.5	12 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
45	d2eg6a1	Alignment	not modelled	99.5	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
46	d1gkpa2	Alignment	not modelled	99.4	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
47	d2fvka2	Alignment	not modelled	99.4	11 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
48	d2uz9a2	Alignment	not modelled	99.4	11 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
49	d2icsa2	Alignment	not modelled	99.4	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
50	d1kcxa2	Alignment	not modelled	99.4	12 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
51	d1onwa2	Alignment	not modelled	99.4	12 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
52	c3jzeC	Alignment	not modelled	99.4	15 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
53	c2vunC	Alignment	not modelled	99.4	14 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
54	d2paja2	Alignment	not modelled	99.3	12 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

					Family: SAH/MTA deaminase-like
55	d2imra2	Alignment	not modelled	99.3	11 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
56	d2i9ua2	Alignment	not modelled	99.3	11 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
57	d1p1ma2	Alignment	not modelled	99.3	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
58	c3e0lB_	Alignment	not modelled	99.3	12 PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
59	d3be7a2	Alignment	not modelled	99.3	21 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
60	d1yrra2	Alignment	not modelled	99.2	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
61	d2r8ca2	Alignment	not modelled	99.2	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
62	d2p9ba2	Alignment	not modelled	99.2	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
63	d2qs8a2	Alignment	not modelled	99.2	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
64	d2bb0a2	Alignment	not modelled	99.2	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
65	c3hpaB_	Alignment	not modelled	99.2	11 PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
66	c1p1mA_	Alignment	not modelled	99.2	14 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
67	c2pajA_	Alignment	not modelled	99.1	12 PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
68	c2ogjB_	Alignment	not modelled	99.1	16 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
69	c2imrA_	Alignment	not modelled	99.1	10 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
70	c2i9uA_	Alignment	not modelled	99.1	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
71	d1un7a2	Alignment	not modelled	99.1	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
72	c2q09A_	Alignment	not modelled	99.1	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
73	d1ra0a2	Alignment	not modelled	99.1	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
74	d1ltua_	Alignment	not modelled	99.1	13 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase
75	c2aqoB_	Alignment	not modelled	99.0	11 PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
76	d2ooda2	Alignment	not modelled	99.0	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
77	c2i5gB_	Alignment	not modelled	99.0	12 PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
78	c2bb0A_	Alignment	not modelled	99.0	16 PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
79	c3lnpA_	Alignment	not modelled	99.0	13 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
80	c3dc8B_	Alignment	not modelled	99.0	15 PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from

					sinorhizobium meliloti
81	c1r9yA_	Alignment	not modelled	99.0	15 PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
82	c3gnhA_	Alignment	not modelled	99.0	17 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.
83	c2gokA_	Alignment	not modelled	98.9	14 PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
84	c1gkpD_	Alignment	not modelled	98.9	17 PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
85	d2q09a2	Alignment	not modelled	98.9	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
86	c3b40A_	Alignment	not modelled	98.9	15 PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
87	c1k1dF_	Alignment	not modelled	98.9	15 PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
88	d2puza2	Alignment	not modelled	98.9	17 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
89	c3hm7A_	Alignment	not modelled	98.9	14 PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
90	c2icsA_	Alignment	not modelled	98.9	15 PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
91	c1gkrA_	Alignment	not modelled	98.9	17 PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aureescens
92	c3d6nA_	Alignment	not modelled	98.8	13 PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
93	c2vr2A_	Alignment	not modelled	98.8	13 PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
94	c2ftwA_	Alignment	not modelled	98.8	16 PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
95	c3lsbA_	Alignment	not modelled	98.8	14 PDB header: hydrolase Chain: A: PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureescens tc1 complexed with zinc and ametrin
96	d1o12a2	Alignment	not modelled	98.8	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
97	c1nfgA_	Alignment	not modelled	98.8	8 PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
98	d4ubpc2	Alignment	not modelled	98.8	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
99	c2gseC_	Alignment	not modelled	98.8	12 PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinase-like 2
100	c2p50C_	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
101	c3ighX_	Alignment	not modelled	98.7	22 PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
102	c3etkA_	Alignment	not modelled	98.7	22 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
103	c2qt3A_	Alignment	not modelled	98.7	13 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
104	c3mduA_	Alignment	not modelled	98.7	13 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
105	c2fvmA_	Alignment	not modelled	98.7	13 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
106	c3fdgA_	Alignment	not modelled	98.6	13 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
107	c2oodA_	Alignment	not modelled	98.6	14 PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
108	c3itcA_	Alignment	not modelled	98.5	16 PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
109	c2ragB_	Alignment	not modelled	98.5	11 PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus
110	c3lu2B_	Alignment	not modelled	98.5	13 PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
111	c2z00A_	Alignment	not modelled	98.5	14 PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
112	c3be7B_	Alignment	not modelled	98.5	20 PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
113	c2p9bA_	Alignment	not modelled	98.5	14 PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
114	c3mpgB_	Alignment	not modelled	98.4	15 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
115	d1m7ja3	Alignment	not modelled	98.4	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
116	c3griB_	Alignment	not modelled	98.4	10 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
117	c3e74D_	Alignment	not modelled	98.3	13 PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at2 the metal center
118	c2qs8A_	Alignment	not modelled	98.3	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
119	c3la4A_	Alignment	not modelled	98.3	13 PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
120	d1j5sa_	Alignment	not modelled	98.3	18 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like