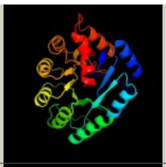
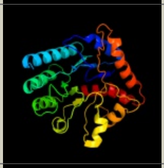
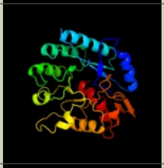
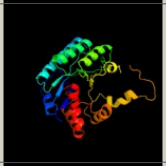
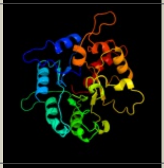
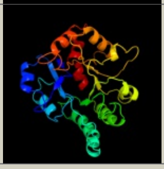
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P39408
Date	Thu Jan 5 12:00:44 GMT 2012
Unique Job ID	db8b4bbb467a679f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zzma1	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
2	c2gzxB_	Alignment		100.0	30	**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.
3	c3ipwA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
4	d1xwya1	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
5	c3rcmA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tatd family hydrolase; **PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
6	d1j6oa_	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
7	c2xioA_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
8	c2y1hA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3; **PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3)
9	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
10	d1yixa1	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
11	c3gg7A_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized metalloprotein; **PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans

12	c3irsB_	Alignment		100.0	15	**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
13	d2f6ka1	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
14	c2wm1A_	Alignment		100.0	16	**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	d2dvta1	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
16	d2ffia1	Alignment		100.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
17	c3nurA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus
18	d2gwga1	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
19	c3guwB_	Alignment		100.0	18	**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
20	c3ij6A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
21	c3cjpA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
22	d2hbva1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
23	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
24	d1bf6a_	Alignment	not modelled	100.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
25	c3f4cA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
26	d1i0da_	Alignment	not modelled	99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
27	c2vc7A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
28	d2d2ja1	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like

29	c3pnzD_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphotriesterase family protein; **PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes
30	c1pscA_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
31	c2zc1A_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
32	c3k2gA_	Alignment	not modelled	99.9	14	**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	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
34	c2qpxA_	Alignment	not modelled	99.8	18	**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
35	d1xrta2	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
36	c3pnuA_	Alignment	not modelled	99.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
37	d2eg6a1	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Dihydroorotase
38	c3jzeC_	Alignment	not modelled	99.7	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
39	d1gkra2	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
40	d1nfga2	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
41	d1k1da2	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
42	d1ynya2	Alignment	not modelled	99.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
43	c3msrA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolases; **PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae
44	d2fvka2	Alignment	not modelled	99.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
45	d1kcxa2	Alignment	not modelled	99.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
46	d2imra2	Alignment	not modelled	99.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**DR0824-like
47	d2icsa2	Alignment	not modelled	99.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenine deaminase-like
48	d2paja2	Alignment	not modelled	99.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
49	d2ftwa2	Alignment	not modelled	99.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
50	d2uz9a2	Alignment	not modelled	99.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
51	d1onwa2	Alignment	not modelled	99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase, catalytic domain
52	d1gkpa2	Alignment	not modelled	99.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
53	d2i9ua2	Alignment	not modelled	99.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
54	c3nqbB_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenine deaminase 2; **PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)

55	c3e0lB_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine deaminase; **PDBTitle:** computationally designed ammelide deaminase
56	c2pajA_	Alignment	not modelled	99.3	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
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	d3be7a2	Alignment	not modelled	99.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
59	d1p1ma2	Alignment	not modelled	99.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
60	d2r8ca2	Alignment	not modelled	99.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
61	c2vunC_	Alignment	not modelled	99.2	14	**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
62	d2bb0a2	Alignment	not modelled	99.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
63	d2ooda2	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
64	d2qs8a2	Alignment	not modelled	99.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
65	c2i9uA_	Alignment	not modelled	99.1	16	**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
66	c3lnpA_	Alignment	not modelled	99.1	15	**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
67	c2q09A_	Alignment	not modelled	99.1	11	**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
68	d2p9ba2	Alignment	not modelled	99.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
69	c2bb0A_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** structure of imidazolonepropionase from bacillus subtilis
70	d1itua_	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
71	c2imrA_	Alignment	not modelled	99.1	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
72	c2ogjB_	Alignment	not modelled	99.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of a dihydroorotase
73	d1un7a2	Alignment	not modelled	99.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
74	d1yrra2	Alignment	not modelled	99.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
75	c3lu2B_	Alignment	not modelled	99.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
76	d2q09a2	Alignment	not modelled	99.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
77	c2vr2A_	Alignment	not modelled	98.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** human dihydropyrimidinase
78	c3v7pA_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase family protein; **PDBTitle:** crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2
79	c3fdgA_	Alignment	not modelled	98.9	15	**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
80	c1p1mA_	Alignment	not modelled	98.9	13	**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
81	d1m7ja3	Alignment	not modelled	98.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**D-aminoacylase, catalytic domain
82	c3hpaB_	Alignment	not modelled	98.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
83	d2puza2	Alignment	not modelled	98.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
84	c2ftwA_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidine amidohydrolase; **PDBTitle:** crystal structure of dihydropyrimidinase from dictyostelium discoideum
85	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
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	c3dc8B_	Alignment	not modelled	98.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from sinorhizobium meliloti
88	c2icsA_	Alignment	not modelled	98.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenine deaminase; **PDBTitle:** crystal structure of an adenine deaminase
89	c3gnhA_	Alignment	not modelled	98.8	14	**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.
90	d1ra0a2	Alignment	not modelled	98.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
91	c2gseC_	Alignment	not modelled	98.8	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydropyrimidinase-related protein 2; **PDBTitle:** crystal structure of human dihydropyrimidinease-like 2
92	c3lsbA_	Alignment	not modelled	98.8	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
93	d1o12a2	Alignment	not modelled	98.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
94	c3ighX_	Alignment	not modelled	98.8	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3
95	d4ubpc2	Alignment	not modelled	98.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
96	c1k1dF_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**d-hydantoinase; **PDBTitle:** crystal structure of d-hydantoinase
97	c3ou8B_	Alignment	not modelled	98.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
98	c2aqoB_	Alignment	not modelled	98.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isoaspartyl dipeptidase; **PDBTitle:** crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
99	c3ou8A_	Alignment	not modelled	98.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
100	c2oodA_	Alignment	not modelled	98.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr3880 protein; **PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum
101	c2i5gB_	Alignment	not modelled	98.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
102	c1gkpD_	Alignment	not modelled	98.6	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**hydantoinase; **PDBTitle:** d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
103	c3mduA_	Alignment	not modelled	98.6	17	**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
104	c1r9yA_	Alignment	not modelled	98.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine deaminase; **PDBTitle:** bacterial cytosine deaminase d314a mutant.
105	c2ragB_	Alignment	not modelled	98.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter

						crescentus
106	c2fvmA_	Alignment	not modelled	98.6	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
107	c1gkrA_	Alignment	not modelled	98.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase; **PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
108	c2qt3A_	Alignment	not modelled	98.5	15	**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
109	d1j5sa_	Alignment	not modelled	98.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Uronate isomerase-like
110	c3etkA_	Alignment	not modelled	98.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
111	c3hm7A_	Alignment	not modelled	98.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125
112	c1nfgA_	Alignment	not modelled	98.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-hydantoinase; **PDBTitle:** structure of d-hydantoinase
113	c3itcA_	Alignment	not modelled	98.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
114	c3rysA_	Alignment	not modelled	98.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
115	c2p50C_	Alignment	not modelled	98.4	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
116	c2q01A_	Alignment	not modelled	98.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uronate isomerase; **PDBTitle:** crystal structure of glucuronate isomerase from caulobacter crescentus
117	c3d6nA_	Alignment	not modelled	98.3	16	**PDB header:**hydrolase/transferase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
118	c3be7B_	Alignment	not modelled	98.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zn-dependent arginine carboxypeptidase; **PDBTitle:** crystal structure of zn-dependent arginine carboxypeptidase
119	d1vfla1	Alignment	not modelled	98.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
120	d1e9yb2	Alignment	not modelled	98.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain