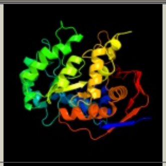
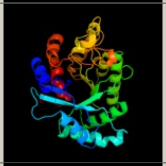
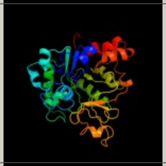
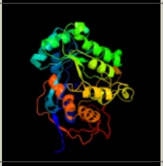
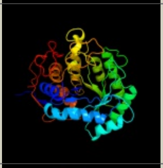
Email	l.a.kelley@imperial.ac.uk
Description	P05020
Date	Thu Jan 5 10:58:35 GMT 2012
Unique Job ID	0f8a88ab9eb58b45

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2eg6a1	Alignment		100.0	99	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Dihydroorotase
2	c3jzeC_	Alignment		100.0	87	**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
3	c3pnuA_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
4	d1k1da2	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
5	d1gkra2	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
6	d1nfga2	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
7	d1ynya2	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
8	d2fvka2	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
9	d1m7ja3	Alignment		100.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**D-aminoacylase, catalytic domain
10	d2ftwa2	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
11	d1gkpa2	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain

12	d1kcxa2	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
13	c2vr2A_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** human dihydropyrimidinase
14	c3dc8B_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from sinorhizobium meliloti
15	c2fvmA_	Alignment		100.0	15	**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
16	c2ftwA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidine amidohydrolase; **PDBTitle:** crystal structure of dihydropyrimidinase from dictyostelium discoideum
17	c2gseC_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydropyrimidinase-related protein 2; **PDBTitle:** crystal structure of human dihydropyrimidinease-like 2
18	c1gkpD_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**hydantoinase; **PDBTitle:** d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
19	c1gkrA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase; **PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
20	c3hm7A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125
21	c1k1dF_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**d-hydantoinase; **PDBTitle:** crystal structure of d-hydantoinase
22	c1nfgA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-hydantoinase; **PDBTitle:** structure of d-hydantoinase
23	c2z00A_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of dihydroorotase from thermus thermophilus
24	c3griB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** the crystal structure of a dihydroorotase from staphylococcus aureus
25	c3e74D_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allantoinase; **PDBTitle:** crystal structure of e. coli allantoinase with iron ions at2 the metal center
26	c2gwnA_	Alignment	not modelled	100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** the structure of putative dihydroorotase from porphyromonas2 gingivalis.
27	c3mpgB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** dihydroorotase from bacillus anthracis
28	c3d6nA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase/transferase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
						Fold:TIM beta/alpha-barrel

29	d1xrta2	Alignment	not modelled	100.0	22	**Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
30	c1xrfA_	Alignment	not modelled	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
31	c3la4A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease; **PDBTitle:** crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
32	d1o12a2	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
33	d1i0da_	Alignment	not modelled	99.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
34	c1pscA_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** phosphotriesterase from pseudomonas diminuta
35	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
36	d2d2ja1	Alignment	not modelled	99.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
37	d4ubpc2	Alignment	not modelled	99.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
38	d1onwa2	Alignment	not modelled	99.9	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Isoaspartyl dipeptidase, catalytic domain
39	c3msrA_	Alignment	not modelled	99.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolases; **PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae
40	c3e0lB_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanine deaminase; **PDBTitle:** computationally designed ammelide deaminase
41	d2icsa2	Alignment	not modelled	99.8	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenine deaminase-like
42	c2vunC_	Alignment	not modelled	99.8	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
43	c1p1mA_	Alignment	not modelled	99.8	15	**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
44	c3nqbB_	Alignment	not modelled	99.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenine deaminase 2; **PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
45	c3lsbA_	Alignment	not modelled	99.7	11	**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
46	c2ubpC_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (urease alpha subunit); **PDBTitle:** structure of native urease from bacillus pasteurii
47	c2aqoB_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isoaspartyl dipeptidase; **PDBTitle:** crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
48	c3gnhA_	Alignment	not modelled	99.7	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.
49	c2pajA_	Alignment	not modelled	99.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/guanine deaminase; **PDBTitle:** crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
50	c3hpaB_	Alignment	not modelled	99.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
51	c2vc7A_	Alignment	not modelled	99.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
52	c1r9yA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine deaminase; **PDBTitle:** bacterial cytosine deaminase d314a mutant.
53	d2p9ba2	Alignment	not modelled	99.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
54	c2r8cB_	Alignment	not modelled	99.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eaj56179
						PDB header:hydrolase

55	c2ogjB_	Alignment	not modelled	99.6	12	**Chain:** B: **PDB Molecule:**dihydroorotase; **PDBTitle:** crystal structure of a dihydroorotase
56	c2q09A_	Alignment	not modelled	99.6	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
57	c3ighX_	Alignment	not modelled	99.6	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
58	c2gokA_	Alignment	not modelled	99.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
59	c1e9yB_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**urease subunit beta; **PDBTitle:** crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
60	c2oodA_	Alignment	not modelled	99.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr3880 protein; **PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum
61	d1xwya1	Alignment	not modelled	99.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
62	c2qt3A_	Alignment	not modelled	99.6	11	**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
63	c3be7B_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zn-dependent arginine carboxypeptidase; **PDBTitle:** crystal structure of zn-dependent arginine carboxypeptidase
64	c2i9uA_	Alignment	not modelled	99.6	13	**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
65	c2bb0A_	Alignment	not modelled	99.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**imidazolonepropionase; **PDBTitle:** structure of imidazolonepropionase from bacillus subtilis
66	d1bf6a_	Alignment	not modelled	99.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Phosphotriesterase-like
67	d1ra0a2	Alignment	not modelled	99.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Cytosine deaminase catalytic domain
68	c2p9bA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible prolidase; **PDBTitle:** crystal structure of putative prolidase from2 bifidobacterium longum
69	c3feqB_	Alignment	not modelled	99.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eah89906
70	d1zzma1	Alignment	not modelled	99.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
71	c2icsA_	Alignment	not modelled	99.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenine deaminase; **PDBTitle:** crystal structure of an adenine deaminase
72	c3gipB_	Alignment	not modelled	99.5	14	**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.
73	c3lnpA_	Alignment	not modelled	99.5	12	**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
74	c2p50C_	Alignment	not modelled	99.5	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
75	c3etkA_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
76	c1fwcC_	Alignment	not modelled	99.4	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**urease; **PDBTitle:** klebsiella aerogenes urease, c319a variant at ph 8.5
77	c3rcmA_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tatd family hydrolase; **PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
78	c3ooqC_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of amidohydrolase from thermotoga maritima msb8
						PDB header:hydrolase

79	c1rjqA_	Alignment	not modelled	99.4	11	**Chain:** A: **PDB Molecule:**d-aminoacylase; **PDBTitle:** the crystal structure of the d-aminoacylase mutant d366a
80	c3mduA_	Alignment	not modelled	99.4	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
81	d2uz9a2	Alignment	not modelled	99.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
82	d2paja2	Alignment	not modelled	99.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
83	c2qs8A_	Alignment	not modelled	99.4	11	**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
84	c3f4cA_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
85	d3be7a2	Alignment	not modelled	99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
86	d1xrta1	Alignment	not modelled	99.4	11	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
87	d1nfga1	Alignment	not modelled	99.4	13	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
88	c2zc1A_	Alignment	not modelled	99.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
89	c2vhlB_	Alignment	not modelled	99.3	11	**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
90	c2imrA_	Alignment	not modelled	99.3	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
91	d1yixa1	Alignment	not modelled	99.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
92	c3egjA_	Alignment	not modelled	99.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
93	d2imra2	Alignment	not modelled	99.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**DR0824-like
94	d2r8ca2	Alignment	not modelled	99.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
95	c2gzxB_	Alignment	not modelled	99.2	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.
96	d1j6oa_	Alignment	not modelled	99.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
97	c1o12B_	Alignment	not modelled	99.2	13	**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
98	d2bb0a2	Alignment	not modelled	99.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
99	c2y1hA_	Alignment	not modelled	99.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3; **PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3)
100	d2i9ua2	Alignment	not modelled	99.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
101	d2ooda2	Alignment	not modelled	99.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
102	d2qs8a2	Alignment	not modelled	99.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
103	d2q09a2	Alignment	not modelled	99.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
104	d1p1ma2	Alignment	not modelled	98.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like

105	d2puza2	Alignment	not modelled	98.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Imidazolonepropionase-like
106	d2dvta1	Alignment	not modelled	98.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
107	d2ffia1	Alignment	not modelled	98.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
108	d1gkra1	Alignment	not modelled	98.8	20	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
109	c2wm1A_	Alignment	not modelled	98.8	19	**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
110	c3gg7A_	Alignment	not modelled	98.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized metalloprotein; **PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
111	c3k2gA_	Alignment	not modelled	98.7	13	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
112	d2gwga1	Alignment	not modelled	98.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
113	c3irsB_	Alignment	not modelled	98.6	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
114	c3guwB_	Alignment	not modelled	98.6	17	**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
115	c2qahA_	Alignment	not modelled	98.6	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
116	c3cjpA_	Alignment	not modelled	98.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
117	c3ij6A_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
118	c3rhgA_	Alignment	not modelled	98.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
119	d2f6ka1	Alignment	not modelled	98.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
120	c3nurA_	Alignment	not modelled	98.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus