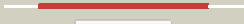



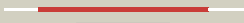




















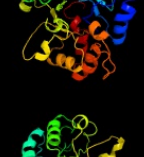
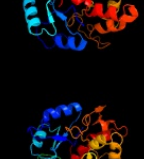
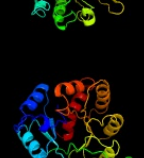


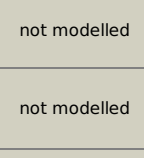


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1008_(tatD)_1127093_1127887
Date	Wed Jul 31 22:05:07 BST 2019
Unique Job ID	4b04ef7002657ffb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zzma1	 Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
2	d1xwya1	 Alignment		100.0	28	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
3	c2gzxB_	 Alignment		100.0	34	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.
4	d1j6oa_	 Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
5	c3ipwA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
6	c2xioA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
7	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
8	d1yixa1	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
9	c3e2vA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
10	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)
11	c3gg7A_	 Alignment		100.0	28	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	19	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	c4do7B	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase 2; PDBTitle: crystal structure of an amidohydrolase (cog3618) from burkholderia2 multivorans (target efi-500235) with bound zn, space group c2
14	c3guwB	Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_1765; PDBTitle: crystal structure of the tatd-like protein (af1765) from archaeoglobus2 fulgidus, northeast structural genomics consortium target gr121
15	d2gwga1	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
16	c5vn5A	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: 2,2',3'-trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl meta- PDBTitle: crystal structure of ligy from sphingobium sp. strain syk-6
17	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
18	c3cjpA	Alignment		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
19	d2ffia1	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
20	c4hk6D	Alignment		100.0	18	PDB header: lyase Chain: D: PDB Molecule: uracil-5-carboxylate decarboxylase; PDBTitle: crystal structure of cordyceps militaris idcase in complex with 5-2 nitro-uracil
21	d2f6ka1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
22	c6dxsB	Alignment	not modelled	100.0	15	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: 4-oxalomesaconate hydratase; PDBTitle: crystal structure of the ligj hydratase e284q mutant substrate complex2 with (3z)-2-keto-4-carboxy-3-hexenedioate
23	d2dvta1	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
24	c4l5pD	Alignment	not modelled	99.9	19	PDB header: lyase Chain: D: PDB Molecule: 5-carboxyvanillate decarboxylase; PDBTitle: crystal structure of 5-carboxyvanillate decarboxylase from2 sphingomonas paucimobilis complexed with 4-hydroxy-3-methoxy-5-3 nitrobenzoic acid
25	c4infA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of amidohydrolase saro_0799 (target efi-505250) from2 novosphingobium aromaticivorans dsm 12444 with bound calcium
26	c4i6kA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase family protein; PDBTitle: crystal structure of probable 2-pyrone-4,6-dicarboxylic acid hydrolase2 abaye1769 (target efi-505029) from acinetobacter baumannii with3 citric acid bound
27	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
						Fold: TIM beta/alpha-barrel

28	d1bf6a_	Alignment	not modelled	99.9	14	Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
29	c3ij6A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from <i>lactobacillus acidophilus</i>
30	c3nurA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from <i>staphylococcus2 aureus</i>
31	c4mupC_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of <i>agrobacterium tumefaciens</i> atu3138 (efi target2 505157), apo structure
32	c3tn6A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: crystal structure of gkap mutant r230h from <i>geobacillus kaustophilus2 hta426</i>
33	d2hbva1	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
34	c2vc7A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
35	c2qahA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: 2-pyrone-4,6-dicarboxylic acid hydrolase; PDBTitle: crystal structure of the 2-pyrone-4,6-dicarboxylic acid hydrolase from <i>2 sphingomonas paucimobilis</i>
36	c6omqA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ptmu3; PDBTitle: crystal structure of ptmu3 complexed with ptm substrate
37	c3pnzD_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from <i>listeria monocytogenes</i>
38	d1i0da_	Alignment	not modelled	99.9	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
39	c4rdzA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group
40	d2d2ja1	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
41	c2zc1A_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from <i>deinococcus radiodurans</i>
42	c4if2A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase homology protein; PDBTitle: structure of the phosphotriesterase from <i>mycobacterium tuberculosis</i>
43	c1pscA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from <i>pseudomonas diminuta</i>
44	c4dziD_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: putative tim-barrel metal-dependent hydrolase; PDBTitle: crystal structure of amidohydrolase map2389c (target efi-500390) from <i>2 mycobacterium avium</i> subsp. <i>paratuberculosis</i> k-10
45	c3k2gA_	Alignment	not modelled	99.9	19	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from <i>2 rhodobacter sphaeroides</i>
46	c3rhgA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from <i>2 proteus mirabilis</i> hi4320
47	d1xrta2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
48	c2qpxA_	Alignment	not modelled	99.7	16	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 <i>lactobacillus casei</i> atcc 334 at 1.40 a resolution
49	c3pnuA_	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from <i>2 campylobacter jejuni</i> .
50	c5v0gE_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: E: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase pyrc from <i>yersinia pestis</i> in2 complex with zinc and unknown ligand at 2.4 a resolution.
51	c3msrA_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from <i>mycoplasma synoviae</i>
52	d1k1da2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
53	d2eg6a1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase

54	c3jzeC_	Alignment	not modelled	99.6	16	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
55	d1nfqa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
56	c4fyB_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
57	c5vgmA_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase pyrc from vibrio cholerae in2 complex with zinc at 1.95 a resolution.
58	d1gkra2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
59	d1ynya2	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
60	d1kcxa2	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
61	c2ogjC_	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
62	d2uz9a2	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
63	d2fvka2	Alignment	not modelled	99.3	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
64	d2paja2	Alignment	not modelled	99.3	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
65	d2imra2	Alignment	not modelled	99.3	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
66	d1p1ma2	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
67	d2icsa2	Alignment	not modelled	99.3	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
68	c1xrfA_	Alignment	not modelled	99.3	15	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
69	c4dzhA_	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolyase; PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
70	d1onwa2	Alignment	not modelled	99.2	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
71	c4dykB_	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolyase; PDBTitle: crystal structure of an adenosine deaminase from pseudomonas2 aeruginosa pao1 (target nysgrc-200449) with bound zn
72	d2ftwa2	Alignment	not modelled	99.2	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
73	d2i9ua2	Alignment	not modelled	99.2	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
74	d1gkpa2	Alignment	not modelled	99.2	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
75	c3e0lB_	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
76	d3be7a2	Alignment	not modelled	99.2	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
77	c3nqbB_	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
78	c6ohaA_	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: probable guanine deaminase; PDBTitle: yeast guanine deaminase
79	c2pajA_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolyase from an environmental sample of2 sargasso sea
80	d2qs8a2	Alianment	not modelled	99.1	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

						Family: Zn-dependent arginine carboxypeptidase-like
81	d2r8ca2	Alignment	not modelled	99.1	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
82	c2vunC_	Alignment	not modelled	99.1	16	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
83	c5ns5A_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase glij; PDBTitle: cys-gly dipeptidase glij in complex with cu2+ and zn2+
84	c4f0rA_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylthioadenosine/s-adenosylhomocysteine deaminase; PDBTitle: crystal structure of an adenosine deaminase homolog from2 chromobacterium violaceum (target nysgrc-019589) bound zn and 5'-3 methylthioadenosine (unproductive complex)
85	d2bb0a2	Alignment	not modelled	99.0	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
86	c3lnpA_	Alignment	not modelled	99.0	15	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase family protein olei01672_1_465; PDBTitle: crystal structure of amidohydrolase family protein olei01672_1_4652 from oleispira antarctica
87	c3lu2B_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
88	d2p9ba2	Alignment	not modelled	99.0	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
89	c2ogjB_	Alignment	not modelled	99.0	20	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
90	d2ooda2	Alignment	not modelled	98.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
91	c2q09A_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxoimidazolidin-4-yl)-propionic acid
92	c2imrA_	Alignment	not modelled	98.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
93	c2i9uA_	Alignment	not modelled	98.9	12	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
94	c3itcA_	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
95	c4i6vA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase 2; PDBTitle: the crystal structure of an amidohydrolase 2 from planctomyces2 limnophilus dsm 3776
96	d1yrra2	Alignment	not modelled	98.9	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
97	c1p1mA_	Alignment	not modelled	98.9	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
98	c2bb0A_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
99	c3v7pA_	Alignment	not modelled	98.9	12	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
100	c2ragB_	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus
101	d1un7a2	Alignment	not modelled	98.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
102	c3b40A_	Alignment	not modelled	98.8	11	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from pseudomonas2 aeruginosa
103	c2gokA_	Alignment	not modelled	98.8	19	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
104	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
105	d2q09a2	Alignment	not modelled	98.8	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

					Family: Imidazolonepropionase-like
106	d2puza2	Alignment	not modelled	98.8	19 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
107	c4c65A_	Alignment	not modelled	98.8	15 PDB header: hydrolase Chain: A: PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
108	c4c6mA_	Alignment	not modelled	98.8	15 PDB header: hydrolase Chain: A: PDB Molecule: cad protein; PDBTitle: crystal structure of the dihydroorotase domain of human cad2 bound to the inhibitor fluoroorotate at ph 7.0
109	d1ra0a2	Alignment	not modelled	98.8	15 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
110	c3gnhA_	Alignment	not modelled	98.8	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.
111	c6ohcB_	Alignment	not modelled	98.8	13 PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: e. coli guanine deaminase
112	c4v1xA_	Alignment	not modelled	98.8	16 PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
113	c3hpaB_	Alignment	not modelled	98.7	13 PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
114	c2vr2A_	Alignment	not modelled	98.7	15 PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
115	c5xqxB_	Alignment	not modelled	98.7	17 PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of colwellia psychrerythraea strain 34h isoaspartyl2 dipeptidase e80q mutant complexed with beta-isoaspartyl lysine
116	c3hm7A_	Alignment	not modelled	98.7	14 PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
117	c1k1dF_	Alignment	not modelled	98.7	15 PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
118	c1gkpD_	Alignment	not modelled	98.7	14 PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
119	c5nnlB_	Alignment	not modelled	98.7	11 PDB header: oxidoreductase Chain: B: PDB Molecule: inactive dihydroorotase-like domain; PDBTitle: inactive dihydroorotase-like domain of chaetomium thermophilum cad-2 like multifunctional protein
120	c2gseC_	Alignment	not modelled	98.6	13 PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2