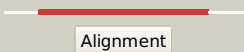

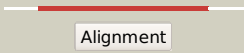

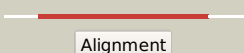

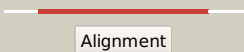
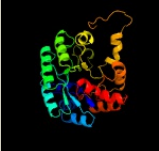


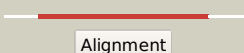

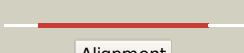




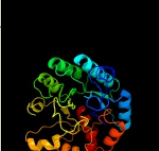

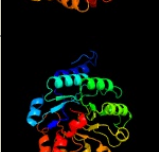
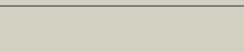












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3510c (-)_3938600_3939436
Date	Fri Aug 9 18:20:18 BST 2019
Unique Job ID	95a7c6a709c7cffc

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3irsB_			100.0	25	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
2	c4l5pD_			100.0	21	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
3	c2wm1A_			100.0	21	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
4	d2dvta1			100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
5	c3nurA_			100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
6	c4infA_			100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of amidohydrolase sar0_0799 (target efi-505250) from2 novosphingobium aromaticivorans dsm 12444 with bound calcium
7	c6omqA_			100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: ptmu3; PDBTitle: crystal structure of ptmu3 complexed with ptm substrate
8	c4hk6D_			100.0	20	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
9	d2f6ka1			100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
10	c5vn5A_			100.0	20	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
11	c3ij6A_			100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 lactobacillus acidophilus

12	d2hbva1	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
13	c3cjpA	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: predicted amidohydrolase, dihydroorotase family; PDBTitle: crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
14	d2gwga1	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
15	c4dziD	Alignment		100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: putative tim-barrel metal-dependent hydrolase; PDBTitle: crystal structure of amidohydrolase map2389c (target efi-500390) from2 mycobacterium avium subsp. paratuberculosis k-10
16	c2qahA	Alignment		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 acid hydrolase from2 sphingomonas paucimobills
17	c6dxsB	Alignment		100.0	22	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
18	c4do7B	Alignment		100.0	15	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
19	d2ffia1	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
20	c4mupC	Alignment		100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure
21	c4i6kA	Alignment	not modelled	100.0	17	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
22	c2gzxB	Alignment	not modelled	100.0	17	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.
23	d1xwya1	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
24	c3rcmA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
25	d1yixa1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
26	d1zzma1	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
27	d1j6oa	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
28	c2y1hA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)

29	c3gg7A_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from <i>deinococcus radiodurans</i>
30	c3guwB_	Alignment	not modelled	100.0	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_1765; PDBTitle: crystal structure of the tatd-like protein (af1765) from <i>archaeoglobus2 fulgidus</i> , northeast structural genomics consortium target gr121
31	c2qpxA_	Alignment	not modelled	99.9	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
32	c2xioA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
33	d1bf6a_	Alignment	not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-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	c3tn6A_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: crystal structure of gkap mutant r230h from <i>geobacillus kaustophilus2</i> hta426
36	c4rdzA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group
37	c3f4cA_	Alignment	not modelled	99.8	10	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from <i>geobacillus2 stearothermophilus</i> strain 10, with glycerol bound
38	c3e2vA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from <i>saccharomyces cerevisiae</i>
39	d2d2ja1	Alignment	not modelled	99.8	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
40	c3ipwA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from <i>entamoeba2 histolytica</i>
41	c4if2A_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase homology protein; PDBTitle: structure of the phosphotriesterase from <i>mycobacterium tuberculosis</i>
42	d1i0da_	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
43	c1pscA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from <i>pseudomonas diminuta</i>
44	c3pnzD_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase Imo2620 from <i>listeria monocytogenes</i>
45	c2zc1A_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from <i>deinococcus radiodurans</i>
46	d1xrt2	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
47	c5v0gE_	Alignment	not modelled	99.5	16	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.
48	c4lfyB_	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from <i>burkholderia cenocepacia2</i> j2315
49	c3pnuA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from <i>campylobacter jejuni</i> .
50	c5vgmA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase pyrc from <i>vibrio cholerae</i> in2 complex with zinc at 1.95 a resolution.
51	c4i6vA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase 2; PDBTitle: the crystal structure of an amidohydrolase 2 from <i>planctomyces2 limnophilus</i> dsm 3776
52	d1itua_	Alignment	not modelled	99.4	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase
53	d2eg6a1	Alignment	not modelled	99.3	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
54	c3k2gA_	Alignment	not modelled	99.3	14	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein

						from2 rhodobacter sphaeroides
55	c3rhgA_	Alignment	not modelled	99.3	11	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
56	d1j5sa_	Alignment	not modelled	99.3	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like
57	c3jzeC_	Alignment	not modelled	99.3	11	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
58	d1nfga2	Alignment	not modelled	99.2	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
59	c3itcA_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
60	d1gkra2	Alignment	not modelled	99.2	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
61	c3lu2B_	Alignment	not modelled	99.1	10	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
62	c2i5gB_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from pseudomonas aeruginosa
63	c2q01A_	Alignment	not modelled	99.1	12	PDB header: isomerase Chain: A: PDB Molecule: uronate isomerase; PDBTitle: crystal structure of glucuronate isomerase from caulobacter crescentus
64	d1k1da2	Alignment	not modelled	99.1	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
65	c5ns5A_	Alignment	not modelled	99.1	18	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase glij; PDBTitle: cys-gly dipeptidase glij in complex with cu2+ and zn2+
66	d1ynya2	Alignment	not modelled	99.1	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
67	c3b40A_	Alignment	not modelled	99.1	19	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from pseudomonas2 aeruginosa
68	c2ragB_	Alignment	not modelled	99.0	21	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus
69	c3msrA_	Alignment	not modelled	99.0	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
70	c3fdgA_	Alignment	not modelled	99.0	18	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
71	d1kcx2	Alignment	not modelled	98.9	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
72	d1gkpa2	Alignment	not modelled	98.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
73	c2vunC_	Alignment	not modelled	98.9	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
74	d2ftwa2	Alignment	not modelled	98.8	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
75	c1xrfA_	Alignment	not modelled	98.8	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
76	c3nqbB_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
77	d2fvka2	Alignment	not modelled	98.5	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
78	d2paja2	Alignment	not modelled	98.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
79	d1p1ma2	Alignment	not modelled	98.4	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
80	c3e0lB_	Alignment	not modelled	98.4	13	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase

81	d2uz9a2	Alignment	not modelled	98.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
82	d2imra2	Alignment	not modelled	98.2	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
83	c4v1xA	Alignment	not modelled	98.2	12	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
84	c2pajA	Alignment	not modelled	98.2	15	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
85	d3be7a2	Alignment	not modelled	98.1	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
86	c4dzhA	Alignment	not modelled	98.1	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
87	d2i9ua2	Alignment	not modelled	98.1	9	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
88	c1nfgA	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
89	c2ogjC	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
90	c4dykB	Alignment	not modelled	98.0	11	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from pseudomonas2 aeruginosa pao1 (target nysgrc-200449) with bound zn
91	c5e5cC	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: C: PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
92	c1gkpD	Alignment	not modelled	98.0	15	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
93	c2bb0A	Alignment	not modelled	98.0	13	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
94	c6ohaA	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: probable guanine deaminase; PDBTitle: yeast guanine deaminase
95	c1k1dF	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
96	d1onwa2	Alignment	not modelled	97.9	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
97	d2icsa2	Alignment	not modelled	97.9	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
98	c2ogjB	Alignment	not modelled	97.9	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
99	d2qs8a2	Alignment	not modelled	97.9	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
100	c6nboA	Alignment	not modelled	97.9	9	PDB header: hydrolase Chain: A: PDB Molecule: n-isopropylammelide isopropylaminohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase from2 burkholderia multivorans atcc 17616
101	c2ftwA	Alignment	not modelled	97.8	20	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
102	c3lsbA	Alignment	not modelled	97.8	14	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
103	d2puza2	Alignment	not modelled	97.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
104	c1p1mA	Alignment	not modelled	97.7	11	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
105	d2ooda2	Alignment	not modelled	97.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
106	d2qeec1	Alignment	not modelled	97.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like
						Fold: TIM beta/alpha-barrel

107	d2bb0a2	Alignment	not modelled	97.7	13	Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
108	d2r8ca2	Alignment	not modelled	97.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
109	c2q09A_	Alignment	not modelled	97.6	14	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
110	c3dc8B_	Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium melliloti
111	d2q09a2	Alignment	not modelled	97.6	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
112	d1un7a2	Alignment	not modelled	97.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
113	c2i9uA_	Alignment	not modelled	97.5	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
114	c3la4A_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
115	c2vr2A_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
116	c2qt3A_	Alignment	not modelled	97.4	8	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
117	c2gokA_	Alignment	not modelled	97.3	16	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
118	c2gseC_	Alignment	not modelled	97.3	18	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
119	d2p9ba2	Alignment	not modelled	97.3	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
120	c3gnhA_	Alignment	not modelled	97.3	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.