



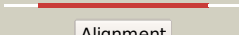

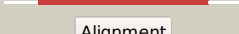



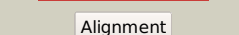

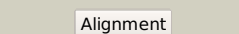











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0230c_(php)_274983_275963
Date	Tue Jul 23 14:50:29 BST 2019
Unique Job ID	69331799a21df281

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4if2A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase homology protein; PDBTitle: structure of the phosphotriesterase from mycobacterium tuberculosis
2	c3k2gA_	 Alignment		100.0	28	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
3	d1i0da_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
4	d2d2ja1	 Alignment		100.0	37	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
5	c2zc1A_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
6	c3tn6A_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
7	c3f4cA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
8	c3rhgA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
9	c3pnzD_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
10	c1pscA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
11	c4rdzA_	 Alignment		100.0	40	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group

12	c2vc7A_	Alignment		100.0	40	PDB header: hydrolase Chain: A; PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
13	d1bf6a_	Alignment		100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
14	c3msrA_	Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
15	c3e2vA_	Alignment		99.9	10	PDB header: hydrolase Chain: A; PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
16	c2xioA_	Alignment		99.9	10	PDB header: hydrolase Chain: A; PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
17	c3ipwA_	Alignment		99.9	11	PDB header: hydrolase Chain: A; PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
18	c2y1hA_	Alignment		99.9	14	PDB header: hydrolase Chain: A; PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
19	d1zzma1	Alignment		99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
20	d1xwya1	Alignment		99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
21	d1yixa1	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
22	d1nfga2	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
23	d1xrta2	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
24	c3rcmA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A; PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
25	d1k1da2	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
26	d1j6oa_	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
27	d1gkra2	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
28	c4i6kA_	Alignment	not modelled	99.8	16	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 PDB header: structural genomics, unknown function

29	c2gzxB_	Alignment	not modelled	99.8	12	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.
30	c4lfyB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
31	d1ynya2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
32	c4mupC_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure
33	d2paja2	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
34	c3gg7A_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
35	c3pnuA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
36	d2eg6a1	Alignment	not modelled	99.8	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
37	c3jzeC_	Alignment	not modelled	99.8	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
38	d2ffia1	Alignment	not modelled	99.8	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
39	c5vgmA_	Alignment	not modelled	99.8	12	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.
40	d2fvka2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
41	c4do7B_	Alignment	not modelled	99.8	8	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
42	c5v0gE_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: E: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase pyrc from yersinia pestis in2 complex with zinc and unknown ligand at 2.4 a resolution.
43	d1kcx2	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
44	c3irsB_	Alignment	not modelled	99.8	13	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
45	d2i9ua2	Alignment	not modelled	99.8	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
46	d1onwa2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
47	d3be7a2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
48	d2uz9a2	Alignment	not modelled	99.8	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
49	c2qahA_	Alignment	not modelled	99.7	15	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 paucimobilis
50	d2ftwa2	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
51	d2qs8a2	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
52	c2ogjC_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
53	c3guwB_	Alignment	not modelled	99.7	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
54	d1gkpa2	Alignment	not modelled	99.7	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain

55	d2r8ca2	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
56	d2icsa2	Alignment	not modelled	99.7	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
57	c2paiA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of 2 sargasso sea
58	c3cjpA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted amidohydrolase, dihydroorotase family; PDBTitle: crystal structure of an uncharacterized amidohydrolase cac3332 from 2 clostridium acetobutylicum
59	d2dvta1	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
60	d1p1ma2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
61	d2imra2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
62	d2ooda2	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
63	c2i9uA	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: cytosine/guanine deaminase related protein; PDBTitle: crystal structure of guanine deaminase from c. acetobutylicum with 2 bound guanine in the active site
64	c3e0lB	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
65	c5nnlB	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: inactive dihydroorotase-like domain; PDBTitle: inactive dihydroorotase-like domain of chaetomium thermophilum cad-2 like multifunctional protein
66	c1xrfA	Alignment	not modelled	99.6	19	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
67	c4c65A	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
68	c3gnhA	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: l-lysine, l-arginine carboxypeptidase cc2672; PDBTitle: crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from 2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine.
69	c3hpaB	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an 2 environmental sample of sargasso sea
70	d2p9ba2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
71	d2hbva1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
72	c4c6mA	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: cad protein; PDBTitle: crystal structure of the dihydroorotase domain of human cad2 bound to the inhibitor fluoro-orotate at ph 7.0
73	c3ij6A	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from 2 lactobacillus acidophilus
74	c4v1xA	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
75	c2wm1A	Alignment	not modelled	99.6	15	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 in 3 complex with 1,3-dihydroxyacetonephosphate suggests a 4 regulatory link between nad synthesis and glycolysis
76	c2vunC	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of amidase at 1.9 a resolution - a 2 new member of the amidohydrolase superfamily
77	c4wgxD	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
78	c5vn5A	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: 2,2',3-trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl meta- PDBTitle: crystal structure of lgy from sphingobium sp. strain syk-6
79	d2gwga1	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

						Family: PP1699/LP2961-like
80	d2bb0a2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
81	c1p1mA	Alignment	not modelled	99.6	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
82	c4hk6D	Alignment	not modelled	99.6	13	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
83	c2ogjB	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
84	c5xgxB	Alignment	not modelled	99.5	18	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
85	d2puza2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
86	c6dxbB	Alignment	not modelled	99.5	12	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
87	c4dykB	Alignment	not modelled	99.5	13	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
88	d2q09a2	Alignment	not modelled	99.5	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
89	c1nfgA	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
90	c4dzhA	Alignment	not modelled	99.5	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
91	c3dc8B	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium melliloti
92	d1ra0a2	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
93	c3lsbA	Alignment	not modelled	99.5	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
94	c2vr2A	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
95	c4l5pD	Alignment	not modelled	99.5	13	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
96	c3d6nA	Alignment	not modelled	99.5	16	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
97	c5e5cC	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: C: PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
98	c3mduA	Alignment	not modelled	99.5	15	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
99	c4whbC	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
100	c2fvmA	Alignment	not modelled	99.5	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
101	c4infA	Alignment	not modelled	99.5	13	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
102	d2f6ka1	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
103	c2q09A	Alignment	not modelled	99.5	15	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

104	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 protein olei01672_1_4652 from oleispira antarctica
105	d1o12a2	Alignment	not modelled	99.5	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
106	c2bb0A	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
107	c2ftwA	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
108	c1r9yA	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
109	c1gkpD	Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
110	c2gokA	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
111	c3be7B	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
112	c3nurA	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
113	d1un7a2	Alignment	not modelled	99.4	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
114	c2aqoB	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
115	c4f0lB	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from brucella melitensis
116	c1k1dF	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
117	c4b91B	Alignment	not modelled	99.4	10	PDB header: signaling protein Chain: B: PDB Molecule: dihydropyrimidinase-related protein 5; PDBTitle: crystal structure of truncated human crmp-5
118	d1m7ja3	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
119	c2gwnA	Alignment	not modelled	99.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
120	c2gseC	Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2