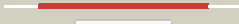



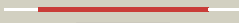




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1879 (-) _2129384_2130520
Date	Fri Aug 2 13:30:49 BST 2019
Unique Job ID	7a155cf1cf792f6a

Detailed template information

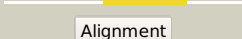
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j5sa_	 Alignment		100.0	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like
2	c2q01A_	 Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: uronate isomerase; PDBTitle: crystal structure of glucuronate isomerase from caulobacter crescentus
3	c3iacA_	 Alignment		100.0	16	PDB header: isomerase Chain: A: PDB Molecule: glucuronate isomerase; PDBTitle: 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
4	c4i6vA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase 2; PDBTitle: the crystal structure of an amidohydrolase 2 from planctomyces2 limnophilus dsm 3776
5	c2qpxA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: predicted metal-dependent hydrolase of the tim-barrel fold; PDBTitle: crystal structure of putative metal-dependent hydrolase (yp_805737.1)2 from lactobacillus casei atcc 334 at 1.40 a resolution
6	d2qeec1	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Uronate isomerase-like
7	c3irsB_	 Alignment		100.0	18	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
8	c2gzxB_	 Alignment		99.9	18	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.
9	c3cjpA_	 Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: predicted amidohydrolase, dihydroorotase family; PDBTitle: crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
10	c4l5pD_	 Alignment		99.9	16	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
11	d2ffia1	 Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like

12	c4hk6D	Alignment		99.9	14	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
13	c6omqA	Alignment		99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ptmu3; PDBTitle: crystal structure of ptmu3 complexed with ptm substrate
14	c2wm1A	Alignment		99.9	14	PDB header: lyase Chain: A: PDB Molecule: 2-amino-3-carboxymuconate-6-semialdehyde PDBTitle: the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis
15	c5vn5A	Alignment		99.9	15	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
16	c3ij6A	Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 lactobacillus acidophilus
17	d1j6oa	Alignment		99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
18	d1zzma1	Alignment		99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
19	d2gwga1	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
20	c4infA	Alignment		99.9	12	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
21	c4do7B	Alignment	not modelled	99.9	17	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
22	d2hbva1	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
23	c2y1hA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
24	c3rcmA	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
25	c2qahA	Alignment	not modelled	99.9	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
26	c3nurA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
27	c6dxsB	Alignment	not modelled	99.9	13	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
28	c4mupC	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure

29	d1xwya1	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
30	c4i6kA	Alignment	not modelled	99.9	13	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
31	c3gg7A	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
32	d2dvta1	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
33	d2f6ka1	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
34	c4dziD	Alignment	not modelled	99.8	15	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
35	d1yixa1	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
36	c4rdzA	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group
37	c3tn6A	Alignment	not modelled	99.6	10	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
38	c3guwB	Alignment	not modelled	99.6	13	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
39	d1bf6a	Alignment	not modelled	99.6	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
40	c2vc7A	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
41	c2xioA	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
42	c3f4cA	Alignment	not modelled	99.4	10	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
43	d1i0da	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
44	c3pnzD	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
45	c1pscA	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
46	c3ipwA	Alignment	not modelled	99.2	10	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
47	c4if2A	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase homology protein; PDBTitle: structure of the phosphotriesterase from mycobacterium tuberculosis
48	c3e2vA	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
49	c2zc1A	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
50	c3k2gA	Alignment	not modelled	99.0	20	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
51	c3rhgA	Alignment	not modelled	98.9	14	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
52	d2d2ja1	Alignment	not modelled	98.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
53	d1gkra2	Alignment	not modelled	98.1	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
54	d1xrta2	Alignment	not modelled	97.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

						Family: Hydantoinase (dihydropyrimidinase), catalytic domain
55	d1itua_	Alignment	not modelled	97.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase
56	c3pnuA_	Alignment	not modelled	97.7	18	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
57	c5ns5A_	Alignment	not modelled	97.6	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase glij; PDBTitle: cys-gly dipeptidase glij in complex with cu2+ and zn2+
58	c3ou8B_	Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: B: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
59	c3lu2B_	Alignment	not modelled	97.6	10	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
60	c3fdgA_	Alignment	not modelled	97.6	17	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
61	d2bb0a2	Alignment	not modelled	97.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
62	c2i5gB_	Alignment	not modelled	97.2	16	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas aeruginosa
63	c2ragB_	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus
64	c3itcA_	Alignment	not modelled	97.1	15	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
65	c3b40A_	Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from pseudomonas2 aeruginosa
66	d1k1da2	Alignment	not modelled	97.0	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
67	c4lfyB_	Alignment	not modelled	97.0	21	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
68	c3msrA_	Alignment	not modelled	96.8	16	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
69	d1nfga2	Alignment	not modelled	96.7	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
70	d2amxa1	Alignment	not modelled	96.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
71	c5v0gE_	Alignment	not modelled	96.4	15	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.
72	d2puza2	Alignment	not modelled	96.3	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
73	d2fvka2	Alignment	not modelled	96.2	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
74	d1ynya2	Alignment	not modelled	96.1	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
75	c3ou8A_	Alignment	not modelled	96.1	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
76	d2eg6a1	Alignment	not modelled	96.0	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
77	c1vliA_	Alignment	not modelled	95.6	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
78	d3be7a2	Alignment	not modelled	95.6	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
79	c2vunC_	Alignment	not modelled	95.4	15	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
						Fold: TIM beta/alpha-barrel

80	d1ra0a2	Alignment	not modelled	95.4	14	Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
81	d1vla2	Alignment	not modelled	95.4	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
82	c5vgmA	Alignment	not modelled	95.3	15	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.
83	d2qs8a2	Alignment	not modelled	95.3	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
84	c1xuzA	Alignment	not modelled	95.0	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siac; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminol
85	c3zeC	Alignment	not modelled	94.9	14	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
86	c3g8rA	Alignment	not modelled	94.7	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
87	c6ii7A	Alignment	not modelled	94.7	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase; PDBTitle: crystal structure of plasmodium falciparum adenosine deaminase2 c27q+l227i mutant co-complexed with zn ion, hypoxanthine and inosine
88	d1p1ma2	Alignment	not modelled	94.4	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
89	d2zdra2	Alignment	not modelled	93.4	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
90	c4v1xA	Alignment	not modelled	93.3	13	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
91	c3lsbA	Alignment	not modelled	93.0	15	PDB header: hydrolase Chain: A: PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aurescens tc1 complexed with zinc and ametrin
92	c3nqbB	Alignment	not modelled	92.4	22	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
93	d2uz9a2	Alignment	not modelled	91.8	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
94	c3e0lB	Alignment	not modelled	89.7	15	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
95	d1kcx2	Alignment	not modelled	89.2	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
96	d2r8ca2	Alignment	not modelled	88.4	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
97	c2bb0A	Alignment	not modelled	88.3	15	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
98	d1o66a	Alignment	not modelled	86.1	12	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
99	c4dykB	Alignment	not modelled	83.8	15	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
100	d2ftwa2	Alignment	not modelled	82.2	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
101	c3hpaB	Alignment	not modelled	81.2	15	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
102	d2paja2	Alignment	not modelled	81.1	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
103	c2pajA	Alignment	not modelled	80.7	12	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
104	d1o12a2	Alignment	not modelled	80.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain

105	c6ncsB_	 Alignment	not modelled	79.5	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminic acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
106	d1onwa2	 Alignment	not modelled	78.7	24	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
107	d1gkpa2	 Alignment	not modelled	78.3	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
108	d2i9ua2	 Alignment	not modelled	77.2	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
109	c3ighX_	 Alignment	not modelled	76.9	15	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 pyrococcus horikoshii ot3
110	c4dzhA_	 Alignment	not modelled	75.3	17	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase nis_0429 (target xanthomonas2 campestris (target nysgrc-200456) with bound zn
111	d2q09a2	 Alignment	not modelled	73.1	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
112	c3v7pA_	 Alignment	not modelled	71.8	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
113	d2icsa2	 Alignment	not modelled	69.2	6	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
114	c3sz8D_	 Alignment	not modelled	67.8	14	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
115	c2gokA_	 Alignment	not modelled	67.5	13	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
116	d1m7ja3	 Alignment	not modelled	66.1	22	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
117	c2ogjB_	 Alignment	not modelled	66.0	21	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
118	c4f0rA_	 Alignment	not modelled	65.7	13	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)
119	c2q09A_	 Alignment	not modelled	64.2	12	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
120	c1p1mA_	 Alignment	not modelled	63.7	14	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