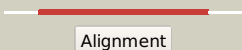

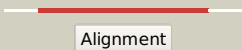

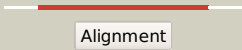







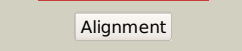

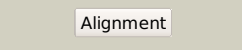



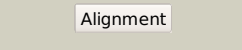
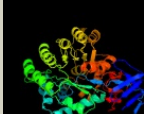
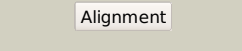



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0552 (-) _642892_644496
Date	Fri Jul 26 01:50:10 BST 2019
Unique Job ID	24527c1b4dd1b397

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ighX_	 Alignment		100.0	22	PDB header: hydrolase Chain: X; PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 pyrococcus horikoshii ot3
2	c3etkA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
3	c4v1xA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
4	c4dzhA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
5	c4dykB_	 Alignment		100.0	22	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
6	c3lsbA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureusens tc1 complexed with zinc and ametrin
7	c2bb0A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
8	c4c65A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
9	c2i9uA_	 Alignment		100.0	16	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
10	c2gokA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
11	c4f0rA_	 Alignment		100.0	17	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)

12	c3lnpA_	Alignment		100.0	18	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
13	c4wgxD_	Alignment		100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
14	c2oodA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
15	c3hpaB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
16	c3e0lB_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
17	c2pajA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
18	c3feqB_	Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
19	c1plmA_	Alignment		100.0	18	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
20	c3gnhA_	Alignment		100.0	20	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.
21	c2q09A_	Alignment	not modelled	100.0	17	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
22	c3be7B_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
23	c2r8cB_	Alignment	not modelled	100.0	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
24	c3dc8B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
25	c4whbC_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
26	c2qs8A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of a xaa-pro dipeptidase with bound methionine in2 the active site
27	c2gseC_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
28	c2ftwA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
						PDB header: hydrolase

29	c5e5cC_	Alignment	not modelled	100.0	16	Chain: C; PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
30	c1gkpD_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D; PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
31	c3v7pA_	Alignment	not modelled	100.0	17	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
32	c4b91B_	Alignment	not modelled	100.0	13	PDB header: signaling protein Chain: B; PDB Molecule: dihydropyrimidinase-related protein 5; PDBTitle: crystal structure of truncated human crmp-5
33	c3hm7A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
34	c1gkrA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
35	c1nfgA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
36	c3ooqC_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C; PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
37	c2vr2A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
38	c3gjpB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: n-acyl-d-glutamate deacylase; PDBTitle: crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.
39	c4f0lB_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from brucella melitensis
40	c1k1dF_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: F; PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
41	c2qt3A_	Alignment	not modelled	100.0	16	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
42	c1r9yA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
43	c4jnrE_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: E; PDB Molecule: putative cytosine deaminase and related metal-dependent PDBTitle: crystal structure of 5-methylcytosine deaminase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 liganded with 5-fluorocytosine
44	c2fvmA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from saccharomyces kluveri2 in complex with the reaction product n-carbamyl-beta-alanine
45	c2p9bA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
46	c1rjqA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
47	c2gwnA_	Alignment	not modelled	100.0	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
48	c1xrfA_	Alignment	not modelled	100.0	18	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
49	c3d6nA_	Alignment	not modelled	100.0	16	PDB header: hydrolase/transferase Chain: A; PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
50	c2z00A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
51	c6nboA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: n-isopropylammelide isopropylaminohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase from2 burkholderia multivorans atcc 17616
52	c3la4A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
53	c2ubpC_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C; PDB Molecule: protein (urease alpha subunit);

						PDBTitle: structure of native urease from bacillus pasteurii
54	c3mduA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: n-formimino-l-glutamate iminohydrolase; PDBTitle: the structure of n-formimino-l-glutamate iminohydrolase from 2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
55	c3mpgB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
56	c3griB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
57	c2vunC_	Alignment	not modelled	100.0	19	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
58	c3e74D_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at the metal2 center
59	c1e9yB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with 2 acetohydroxamic acid
60	c3nqbB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
61	c1fwcC_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5
62	c5t5mA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwda; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from 2 methanothermobacter wolfeii, trigonal form at 2.5 a.
63	c2vhlB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: the three-dimensional structure of the n-acetylglucosamine-2 6-phosphate deacetylase from bacillus subtilis
64	c2aaqB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
65	c4z42L_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: L: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of urease from yersinia enterocolitica
66	c5xgxB_	Alignment	not modelled	100.0	19	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
67	c2p50C_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
68	c2icsA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
69	c3egjA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
70	c2imrA_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from 2 deinococcus radiodurans
71	c1o12B_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: crystal structure of n-acetylglucosamine-6-phosphate deacetylase2 (tm0814) from thermotoga maritima at 2.5 a resolution
72	c2ogjB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
73	c6fv3D_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 from mycobacterium smegmatis.
74	d2uz9a2	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
75	c4c6mA_	Alignment	not modelled	99.9	13	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
76	c2ogjC_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
77	d2i9ua2	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

						Family: SAH/MTA deaminase-like
78	c5nnbB_	Alignment	not modelled	99.8	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
79	d2ooda2	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
80	d1ra0a2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
81	d2r8ca2	Alignment	not modelled	99.8	23	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
82	d2bb0a2	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
83	d3be7a2	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
84	c3msrA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
85	d2paja2	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
86	c3pnuA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
87	d2qs8a2	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
88	d2q09a2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
89	d2puza2	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
90	d1p1ma2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
91	d2imra2	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
92	c3ggmB_	Alignment	not modelled	99.7	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bt9727_2919; PDBTitle: crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
93	d1gkpa2	Alignment	not modelled	99.7	20	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
94	d1ejxc1	Alignment	not modelled	99.7	25	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
95	d1kcx2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
96	d2p9ba2	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
97	d1gkra2	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
98	d1k1da2	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
99	d1i0da_	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
100	d2ftwa2	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
101	d4ubpc2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
102	d1nfga2	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
103	d1e9yb1	Alignment	not modelled	99.6	13	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
104	c4fyB_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315

105	d1ynya2	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
106	d1onwa1	Alignment	not modelled	99.6	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: !soaspartyl dipeptidase
107	d2eg6a1	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
108	d2fvka2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
109	d2fvka1	Alignment	not modelled	99.6	21	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
110	d2p9ba1	Alignment	not modelled	99.6	24	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: !imidazolonepropionase-like
111	c3jzeC_	Alignment	not modelled	99.5	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
112	d1xrta2	Alignment	not modelled	99.5	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
113	d1yrra1	Alignment	not modelled	99.5	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
114	d2d2ja1	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
115	d2r8ca1	Alignment	not modelled	99.5	30	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
116	c5v0gE_	Alignment	not modelled	99.5	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.
117	c5vgmA_	Alignment	not modelled	99.4	18	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.
118	c1pscA_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
119	d1k1da1	Alignment	not modelled	99.3	25	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
120	c4rdzA_	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group