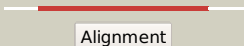



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0074 (-)_82745_83980
Date	Tue Jul 23 14:50:10 BST 2019
Unique Job ID	2468bc2376324c26

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wgxD_	 Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
2	c3be7B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
3	c3gnhA_	 Alignment		100.0	29	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.
4	c4c65A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
5	c4whbC_	 Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
6	c2qs8A_	 Alignment		100.0	28	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
7	c2r8cB_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
8	c3feqB_	 Alignment		100.0	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
9	c4v1xA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
10	c2p9bA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
11	c4dykB_	 Alignment		100.0	20	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

12	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
13	c4dzhA_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
14	c3hpaB_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
15	c3lsbA_	Alignment		100.0	17	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
16	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
17	c2q09A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxoimidazolidin-4-yl)-propionic acid
18	c3nqbB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
19	c2gokA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
20	c2bb0A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
21	c4f0rA_	Alignment	not modelled	100.0	20	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)
22	c1p1mA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tm0936; PDBTitle: structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine
23	c3e0lB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
24	c5e5cC_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
25	c1r9yA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
26	c3gipB_	Alignment	not modelled	100.0	21	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.
27	c2fvmA_	Alignment	not modelled	100.0	15	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
						PDB header: signaling protein

28	c4b91B_	Alignment	not modelled	100.0	18	Chain: B; PDB Molecule: dihydropyrimidinase-related protein 5; PDBTitle: crystal structure of truncated human crmp-5
29	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
30	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
31	c3dc8B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium melliloti
32	c6nboA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: n-isopropylammelide isopropylaminohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase from2 burkholderia multivorans atcc 17616
33	c2qt3A_	Alignment	not modelled	100.0	15	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
34	c1nfgA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
35	c2ftwA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
36	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 aureus
37	c2gseC_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C; PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinase-like 2
38	c1xrfA_	Alignment	not modelled	100.0	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
39	c1gkpD_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D; PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221
40	c2vr2A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
41	c2i9uA_	Alignment	not modelled	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
42	c1k1dF_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: F; PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
43	c2aqoB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B; PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
44	c2gwnA_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
45	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
46	c2ubpC_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C; PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
47	c5xgxB_	Alignment	not modelled	100.0	16	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
48	c2vunC_	Alignment	not modelled	100.0	20	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
49	c4f0lB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from brucella melitensis
50	c3ooqC_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C; PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
51	c3hm7A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
						PDB header: hydrolase Chain: C; PDB Molecule: n-acetylglucosamine-6-phosphate

52	c2p50C_	Alignment	not modelled	100.0	21	deacetylase; PDBTitle: crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
53	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 with2 acetohydroxamic acid
54	c3v7pA_	Alignment	not modelled	100.0	15	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
55	c2oodA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
56	c1fwcC_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5
57	c3e74D_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at the metal2 center
58	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)
59	c2vhlB_	Alignment	not modelled	100.0	17	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
60	c2z00A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
61	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
62	c5t5mA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdA; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, trigonal form at 2.5 a.
63	c3mpgB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
64	c3mduA_	Alignment	not modelled	100.0	18	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
65	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
66	c3egiA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
67	c3etkA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
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	c3ighX_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 pyrococcus horikoshii ot3
70	c6fv3D_	Alignment	not modelled	100.0	19	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.
71	c2ogjB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
72	c1o12B_	Alignment	not modelled	100.0	15	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
73	c2imrA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
74	d2qs8a2	Alignment	not modelled	99.9	29	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
75	c2ogjC_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
						PDB header: oxidoreductase

76	c5nnlB_	Alignment	not modelled	99.9	15	Chain: B: PDB Molecule: inactive dihydroorotase-like domain; PDBTitle: inactive dihydroorotase-like domain of chaetomium thermophilum cad-2 like multifunctional protein
77	c4c6mA_	Alignment	not modelled	99.9	18	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
78	d3be7a2	Alignment	not modelled	99.9	30	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
79	d2r8ca2	Alignment	not modelled	99.9	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
80	c3msrA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
81	d2uz9a2	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
82	d2p9ba2	Alignment	not modelled	99.9	29	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
83	d2paja2	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
84	d1ra0a2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
85	d2ooda2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
86	d2i9ua2	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
87	d2imra2	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
88	d2puza2	Alignment	not modelled	99.8	23	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
89	d2q09a2	Alignment	not modelled	99.7	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
90	d2bb0a2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
91	d4ubpc2	Alignment	not modelled	99.7	20	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
92	d1p1ma2	Alignment	not modelled	99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
93	c3pnuA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
94	d1i0da_	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
95	d1kcxa2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
96	d1gkpa2	Alignment	not modelled	99.7	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
97	d1e9yb1	Alignment	not modelled	99.6	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
98	d1onwa2	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
99	d2ftwa2	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
100	d2d2ja1	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Phosphotriesterase-like
101	c4lfyB_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
102	d2eg6a1	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
103	d1ynya2	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

						Family: Hydantoinase (dihydropyrimidinase), catalytic domain
104	c1pscA_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: phosphotriesterase from pseudomonas diminuta
105	d1ejxc1	Alignment	not modelled	99.6	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
106	c3jzeC_	Alignment	not modelled	99.6	13	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
107	c2zc1A_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: organophosphorus hydrolase from deinococcus radiodurans
108	d1k1da2	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
109	d2icsa2	Alignment	not modelled	99.5	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
110	c4rdzA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group
111	d1un7a2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
112	c5v0gE_	Alignment	not modelled	99.5	12	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.
113	c3ggmB_	Alignment	not modelled	99.5	23	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
114	d2fvka1	Alignment	not modelled	99.5	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
115	d1xrta2	Alignment	not modelled	99.5	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
116	d1yrra2	Alignment	not modelled	99.5	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
117	c5vgmA_	Alignment	not modelled	99.5	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.
118	d1gkra2	Alignment	not modelled	99.5	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
119	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
120	c3f4cA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound