











Phyre2

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Description	RVBD2913c_(-)_3219873_3221708
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Unique Job ID	c6b43eca0d4d1803

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gipB_	 Alignment		100.0	27	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.
2	c1rjqA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
3	c2fvmA_	 Alignment		100.0	17	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
4	c4b91B_	 Alignment		100.0	15	PDB header: signaling protein Chain: B: PDB Molecule: dihydropyrimidinase-related protein 5; PDBTitle: crystal structure of truncated human crmp-5
5	c5e5cC_	 Alignment		100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
6	c1gkrA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
7	c2ftwA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
8	c2gseC_	 Alignment		100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
9	c1k1dF_	 Alignment		100.0	19	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
10	c2vr2A_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
11	c1nfgA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase

12	c3dc8B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
13	c1gkpD_	Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
14	c4v1xA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
15	c3hm7A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
16	c3e74D_	Alignment		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
17	c3hpaB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 environmental sample of sargasso sea
18	c1p1mA_	Alignment		100.0	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
19	c4dykB_	Alignment		100.0	18	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
20	c3d6nA_	Alignment		100.0	19	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
21	c3lnpA_	Alignment	not modelled	100.0	14	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
22	c4dzhA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
23	c3lsbA_	Alignment	not modelled	100.0	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
24	c2pajA_	Alignment	not modelled	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
25	c4f0rA_	Alignment	not modelled	100.0	15	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)
26	c2gwnA_	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
27	c5t5mA_	Alignment	not modelled	100.0	12	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.
28	c2z00A_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
29	c3mpgB_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
30	c1xrfA_	Alignment	not modelled	100.0	21 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
31	c3la4A_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
32	c2ubpC_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
33	c1fwcC_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5
34	c6nboA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A: PDB Molecule: n-isopropylammelide isopropylaminohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase from2 burkholderia multivorans atcc 17616
35	c1e9yB_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
36	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
37	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
38	c2p9bA_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
39	c4wgxD_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
40	c6ohaA_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: probable guanine deaminase; PDBTitle: yeast guanine deaminase
41	c2i9uA_	Alignment	not modelled	100.0	15 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	c4z42L_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: L: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of urease from yersinia enterocolitica
43	c2bb0A_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
44	c4f0lB_	Alignment	not modelled	100.0	12 PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from brucella melitensis
45	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
46	c3be7B_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
47	c4whbC_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
48	c2aqqB_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
49	c4c65A_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
50	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)
51	c3gnhA_	Alignment	not modelled	100.0	15 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.
52	c3v7pA_	Alignment	not modelled	100.0	13 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
53	c2qs8A_	Alignment	not modelled	100.0	14 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
54	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
55	c2r8cB_	Alignment	not modelled	100.0	19 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
56	c3feqB_	Alignment	not modelled	100.0	18 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
57	c4jnrE_	Alignment	not modelled	100.0	15 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
58	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
59	c3e0lB_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
60	c1r9yA_	Alignment	not modelled	100.0	12 PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
61	c3mduA_	Alignment	not modelled	100.0	16 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
62	c2vhlB_	Alignment	not modelled	100.0	16 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
63	c2gokA_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
64	c2icsA_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
65	c3ooqC_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
66	c3ighX_	Alignment	not modelled	100.0	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
67	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
68	c3etkA_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
69	c6ohcB_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: e. coli guanine deaminase
70	c2p50C_	Alignment	not modelled	100.0	15 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
71	c6fv3D_	Alignment	not modelled	100.0	18 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.
72	c3egiA_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
73	c2ogjB_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
74	c1o12B_	Alignment	not modelled	100.0	19 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
75	c2imrA_	Alignment	not modelled	99.9	13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2

						deinococcus radiodurans
76	c4c6mA	Alignment	not modelled	99.9	15	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
77	c5nnbB	Alignment	not modelled	99.9	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
78	d1m7ja3	Alignment	not modelled	99.9	23	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
79	c2ogjC	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
80	c3ggmB	Alignment	not modelled	99.7	24	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
81	d1k1da1	Alignment	not modelled	99.7	41	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
82	d1e9yb1	Alignment	not modelled	99.7	19	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
83	d1ejxc1	Alignment	not modelled	99.6	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
84	d4ubpc2	Alignment	not modelled	99.6	21	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
85	d1kcxal	Alignment	not modelled	99.6	28	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
86	d1gkpa1	Alignment	not modelled	99.6	43	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
87	d1ynya1	Alignment	not modelled	99.6	38	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
88	d2fvka1	Alignment	not modelled	99.6	27	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
89	d2fvka2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
90	d1onwa1	Alignment	not modelled	99.5	13	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Isospartyl dipeptidase
91	d2p9ba1	Alignment	not modelled	99.5	13	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
92	d1nfga1	Alignment	not modelled	99.5	14	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
93	c3pnuA	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
94	d2paja1	Alignment	not modelled	99.4	14	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
95	c3msrA	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
96	c4fyB	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
97	d1gkpa2	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
98	d1ynya2	Alignment	not modelled	99.4	18	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
99	d2r8ca1	Alignment	not modelled	99.4	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
100	d1yrra1	Alignment	not modelled	99.4	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
101	c3jzeC	Alignment	not modelled	99.4	15	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
102	d2eg6a1	Alignment	not modelled	99.4	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases

				Family:Dihydroorotase	
103	d1gkra1	Alignment	not modelled	99.4	18 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
104	d1ra0a2	Alignment	not modelled	99.4	11 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
105	d1gkra2	Alignment	not modelled	99.3	20 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
106	d1kcxa2	Alignment	not modelled	99.3	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
107	c5v0gE_	Alignment	not modelled	99.3	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.
108	d2uz9a2	Alignment	not modelled	99.3	16 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
109	d2ftwa2	Alignment	not modelled	99.3	21 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
110	c5vgmA_	Alignment	not modelled	99.3	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.
111	d1p1ma1	Alignment	not modelled	99.3	16 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
112	d1nfga2	Alignment	not modelled	99.3	17 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
113	d1k1da2	Alignment	not modelled	99.3	14 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
114	d1m7ja1	Alignment	not modelled	99.2	30 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
115	d1m7ja2	Alignment	not modelled	99.2	31 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
116	d2i9ua2	Alignment	not modelled	99.2	12 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
117	d1xrta2	Alignment	not modelled	99.2	20 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
118	d2paja2	Alignment	not modelled	99.1	23 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
119	d2p9ba2	Alignment	not modelled	99.1	20 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
120	d2ftwa1	Alignment	not modelled	99.1	16 Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)