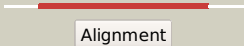

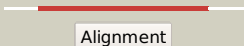

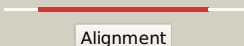







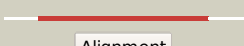











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1381_(pyrC)_1554194_1555486
Date	Wed Jul 31 22:05:48 BST 2019
Unique Job ID	718c720ea5a7f54b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5e5cC_</a>			100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> d-hydantoinase/dihydropyrimidinase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
2	<a href="#">c1gkrA_</a>			100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-atp dependent l-selective hydantoinase; <b>PDBTitle:</b> l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aureus
3	<a href="#">c4b91B_</a>			100.0	22	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropyrimidinase-related protein 5; <b>PDBTitle:</b> crystal structure of truncated human crmp-5
4	<a href="#">c2ftwA_</a>			100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropyrimidine amidohydrolase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from dictyostelium discoideum
5	<a href="#">c1gkpD_</a>			100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> hydantoinase; <b>PDBTitle:</b> d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
6	<a href="#">c3dc8B_</a>			100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from sinorhizobium meliloti
7	<a href="#">c2gseC_</a>			100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydropyrimidinase-related protein 2; <b>PDBTitle:</b> crystal structure of human dihydropyrimidinease-like 2
8	<a href="#">c1k1dF_</a>			100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> d-hydantoinase; <b>PDBTitle:</b> crystal structure of d-hydantoinase
9	<a href="#">c1nfgA_</a>			100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-hydantoinase; <b>PDBTitle:</b> structure of d-hydantoinase
10	<a href="#">c3hm7A_</a>			100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> allantoinase; <b>PDBTitle:</b> crystal structure of allantoinase from bacillus halodurans c-125
11	<a href="#">c3mpgB_</a>			100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> dihydroorotase from bacillus anthracis

12	<a href="#">c2vr2A_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> human dihydropyrimidinase
13	<a href="#">c3griB_</a>	Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the crystal structure of a dihydroorotase from staphylococcus aureus
14	<a href="#">c3d6nA_</a>	Alignment		100.0	39	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
15	<a href="#">c2fvmA_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropyrimidinase; <b>PDBTitle:</b> crystal structure of dihydropyrimidinase from saccharomyces kluuyveri2 in complex with the reaction product n-carbamyl-beta-alanine
16	<a href="#">c2z00A_</a>	Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase from thermus thermophilus
17	<a href="#">c3e74D_</a>	Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> allantoinase; <b>PDBTitle:</b> crystal structure of e. coli allantoinase with iron ions at the metal2 center
18	<a href="#">c2gwnA_</a>	Alignment		100.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the structure of putative dihydroorotase from porphyromonas2 gingivalis.
19	<a href="#">c1xrfA_</a>	Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution
20	<a href="#">c4v1xA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atrazine chlorohydrolase; <b>PDBTitle:</b> the structure of the hexameric atrazine chlorohydrolase, atza
21	<a href="#">c4wgxD_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> molinate hydrolase; <b>PDBTitle:</b> crystal structure of molinate hydrolase
22	<a href="#">c3lsbA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> triazine hydrolase; <b>PDBTitle:</b> crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureuscsens tc1 complexed with zinc and ametrin
23	<a href="#">c2pajA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytosine/guanine deaminase; <b>PDBTitle:</b> crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
24	<a href="#">c4dykB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an adenosine deaminase from pseudomonas2 aeruginosa pao1 (target nysgrc-200449) with bound zn
25	<a href="#">c3lnpA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase family protein olei01672_1_465; <b>PDBTitle:</b> crystal structure of amidohydrolase family protein olei01672_1_4652 from oleispira antarctica
26	<a href="#">c3hpaB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
27	<a href="#">c5xgxB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> isoaspartyl dipeptidase; <b>PDBTitle:</b> crystal structure of colwellia psychrerythraea strain 34h isoaspartyl2 dipeptidase e80q mutant complexed with beta-isoaspartyl lysine
						<b>PDB header:</b> hydrolase

28	<a href="#">c2qt3A</a>	Alignment	not modelled	100.0	15	<b>Chain:</b> A; <b>PDB Molecule:</b> n-isopropylammelide isopropyl amidohydrolase; <b>PDBTitle:</b> crystal structure of n-isopropylammelide isopropylaminohydrolase atz2 from pseudomonas sp. strain adp complexed with zn
29	<a href="#">c4dzhA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
30	<a href="#">c1p1mA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein tm0936; <b>PDBTitle:</b> structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine
31	<a href="#">c4whbC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> phenylurea hydrolase b; <b>PDBTitle:</b> crystal structure of phenylurea hydrolase b
32	<a href="#">c6nboA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-isopropylammelide isopropylaminohydrolase; <b>PDBTitle:</b> crystal structure of n-isopropylammelide isopropylaminohydrolase from2 burkholderia multivorans atcc 17616
33	<a href="#">c2aqaB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> isoaspartyl dipeptidase; <b>PDBTitle:</b> crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
34	<a href="#">c4f0rA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-methylthioadenosine/s-adenosylhomocysteine deaminase; <b>PDBTitle:</b> crystal structure of an adenosine deaminase homolog from2 chromobacterium violaceum (target nysgrc-019589) bound zn and 5'-3 methylthioadenosine (unproductive complex)
35	<a href="#">c3nqbB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> adenine deaminase 2; <b>PDBTitle:</b> crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
36	<a href="#">c4c65A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ochratoxinase; <b>PDBTitle:</b> crystal structure of a. niger ochratoxinase
37	<a href="#">c2r8cB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative amidohydrolase; <b>PDBTitle:</b> crystal structure of uncharacterized protein eaj56179
38	<a href="#">c2bb0A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> structure of imidazolonepropionase from bacillus subtilis
39	<a href="#">c3qipB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> n-acyl-d-glutamate deacylase; <b>PDBTitle:</b> crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.
40	<a href="#">c3gnhA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> l-lysine, l-arginine carboxypeptidase cc2672; <b>PDBTitle:</b> crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine.
41	<a href="#">c6ohaA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable guanine deaminase; <b>PDBTitle:</b> yeast guanine deaminase
42	<a href="#">c2gokA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution
43	<a href="#">c2q09A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> imidazolonepropionase; <b>PDBTitle:</b> crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxo-imidazolidin-4-yl)-propionic acid
44	<a href="#">c1rjqA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> d-aminoacylase; <b>PDBTitle:</b> the crystal structure of the d-aminoacylase mutant d366a
45	<a href="#">c2vhlB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> the three-dimensional structure of the n-acetylglucosamine-2 6-phosphate deacetylase from bacillus subtilis
46	<a href="#">c5t5mA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdA; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, trigonal form at 2.5 a.
47	<a href="#">c2vunC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> enamidase; <b>PDBTitle:</b> the crystal structure of enamidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
48	<a href="#">c2p9bA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> possible prolidase; <b>PDBTitle:</b> crystal structure of putative prolidase from2 bifidobacterium longum
49	<a href="#">c4jnrE</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> putative cytosine deaminase and related metal-dependent <b>PDBTitle:</b> crystal structure of 5-methylcytosine deaminase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 liganded with 5-fluorocytosine
50	<a href="#">c3e0lB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> guanine deaminase; <b>PDBTitle:</b> computationally designed ammeline deaminase
						<b>PDB header:</b> hydrolase

51	<a href="#">c3be7B_</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> B; <b>PDB Molecule:</b> zn-dependent arginine carboxypeptidase; <b>PDBTitle:</b> crystal structure of zn-dependent arginine carboxypeptidase
52	<a href="#">c3feqB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative amidohydrolase; <b>PDBTitle:</b> crystal structure of uncharacterized protein eah89906
53	<a href="#">c3la4A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> urease; <b>PDBTitle:</b> crystal structure of the first plant urease from jack bean ( <i>canavalia2 ensiformis</i> )
54	<a href="#">c2p50C_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn
55	<a href="#">c2i9uA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cytosine/guanine deaminase related protein; <b>PDBTitle:</b> crystal structure of guanine deaminase from <i>c. acetobutylicum</i> with2 bound guanine in the active site
56	<a href="#">c1r9yA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cytosine deaminase; <b>PDBTitle:</b> bacterial cytosine deaminase d314a mutant.
57	<a href="#">c2qs8A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of a xaa-pro dipeptidase with bound methionine in2 the active site
58	<a href="#">c2ubpC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> protein (urease alpha subunit); <b>PDBTitle:</b> structure of native urease from bacillus pasteurii
59	<a href="#">c3ooqC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase from thermotoga maritima msb8
60	<a href="#">c6ohcB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> guanine deaminase; <b>PDBTitle:</b> e. coli guanine deaminase
61	<a href="#">c1e9yB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> urease subunit beta; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
62	<a href="#">c2oodA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> blr3880 protein; <b>PDBTitle:</b> crystal structure of guanine deaminase from bradyrhizobium japonicum
63	<a href="#">c3v7pA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> amidohydrolase family protein; <b>PDBTitle:</b> crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2
64	<a href="#">c1fwcC_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> urease; <b>PDBTitle:</b> klebsiella aerogenes urease, c319a variant at ph 8.5
65	<a href="#">c4f0lB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase from brucella melitensis
66	<a href="#">c3egjA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
67	<a href="#">c4z42L_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> L; <b>PDB Molecule:</b> urease subunit alpha; <b>PDBTitle:</b> crystal structure of urease from yersinia enterocolitica
68	<a href="#">c2icsA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> adenine deaminase; <b>PDBTitle:</b> crystal structure of an adenine deaminase
69	<a href="#">c4c6mA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cad protein; <b>PDBTitle:</b> crystal structure of the dihydroorotase domain of human cad2 bound to the inhibitor fluoroorotate at ph 7.0
70	<a href="#">c3mduA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-formimino-l-glutamate iminohydrolase; <b>PDBTitle:</b> the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate
71	<a href="#">c6fv3D_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 from mycobacterium smegmatis.
72	<a href="#">c1o12B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-6-phosphate deacetylase2 (tm0814) from thermotoga maritima at 2.5 a resolution
73	<a href="#">c5nnlB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> inactive dihydroorotase-like domain; <b>PDBTitle:</b> inactive dihydroorotase-like domain of chaetomium thermophilum cad-2 like multifunctional protein
74	<a href="#">c2ogjB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of a dihydroorotase
75	<a href="#">c3ighX_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> X; <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase;

						<b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent hydrolase from2 pyrococcus horikoshii ot3
76	<a href="#">c3etkA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus
77	<a href="#">d1k1da2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
78	<a href="#">c3pnuA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
79	<a href="#">c4fybB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
80	<a href="#">d1gkra2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
81	<a href="#">d1nfga2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
82	<a href="#">d1gkpa2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
83	<a href="#">d2eg6a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Dihydroorotase
84	<a href="#">c5vgmA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase pyrc from vibrio cholerae in2 complex with zinc at 1.95 a resolution.
85	<a href="#">d1ynya2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
86	<a href="#">c3jzeC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
87	<a href="#">c5v0gE_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase pyrc from yersinia pestis in2 complex with zinc and unknown ligand at 2.4 a resolution.
88	<a href="#">c2imrA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dr_0824; <b>PDBTitle:</b> crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
89	<a href="#">d2ftwa2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
90	<a href="#">d1kcx2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
91	<a href="#">d2fvka2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
92	<a href="#">c2ogjC_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of a dihydroorotase
93	<a href="#">c3msrA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolases; <b>PDBTitle:</b> the crystal structure of an amidohydrolase from mycoplasma synoviae
94	<a href="#">d1xrta2</a>	Alignment	not modelled	99.9	45	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase), catalytic domain
95	<a href="#">d4ubpc2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> alpha-subunit of urease, catalytic domain
96	<a href="#">d2uz9a2</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
97	<a href="#">d1m7ja3</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> D-aminoacylase, catalytic domain
98	<a href="#">d2bb0a2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
99	<a href="#">d2paja2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
100	<a href="#">d2p9ba2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
101	<a href="#">d1ra0a2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Cytosine deaminase catalytic domain



102	<a href="#">d1nfga1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
103	<a href="#">d2i9ua2</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
104	<a href="#">d1i0da_</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
105	<a href="#">d2puza2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
106	<a href="#">d2r8ca2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
107	<a href="#">d2imra2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> DR0824-like
108	<a href="#">d2q09a2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Imidazolonepropionase-like
109	<a href="#">d2ooda2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
110	<a href="#">d1onwa2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Isoaspartyl dipeptidase, catalytic domain
111	<a href="#">d3be7a2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
112	<a href="#">d2qs8a2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like
113	<a href="#">d1e9yb1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
114	<a href="#">d1o12a2</a>	Alignment	not modelled	99.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
115	<a href="#">d2fvka1</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
116	<a href="#">d1ejxc1</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
117	<a href="#">d1gkra1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Hydantoinase (dihydropyrimidinase)
118	<a href="#">d1p1ma2</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
119	<a href="#">d1onwa1</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Isoaspartyl dipeptidase
120	<a href="#">d2r8ca1</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> Zn-dependent arginine carboxypeptidase-like