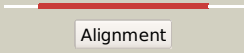

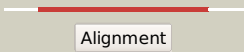

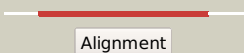
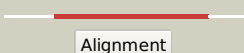


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1850_(ureC)_2097968_2099701
Date	Fri Aug 2 13:30:46 BST 2019
Unique Job ID	9e3ad150fa8ab1d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1e9yB_	 Alignment		100.0	55	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
2	c4z42L_	 Alignment		100.0	57	PDB header: hydrolase Chain: L: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of urease from yersinia enterocolitica
3	c1fwcC_	 Alignment		100.0	61	PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5
4	c2ubpC_	 Alignment		100.0	57	PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
5	c3la4A_	 Alignment		100.0	60	PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
6	d1e9yb2	 Alignment		100.0	53	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
7	d1ejxc2	 Alignment		100.0	62	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
8	d4ubpc2	 Alignment		100.0	57	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
9	d4ubpc1	 Alignment		100.0	63	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
10	d1e9yb1	 Alignment		100.0	44	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
11	d1ejxc1	 Alignment		100.0	44	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease

12	c5e5cC_	Alignment		100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
13	c3hm7A_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
14	c1gkpD_	Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
15	c2ftwA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
16	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
17	c1gkrA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
18	c1k1dF_	Alignment		100.0	17	PDB header: hydrolase Chain: F: PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
19	c3dc8B_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium melloti
20	c2gseC_	Alignment		100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
21	c2fvmA_	Alignment	not modelled	100.0	16	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
22	c2vr2A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
23	c1nfgA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
24	c3e74D_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at the metal2 center
25	c2gwnA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydroorotase; PDBTitle: the structure of putative dihydroorotase from porphyromonas2 gingivalis.
26	c3nqbB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
27	c3d6nA_	Alignment	not modelled	100.0	17	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
28	c4v1xA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza

29	c3mpgB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
30	c3griB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
31	c2z00A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
32	c4wgxD_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
33	c4dykB_	Alignment	not modelled	100.0	19	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
34	c2gokA_	Alignment	not modelled	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
35	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.
36	c4f0rA_	Alignment	not modelled	100.0	19	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)
37	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
38	c4dzhA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an adenosine deaminase from xanthomonas2 campestris (target nysgrc-200456) with bound zn
39	c2bb0A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
40	c3lnpA_	Alignment	not modelled	100.0	17	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
41	c2q09A_	Alignment	not modelled	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-dioxo-imidazolidin-4-yl)-propionic acid
42	c4whbC_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
43	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
44	c3hpaB_	Alignment	not modelled	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
45	c5t5mA_	Alignment	not modelled	100.0	15	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.
46	c2pajA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
47	c3gnhA_	Alignment	not modelled	100.0	16	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.
48	c2vunC_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of amidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily
49	c6ohaA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: probable guanine deaminase; PDBTitle: yeast guanine deaminase
50	c2p9bA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum
51	c3be7B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: zn-dependent arginine carboxypeptidase; PDBTitle: crystal structure of zn-dependent arginine carboxypeptidase
52	c3lsbA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: triazine hydrolase; PDBTitle: crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aureus tc1 complexed

					with zinc and ametrin 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
53	c2vhlB_	Alignment	not modelled	100.0	15
54	c1r9yA_	Alignment	not modelled	100.0	14
55	c3ighX_	Alignment	not modelled	100.0	14
56	c4c65A_	Alignment	not modelled	100.0	15
57	c3feqB_	Alignment	not modelled	100.0	19
58	c2i9uA_	Alignment	not modelled	100.0	14
59	c1p1mA_	Alignment	not modelled	100.0	14
60	c2qt3A_	Alignment	not modelled	100.0	19
61	c2aqoB_	Alignment	not modelled	100.0	15
62	c6nboA_	Alignment	not modelled	100.0	14
63	c2r8cB_	Alignment	not modelled	100.0	18
64	c5xgxB_	Alignment	not modelled	100.0	13
65	c3etkA_	Alignment	not modelled	100.0	13
66	c2qs8A_	Alignment	not modelled	100.0	13
67	c3ooqC_	Alignment	not modelled	100.0	13
68	c4jnrE_	Alignment	not modelled	100.0	13
69	c3v7pA_	Alignment	not modelled	100.0	16
70	c3e0lB_	Alignment	not modelled	100.0	15
71	c2oodA_	Alignment	not modelled	100.0	14
72	c3egiA_	Alignment	not modelled	100.0	12
73	c2p50C_	Alignment	not modelled	100.0	16
74	c6ohcB_	Alignment	not modelled	100.0	11
75	c1o12B_	Alignment	not modelled	100.0	13

						deacetylase2 (tm0814) from thermotoga maritima at 2.5 a resolution
76	c2icsA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
77	c6fv3D	Alignment	not modelled	100.0	12	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.
78	c4f0IB	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from brucella melitensis
79	c2ogjB	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
80	c3mduA	Alignment	not modelled	99.9	15	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
81	c2imrA	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans
82	c5nnlB	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
83	d1gkra2	Alignment	not modelled	99.8	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
84	c4lfyB	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
85	d1k1da2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
86	c3pnuA	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
87	c4c6mA	Alignment	not modelled	99.8	16	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
88	c5vgmA	Alignment	not modelled	99.8	14	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.
89	d1ynya2	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
90	d1nfga2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
91	d1gkpa2	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
92	c3jzeC	Alignment	not modelled	99.8	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
93	c2ogjC	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
94	d2eg6a1	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
95	c5v0gE	Alignment	not modelled	99.7	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.
96	d1kcxa2	Alignment	not modelled	99.7	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
97	d2fvka2	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
98	d2ftwa2	Alignment	not modelled	99.7	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
99	d2fvka1	Alignment	not modelled	99.6	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
100	c3msrA	Alignment	not modelled	99.6	10	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
101	c3gpmB	Alignment	not modelled	99.6	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bt9727_2919;

101	d3ygmh	Alignment	not modelled	99.0	24	PDBTitle: crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
102	d1onwa1	Alignment	not modelled	99.5	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Isoaspartyl dipeptidase
103	d2p9ba1	Alignment	not modelled	99.5	18	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
104	d1yrra1	Alignment	not modelled	99.4	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
105	d2puza2	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
106	d1k1da1	Alignment	not modelled	99.4	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
107	d1ra0a2	Alignment	not modelled	99.4	10	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
108	d2r8ca1	Alignment	not modelled	99.4	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
109	d1xrta2	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
110	d2p9ba2	Alignment	not modelled	99.3	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
111	d2uz9a2	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
112	d2ftwa1	Alignment	not modelled	99.3	13	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
113	d2bb0a2	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
114	d1ynya1	Alignment	not modelled	99.3	25	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
115	d2q09a2	Alignment	not modelled	99.3	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
116	d1gkpa1	Alignment	not modelled	99.2	31	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
117	d2paja2	Alignment	not modelled	99.2	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
118	d2qs8a2	Alignment	not modelled	99.1	20	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
119	d2i9ua2	Alignment	not modelled	99.1	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
120	d1m7ja3	Alignment	not modelled	99.1	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain