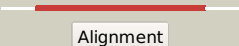



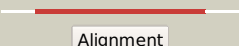





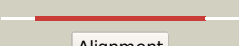













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3332_(nagA)_3718766_3719917
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	09b69dd765fc2b6f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vhlB_	 Alignment		100.0	29	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
2	c6fv3D_	 Alignment		100.0	53	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.
3	c3egiA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-phosphate deacetylase; PDBTitle: n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
4	c2p50C_	 Alignment		100.0	30	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
5	c1o12B_	 Alignment		100.0	28	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
6	c6ohaA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: probable guanine deaminase; PDBTitle: yeast guanine deaminase
7	c2i9uA_	 Alignment		100.0	13	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
8	c2pajA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative cytosine/guanine deaminase; PDBTitle: crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea
9	c2aqoB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: isoaspartyl dipeptidase; PDBTitle: crystal structure of e. coli isoaspartyl dipeptidase mutant e77q
10	c5xgxB_	 Alignment		100.0	15	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
11	c4b91B_	 Alignment		100.0	17	PDB header: signaling protein Chain: B: PDB Molecule: dihydropyrimidinase-related protein 5; PDBTitle: crystal structure of truncated human crmp-5

12	c5e5cC_	Alignment		100.0	14	PDB header: hydrolase Chain: C; PDB Molecule: d-hydantoinase/dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from pseudomonas aeruginosa2 pao1
13	c1xrfA_	Alignment		100.0	14	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
14	c1nfgA_	Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: d-hydantoinase; PDBTitle: structure of d-hydantoinase
15	c3gnhA_	Alignment		100.0	23	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.
16	c4v1xA_	Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: atrazine chlorohydrolase; PDBTitle: the structure of the hexameric atrazine chlorohydrolase, atza
17	c1k1dF_	Alignment		100.0	15	PDB header: hydrolase Chain: F; PDB Molecule: d-hydantoinase; PDBTitle: crystal structure of d-hydantoinase
18	c4dykB_	Alignment		100.0	17	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
19	c2ftwA_	Alignment		100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidine amidohydrolase; PDBTitle: crystal structure of dihydropyrimidinase from dictyostelium discoideum
20	c3lsbA_	Alignment		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 aureuscsens tc1 complexed with zinc and ametrin
21	c2bb0A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: imidazolonepropionase; PDBTitle: structure of imidazolonepropionase from bacillus subtilis
22	c2gseC_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C; PDB Molecule: dihydropyrimidinase-related protein 2; PDBTitle: crystal structure of human dihydropyrimidinease-like 2
23	c2vr2A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidinase; PDBTitle: human dihydropyrimidinase
24	c3e0lB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B; PDB Molecule: guanine deaminase; PDBTitle: computationally designed ammelide deaminase
25	c2fvmA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine
26	c3dc8B_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B; PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from sinorhizobium meliloti
27	c3nqbB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
28	c2gokA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: imidazolonepropionase; PDBTitle: crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution

29	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
30	c4f0rA	Alignment	not modelled	100.0	18	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)
31	c2oodA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: blr3880 protein; PDBTitle: crystal structure of guanine deaminase from bradyrhizobium japonicum
32	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.
33	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
34	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
35	c2q09A	Alignment	not modelled	100.0	16	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
36	c2z00A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of dihydroorotase from thermus thermophilus
37	c1gkpD	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: D: PDB Molecule: hydantoinase; PDBTitle: d-hydantoinase (dihydropyrimidinase) from thermus sp. in space group2 c2221
38	c3hpaB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea
39	c4c65A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ochratoxinase; PDBTitle: crystal structure of a. niger ochratoxinase
40	c2vunC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: enamidase; PDBTitle: the crystal structure of amidohydrolase superfamily
41	c4wgxD	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: molinate hydrolase; PDBTitle: crystal structure of molinate hydrolase
42	c6ohcB	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: guanine deaminase; PDBTitle: e. coli guanine deaminase
43	c3d6nA	Alignment	not modelled	100.0	15	PDB header: hydrolase/transferase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
44	c1gkrA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: non-atp dependent l-selective hydantoinase; PDBTitle: l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens
45	c3v7pA	Alignment	not modelled	100.0	14	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
46	c3griB	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: the crystal structure of a dihydroorotase from staphylococcus aureus
47	c2ubpC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
48	c3e74D	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: allantoinase; PDBTitle: crystal structure of e. coli allantoinase with iron ions at the metal2 center
49	c3mpgB	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: dihydroorotase from bacillus anthracis
50	c1e9yB	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
51	c4whbC	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: phenylurea hydrolase b; PDBTitle: crystal structure of phenylurea hydrolase b
52	c2qs8A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: crystal structure of a xaa-pro dipeptidase with bound methionine in2 the active site
53	c2p9bA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: possible prolidase; PDBTitle: crystal structure of putative prolidase from2 bifidobacterium longum

54	c3feqB	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eah89906
55	c1r9yA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: cytosine deaminase; PDBTitle: bacterial cytosine deaminase d314a mutant.
56	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
57	c3hm7A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: allantoinase; PDBTitle: crystal structure of allantoinase from bacillus halodurans c-125
58	c1fwcC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: urease; PDBTitle: klebsiella aerogenes urease, c319a variant at ph 8.5
59	c1p1mA	Alignment	not modelled	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
60	c3la4A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
61	c4jnrE	Alignment	not modelled	100.0	13	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
62	c3gipB	Alignment	not modelled	100.0	19	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.
63	c1rjqA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
64	c2qt3A	Alignment	not modelled	100.0	14	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
65	c6nboA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: n-isopropylammelide isopropylaminohydrolase; PDBTitle: crystal structure of n-isopropylammelide isopropylaminohydrolase from2 burkholderia multivorans atcc 17616
66	c4f0lB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from brucella melitensis
67	d1un7a2	Alignment	not modelled	100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
68	c3oogC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of amidohydrolase from thermotoga maritima msb8
69	c4z42L	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: L: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of urease from yersinia enterocolitica
70	c2icsA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: adenine deaminase; PDBTitle: crystal structure of an adenine deaminase
71	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
72	c5t5mA	Alignment	not modelled	100.0	16	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.
73	d1yrra2	Alignment	not modelled	100.0	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
74	c2ogjB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
75	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
76	c3ighX	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent hydrolase from2 pyrococcus horikoshii ot3
77	c2imrA	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dr_0824; PDBTitle: crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans

78	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
79	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
80	c2ogjC	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase
81	d1o12a2	Alignment	not modelled	99.8	30	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
82	c3msrA	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolases; PDBTitle: the crystal structure of an amidohydrolase from mycoplasma synoviae
83	d2uz9a2	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
84	d2ooda2	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
85	d2i9ua2	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
86	d1gkpa2	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
87	d2paja2	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: SAH/MTA deaminase-like
88	d4ubpc2	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
89	d1kcxa2	Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
90	d1ra0a2	Alignment	not modelled	99.6	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Cytosine deaminase catalytic domain
91	d1yrra1	Alignment	not modelled	99.6	21	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
92	d2ftwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
93	c3pnuA	Alignment	not modelled	99.5	8	PDB header: hydrolase Chain: A: PDB Molecule: dihydroorotase; PDBTitle: 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
94	d2bb0a2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
95	d2p9ba2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
96	d3be7a2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
97	d2q09a2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
98	d1onwa1	Alignment	not modelled	99.5	15	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Isoaspartyl dipeptidase
99	d1ynya2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
100	d2imra2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: DR0824-like
101	d2puza2	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Imidazolonepropionase-like
102	d1nfga2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
103	c3ggmB	Alignment	not modelled	99.5	19	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
104	c5vgmA	Alignment	not modelled	99.5	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. Fold: TIM beta/alpha-barrel

105	d2qs8a2	Alignment	not modelled	99.5	20	Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
106	d1ejxc1	Alignment	not modelled	99.5	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
107	d1onwa2	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Isoaspartyl dipeptidase, catalytic domain
108	d2p9ba1	Alignment	not modelled	99.5	21	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
109	d1k1da2	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
110	d1e9yb1	Alignment	not modelled	99.5	17	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: alpha-Subunit of urease
111	d1xrta2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
112	d2fvka1	Alignment	not modelled	99.5	12	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
113	d2r8ca2	Alignment	not modelled	99.4	19	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
114	c4lfbB	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315
115	d2icsa2	Alignment	not modelled	99.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenine deaminase-like
116	d1gkra2	Alignment	not modelled	99.4	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
117	c3jzeC	Alignment	not modelled	99.4	12	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
118	d2fvka2	Alignment	not modelled	99.4	14	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
119	d2eg6a1	Alignment	not modelled	99.4	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
120	d2r8ca1	Alignment	not modelled	99.4	14	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like