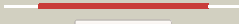


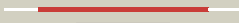














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3594 (-) _4036036_4036863
Date	Fri Aug 9 18:20:27 BST 2019
Unique Job ID	b7454c107bceb617

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bh7A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-L-alanine amidase; PDBTitle: crystal structure of a semet derivative of amid at 2.22 angstroms
2	c4bxdB_	 Alignment		100.0	19	PDB header: hydrolase/peptide Chain: B: PDB Molecule: ampdh3; PDBTitle: crystal structure of ampdh3 from pseudomonas aeruginosa in2 complex with tetrasaccharide pentapeptide
3	c4bolA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: ampdh2; PDBTitle: crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
4	d1j3ga_	 Alignment		100.0	26	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
5	d2bgxa2	 Alignment		100.0	17	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
6	c3hmaA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-L-alanine amidase xlya; PDBTitle: amidase from bacillus subtilis
7	d1yb0a1	 Alignment		99.9	16	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
8	c4ivvA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
9	c4olsA_	 Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: endolysin; PDBTitle: the amidase-2 domain of lysgh15
10	d1sk4a_	 Alignment		99.9	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
11	d1ycka1	 Alignment		99.9	19	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like

12	c2xz4A_	Alignment		99.9	13	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein lf; PDBTitle: crystal structure of the lfz ectodomain of the2 peptidoglycan recognition protein lf
13	c2rkqA_	Alignment		99.9	12	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein-sd; PDBTitle: crystal structure of drosophila peptidoglycan recognition2 protein sd (pgrp-sd)
14	d1ohta_	Alignment		99.9	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
15	c1ohta_	Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cg14704 protein; PDBTitle: peptidoglycan recognition protein-lb
16	d2cb3a1	Alignment		99.9	14	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
17	d2f2lx1	Alignment		99.9	14	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
18	d1lbaa_	Alignment		99.9	24	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
19	c3latB_	Alignment		99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: bifunctional autolysin; PDBTitle: crystal structure of staphylococcus peptidoglycan hydrolase2 amie
20	c5xz3D_	Alignment		99.8	14	PDB header: immune system Chain: D: PDB Molecule: peptidoglycan-recognition protein; PDBTitle: the x-ray structure of apis mellifera pgrp-sa
21	c6ckhA_	Alignment	not modelled	99.8	15	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein; PDBTitle: manduca sexta peptidoglycan recognition protein-1
22	d1sxra_	Alignment	not modelled	99.8	18	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
23	c1s2jA_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein sa cg11709-pa; PDBTitle: crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
24	d2f2la1	Alignment	not modelled	99.8	12	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
25	c6fhgB_	Alignment	not modelled	99.8	18	PDB header: antimicrobial protein Chain: B: PDB Molecule: lyst endolysin; PDBTitle: crystal structure of the ts2631 endolysin from thermus scotoductus2 phage with the unique n-terminal moiety responsible for peptidoglycan3 anchoring
26	c3ep1B_	Alignment	not modelled	99.7	17	PDB header: immune system Chain: B: PDB Molecule: pgrp-hd - peptidoglycan recognition protein PDBTitle: structure of the pgrp-hd from alvinella pompejana
27	c4z8iA_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein 3; PDBTitle: crystal structure of branchiostoma belcheri tsingtauense peptidoglycan2 recognition protein 3
28	c4x36A_	Alignment	not modelled	99.1	20	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: crystal structure of the autolysin lyta from streptococcus

						pneumoniae2 tigr4 PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein lf; PDBTitle: crystal structure of the lfw ectodomain of the2 peptidoglycan recognition protein lf
29	c2xz8A_	Alignment	not modelled	99.0	10	Fold: PGBD-like Superfamily: PGBD-like Family: Peptidoglycan binding domain, PGBD
30	d2bgxa1	Alignment	not modelled	98.5	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
31	c3ds8A_	Alignment	not modelled	52.2	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: TTHA1544-like
32	d2dsta1	Alignment	not modelled	51.5	10	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan-binding domain 1; PDBTitle: crystal structure of burkholderia ap3 phage endolysin
33	c5nm7A_	Alignment	not modelled	48.6	13	Fold: PGBD-like Superfamily: PGBD-like Family: Peptidoglycan binding domain, PGBD
34	d1lbuA1	Alignment	not modelled	42.7	5	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidoglycan-binding/hydrolysing protein; PDBTitle: 2.05 angstrom resolution crystal structure of peptidoglycan-binding2 protein from clostridioides difficile in complex with glutamine3 hydroxamate.
35	c5tv7A_	Alignment	not modelled	42.6	5	PDB header: hydrolase Chain: A: PDB Molecule: erfk/ybis/ycfcs/ynhg family protein; PDBTitle: crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
36	c5bmqa_	Alignment	not modelled	42.0	6	PDB header: hydrolase Chain: A: PDB Molecule: muramoyl-pentapeptide carboxypeptidase; PDBTitle: hydrolase metallo (zn) dd-peptidase
37	c1lbuA_	Alignment	not modelled	39.1	5	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
38	c1qgeD_	Alignment	not modelled	32.0	15	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
39	c2odaB_	Alignment	not modelled	31.0	18	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
40	c2vavL_	Alignment	not modelled	30.0	13	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan hydrolase flgj; PDBTitle: crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
41	c2zycA_	Alignment	not modelled	27.9	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
42	c3i1a_	Alignment	not modelled	25.8	13	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Steroid-binding domain
43	d1t0ga_	Alignment	not modelled	24.3	16	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
44	d2q3la1	Alignment	not modelled	23.9	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
45	d1h41a1	Alignment	not modelled	23.9	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
46	d1cvla_	Alignment	not modelled	22.8	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
47	c1cr6A_	Alignment	not modelled	22.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
48	c4gxtA_	Alignment	not modelled	22.3	18	PDB header: transferase Chain: A: PDB Molecule: dyne8; PDBTitle: crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
49	c4ammA_	Alignment	not modelled	21.8	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
50	d2pl5a1	Alignment	not modelled	21.7	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
51	d1ex9a_	Alignment	not modelled	21.4	13	PDB header: hydrolase Chain: D: PDB Molecule: phosphorylcholine phosphatase; PDBTitle: pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
52	c4as2D_	Alignment	not modelled	21.3	20	PDB header: hydrolase Chain: A: PDB Molecule: lmo1076 protein; PDBTitle: crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
53	c3fi7A_	Alignment	not modelled	20.5	28	PDB header: hydrolase

54	c3bkhA	Alignment	not modelled	20.4	9	Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
55	c1gqkB	Alignment	not modelled	20.1	26	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
56	c4gw3A	Alignment	not modelled	20.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
57	c3rgiA	Alignment	not modelled	19.7	12	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
58	c3im8A	Alignment	not modelled	18.7	19	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
59	c1u0iB	Alignment	not modelled	18.4	35	PDB header: de novo protein Chain: B: PDB Molecule: iaal-k3; PDBTitle: iaal-e3/k3 heterodimer
60	c3fleB	Alignment	not modelled	17.2	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
61	c6cl4A	Alignment	not modelled	16.8	13	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
62	c2op6A	Alignment	not modelled	16.4	21	PDB header: peptide binding protein Chain: A: PDB Molecule: heat shock 70 kda protein d; PDBTitle: peptide-binding domain of heat shock 70 kda protein d precursor from2 c.elegans
63	c3rxyA	Alignment	not modelled	16.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nif3 protein; PDBTitle: crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
64	c3lp5A	Alignment	not modelled	16.0	24	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51
65	c3i28A	Alignment	not modelled	16.0	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
66	c5ijkA	Alignment	not modelled	15.6	29	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
67	d4lipd	Alignment	not modelled	15.2	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
68	c4x8yA	Alignment	not modelled	14.6	20	PDB header: membrane protein Chain: A: PDB Molecule: membrane-associated progesterone receptor component 1; PDBTitle: crystal structure of human pgrmc1 cytochrome b5-like domain
69	d1j03a	Alignment	not modelled	14.5	16	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Steroid-binding domain
70	c3tzzA	Alignment	not modelled	14.5	23	PDB header: transferase Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
71	c2jfkD	Alignment	not modelled	14.3	19	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
72	c5znsA	Alignment	not modelled	14.3	12	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: insect chitin deacetylase
73	c4qbuA	Alignment	not modelled	14.1	27	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
74	c3g87A	Alignment	not modelled	13.9	25	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
75	c4rr5A	Alignment	not modelled	13.7	23	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
76	c5czcA	Alignment	not modelled	13.4	17	PDB header: transferase Chain: A: PDB Molecule: malonyl-coa-[acyl-carrier-protein] transacylase; PDBTitle: the structure of vink
77	c4lpqA	Alignment	not modelled	12.6	10	PDB header: transferase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of the l,d-transpeptidase (residues 123-326) from2 xylanimonas cellulositytica dsm 15894
78	c2qhvA	Alignment	not modelled	12.6	9	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase; PDBTitle: structural basis of octanoic acid recognition by lipoyl-protein2 ligase b
79	c2qhvA	Alignment	not modelled	12.6	9	PDB header: transferase Chain: A: PDB Molecule: lipoyltransferase;

79	c2qnsA	Alignment	not modelled	12.6	9	PDBTitle: structural basis of octanoic acid recognition by lipotein2 ligase b PDB header: biosynthetic protein
80	c6fikA	Alignment	not modelled	12.5	23	Chain: A: PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
81	c2q0xA	Alignment	not modelled	12.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
82	c4qnnC	Alignment	not modelled	12.2	28	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
83	c6iyrA	Alignment	not modelled	12.2	23	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase
84	c2zyiB	Alignment	not modelled	12.2	17	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
85	c2jv8A	Alignment	not modelled	12.2	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ne1242; PDBTitle: solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4
86	c3ptwA	Alignment	not modelled	11.9	19	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
87	d2juza1	Alignment	not modelled	11.9	19	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
88	c3d0kA	Alignment	not modelled	11.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
89	c3hhdC	Alignment	not modelled	11.8	16	PDB header: transferase, hydrolase Chain: C: PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.
90	d1k8qa	Alignment	not modelled	11.2	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
91	c5z7iC	Alignment	not modelled	10.9	24	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
92	d1afra	Alignment	not modelled	10.8	10	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
93	c4xxtA	Alignment	not modelled	10.7	8	PDB header: hydrolase Chain: A: PDB Molecule: fusion of predicted zn-dependent amidase/peptidase (cell PDBTitle: crystal structure of fused zn-dependent2 amidase/peptidase/peptidoglycan-binding domain-containing protein3 from clostridium acetobutylicum atcc 824
94	d1rp1a2	Alignment	not modelled	10.4	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
95	d1f06a2	Alignment	not modelled	10.3	50	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
96	c4mz0B	Alignment	not modelled	10.2	19	PDB header: transferase Chain: B: PDB Molecule: curl; PDBTitle: structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
97	d1lpbb2	Alignment	not modelled	10.1	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
98	c5w8pA	Alignment	not modelled	10.0	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
99	d1yuwa1	Alignment	not modelled	10.0	21	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain