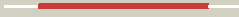












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2323c_(-)_2595371_2596279
Date	Mon Aug 5 13:25:47 BST 2019
Unique Job ID	ccdb13a61bd4f744

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h70a_	 Alignment		100.0	20	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Dimethylarginine dimethylaminohydrolase DDAH
2	c2ci6A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: ng, ng-dimethylarginine dimethylaminohydrolase 1; PDBTitle: crystal structure of dimethylarginine2 dimethylaminohydrolase i bound with zinc low ph
3	c3i4aA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: n(g),n(g)-dimethylarginine dimethylaminohydrolase 1; PDBTitle: crystal structure of dimethylarginine dimethylaminohydrolase-1 (ddah-2 1) in complex with n5-(1-iminopropyl)-l-ornithine
4	d1s9ra_	 Alignment		100.0	19	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Arginine deiminase
5	c4e4jl_	 Alignment		100.0	22	PDB header: hydrolase Chain: J: PDB Molecule: arginine deiminase; PDBTitle: crystal structure of arginine deiminase from mycoplasma penetrans
6	c4bofA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: arginine deiminase; PDBTitle: crystal structure of arginine deiminase from group a streptococcus
7	c5wpiB_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: hsva; PDBTitle: the virulence-associated protein hsva from the fire blight pathogen2 erwinia amylovora is a polyamine amidinotransferase
8	d1bwda_	 Alignment		100.0	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Amidinotransferase
9	c8jdwA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: protein (l-arginine:glycine amidinotransferase); PDBTitle: crystal structure of human l-arginine:glycine amidinotransferase in2 complex with l-alanine
10	c1jdwA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: l-arginine\glycine amidinotransferase; PDBTitle: crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
11	d1jdwA_	 Alignment		100.0	15	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Amidinotransferase

12	d1rxxa_	Alignment		100.0	21	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Arginine deiminase
13	d1vkpa_	Alignment		99.6	15	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
14	c6b2wB_	Alignment		99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: putative peptidyl-arginine deiminase family protein; PDBTitle: c. jejuni c315s agmatine deiminase with substrate bound
15	d2ewoa1	Alignment		99.6	20	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
16	d1xkna_	Alignment		99.5	18	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
17	d2jera1	Alignment		99.5	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
18	c2jerG_	Alignment		99.5	17	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
19	d1zbra1	Alignment		99.5	20	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
20	d2cmua1	Alignment		99.4	20	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
21	c4ytgA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidylarginine deiminase; PDBTitle: crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
22	d1ynha1	Alignment	not modelled	97.0	22	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Succinylarginine dihydrolase-like
23	c4n2kA_	Alignment	not modelled	92.5	26	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-2; PDBTitle: crystal structure of protein arginine deiminase 2 (q350a, 0 mm ca2+)
24	c4n2gA_	Alignment	not modelled	92.4	26	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-2; PDBTitle: crystal structure of protein arginine deiminase 2 (d169a, 10 mm ca2+)
25	d2dexx3	Alignment	not modelled	91.6	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Peptidylarginine deiminase Pad4, catalytic C-terminal domain
26	c2dexX_	Alignment	not modelled	90.4	17	PDB header: hydrolase Chain: X: PDB Molecule: protein-arginine deiminase type iv; PDBTitle: crystal structure of human peptidylarginine deiminase 4 in complex2 with histone h3 n-terminal peptide including arg17
27	c5hp5A_	Alignment	not modelled	90.1	20	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-1; PDBTitle: srtucture of human peptidylarginine deiminase type i (pad1)
28	c3ff4A_	Alignment	not modelled	85.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412

29	d1hx0a2	Alignment	not modelled	82.6	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
30	d3dhp2	Alignment	not modelled	81.5	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
31	d1wd7a_	Alignment	not modelled	78.6	18	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
32	d1iuka_	Alignment	not modelled	72.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
33	d1g94a2	Alignment	not modelled	69.8	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
34	d2d59a1	Alignment	not modelled	68.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
35	d1jaea2	Alignment	not modelled	59.5	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
36	d1y81a1	Alignment	not modelled	55.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
37	c3mw8A_	Alignment	not modelled	54.7	19	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from shewanella amazonensis sb2b at 1.65 a resolution
38	c1sr9A_	Alignment	not modelled	44.2	22	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
39	c2duwA_	Alignment	not modelled	41.7	19	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of klebsiella pneumoniae
40	d1q7ra_	Alignment	not modelled	37.5	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	d1uc8a1	Alignment	not modelled	36.8	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
42	c2ywdA_	Alignment	not modelled	35.9	9	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
43	d1a9xb2	Alignment	not modelled	32.9	6	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
44	c3b1pX_	Alignment	not modelled	31.4	18	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
45	c3x27C_	Alignment	not modelled	30.0	20	PDB header: lyase Chain: C: PDB Molecule: cucumopine synthase; PDBTitle: structure of mcbb in complex with tryptophan
46	d1mgta2	Alignment	not modelled	29.5	21	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
47	c2issF_	Alignment	not modelled	29.3	12	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
48	c1keeH_	Alignment	not modelled	25.5	8	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
49	d2ex4a1	Alignment	not modelled	24.7	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
50	c2jrbA_	Alignment	not modelled	23.9	25	PDB header: rna binding protein Chain: A: PDB Molecule: orf 1 protein; PDBTitle: c-terminal domain of orf1p from mouse line-1
51	c6rdu2_	Alignment	not modelled	22.1	17	PDB header: proton transport Chain: 2: PDB Molecule: asa-2: polytomella f-atp synthase associated subunit 2; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
52	d1jida_	Alignment	not modelled	20.7	16	Fold: SRP19 Superfamily: SRP19 Family: SRP19
53	c6eznG_	Alignment	not modelled	20.5	8	PDB header: membrane protein Chain: G: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
54	c2x4bA_	Alignment	not modelled	20.4	17	PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin PDB header: hydrolase

55	c4qawA_	Alignment	not modelled	20.4	13	Chain: A: PDB Molecule: xyn30d; PDBTitle: structure of modular xyn30d from paenibacillus barcinonensis
56	c4rvqA_	Alignment	not modelled	20.4	19	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
57	d1ka9h_	Alignment	not modelled	20.4	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
58	c5nc8B_	Alignment	not modelled	19.6	18	PDB header: transport protein Chain: B: PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form
59	d1lnga_	Alignment	not modelled	18.6	14	Fold: SRP19 Superfamily: SRP19 Family: SRP19
60	c5nbrB_	Alignment	not modelled	16.7	16	PDB header: transferase Chain: B: PDB Molecule: deoxyribosyltransferase; PDBTitle: 2-desoxiribosyltransferase from leishmania mexicana
61	d1f52a1	Alignment	not modelled	16.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
62	d1a77a2	Alignment	not modelled	16.4	13	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
63	c5j8jA_	Alignment	not modelled	16.2	16	PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase hda1; PDBTitle: a histone deacetylase from saccharomyces cerevisiae
64	c3faxA_	Alignment	not modelled	16.2	17	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
65	d1kwqa3	Alignment	not modelled	16.1	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: A4 beta-galactosidase middle domain
66	c4nx0G_	Alignment	not modelled	16.1	16	PDB header: hydrolase Chain: G: PDB Molecule: abp, a gh27 beta-l-arabinopyranosidase; PDBTitle: crystal structure of abp-wt, a gh27-b-l-arabinopyranosidase from2 geobacillus stearothermophilus
67	d1xtpa_	Alignment	not modelled	15.4	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: AD-003 protein-like
68	d1p88a_	Alignment	not modelled	15.1	17	Fold: IF3-like Superfamily: EPT/RTPC-like Family: Enolpyruvate transferase, EPT
69	d1rxwa2	Alignment	not modelled	15.0	8	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
70	c3vpbC_	Alignment	not modelled	14.7	9	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
71	c4zhjA_	Alignment	not modelled	14.2	13	PDB header: metal binding protein Chain: A: PDB Molecule: mg-chelatase subunit chlh; PDBTitle: crystal structure of the catalytic subunit of magnesium chelatase
72	d1xpja_	Alignment	not modelled	14.0	8	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
73	c3cueM_	Alignment	not modelled	13.6	9	PDB header: protein transport Chain: M: PDB Molecule: transport protein particle 23 kda subunit; PDBTitle: crystal structure of a trapp subassembly activating the rab ypt1p
74	c4gudA_	Alignment	not modelled	13.4	17	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
75	c2j3tC_	Alignment	not modelled	13.3	13	PDB header: transport Chain: C: PDB Molecule: trafficking protein particle complex subunit 1; PDBTitle: the crystal structure of the bet3-trs33-bet5-trs23 complex.
76	c4egjD_	Alignment	not modelled	13.3	10	PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
77	d1ul1x2	Alignment	not modelled	13.2	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
78	c2kjaA_	Alignment	not modelled	13.1	17	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the permutant p54-55
79	d1gjwa2	Alignment	not modelled	13.1	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
80	c2k2wA_	Alignment	not modelled	12.8	14	PDB header: cell cycle Chain: A: PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
81	c2muyA_	Alignment	not modelled	12.5	22	PDB header: nucleotide binding protein Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsh;

					PDBTitle: the solution structure of the ftsh periplasmic n-domain
82	d1zcza1	Alignment	not modelled	12.4	13 Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
83	c3ndjA	Alignment	not modelled	12.0	16 PDB header: transferase Chain: A; PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
84	d1i1qb	Alignment	not modelled	11.9	12 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
85	c6c3aB	Alignment	not modelled	11.7	8 PDB header: biosynthetic protein Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
86	c5ubbA	Alignment	not modelled	11.7	21 PDB header: transferase Chain: A; PDB Molecule: alpha n-terminal protein methyltransferase 1b; PDBTitle: crystal structure of human alpha n-terminal protein methyltransferase2 1b
87	d1qjpa	Alignment	not modelled	11.4	6 Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Glyoxalase I (lactoylglutathione lyase)
88	c3hh1D	Alignment	not modelled	11.3	17 PDB header: transferase Chain: D; PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
89	c3u7jA	Alignment	not modelled	11.3	18 PDB header: isomerase Chain: A; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
90	d2f06a2	Alignment	not modelled	11.2	17 Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
91	c5dmxC	Alignment	not modelled	11.2	14 PDB header: ligase Chain: C; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
92	d1bf2a3	Alignment	not modelled	11.1	11 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	c2pr7A	Alignment	not modelled	11.1	11 PDB header: hydrolase Chain: A; PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
94	c3g12A	Alignment	not modelled	10.9	9 PDB header: lyase Chain: A; PDB Molecule: putative lactoylglutathione lyase; PDBTitle: crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
95	c4egqD	Alignment	not modelled	10.7	11 PDB header: ligase Chain: D; PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
96	d1vsra	Alignment	not modelled	10.7	18 Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
97	c1kmcB	Alignment	not modelled	10.7	14 PDB header: apoptosis/hydrolase Chain: B; PDB Molecule: caspase-7; PDBTitle: crystal structure of the caspase-7 / xiap-bir2 complex
98	c3d8tB	Alignment	not modelled	10.5	14 PDB header: lyase Chain: B; PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
99	c4x84C	Alignment	not modelled	10.5	33 PDB header: isomerase Chain: C; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa