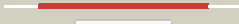



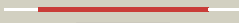







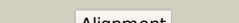













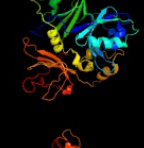


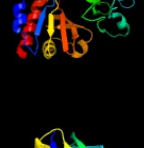
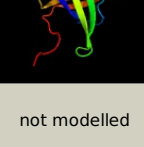


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2211c_gcvT_2476050_2477189
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	e5d2ec54856bf9bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4p9sA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgh
2	c1pj6A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
3	c1x31A_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
4	c1v5vA_	 Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
5	c1yx2B_	 Alignment		100.0	40	PDB header: transferase Chain: B; PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of the probable aminomethyltransferase2 from bacillus subtilis
6	c1worA_	 Alignment		100.0	39	PDB header: transferase Chain: A; PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of t-protein of the glycine cleavage2 system
7	c3girA_	 Alignment		100.0	32	PDB header: transferase Chain: A; PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae
8	c1wsrA_	 Alignment		100.0	29	PDB header: transferase Chain: A; PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of human t-protein of glycine cleavage2 system
9	c3tfhB_	 Alignment		100.0	19	PDB header: transferase Chain: B; PDB Molecule: gcvt-like aminomethyltransferase protein; PDBTitle: dmsp-dependent demethylase from p. ubiquie - apo
10	c1vloA_	 Alignment		100.0	38	PDB header: transferase Chain: A; PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution
11	c5tl4C_	 Alignment		100.0	23	PDB header: transferase Chain: C; PDB Molecule: vanillate/3-o-methylgallate o-demethylase; PDBTitle: crystal structure of sphingomonas paucimobilis aryl o-demethylase ligm

12	d1pj5a4	Alignment		100.0	31	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
13	d1v5va2	Alignment		100.0	36	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
14	d1wosa2	Alignment		100.0	39	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
15	d1vloa2	Alignment		100.0	38	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
16	c1vlyA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: unknown protein from 2d-page; PDBTitle: crystal structure of a putative aminomethyltransferase (ygfz) from2 escherichia coli at 1.30 a resolution
17	c5oliA_	Alignment		100.0	24	PDB header: protein binding Chain: A: PDB Molecule: putative transferase caf17, mitochondrial; PDBTitle: crystal structure of human iba57
18	d1vlyva2	Alignment		100.0	14	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
19	c2gagC_	Alignment		100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: heterotetrameric sarcosine oxidase gamma-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin metalloenzyme at2 1.85 a resolution
20	d1v5va1	Alignment		99.9	38	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
21	d1wosa1	Alignment	not modelled	99.8	40	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
22	d1pj5a1	Alignment	not modelled	99.8	23	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
23	c6ahrB_	Alignment	not modelled	99.8	25	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonucleases p/mrp protein subunit pop1; PDBTitle: cryo-em structure of human ribonuclease p
24	d1vloa1	Alignment	not modelled	99.8	41	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
25	c6ah3B_	Alignment	not modelled	99.7	21	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonucleases p/mrp protein subunit pop1; PDBTitle: cryo-em structure of yeast ribonuclease p with pre-trna substrate
26	d1vlyva1	Alignment	not modelled	96.2	15	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
27	c1xzqA_	Alignment	not modelled	95.7	26	PDB header: hydrolase Chain: A: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
28	c3geiB_	Alignment	not modelled	95.6	22	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
29	c1xzqB_	Alignment	not modelled	93.9	18	PDB header: hydrolase Chain: B: PDB Molecule: probable trna modification gtpase trme;

29	c1xzqb_	Alignment	not modelled	93.9	10	PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf PDB header: hydrolase
30	c3gehA_	Alignment	not modelled	92.7	16	Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
31	d1xzpa3	Alignment	not modelled	92.6	20	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: TrmE formyl-THF-binding domain
32	c5uvnB_	Alignment	not modelled	85.5	18	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
33	c5uvnC_	Alignment	not modelled	85.5	18	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
34	c5uvnD_	Alignment	not modelled	85.5	18	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
35	c5uvnA_	Alignment	not modelled	85.5	18	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
36	c5uvnF_	Alignment	not modelled	85.5	18	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
37	c5uvnE_	Alignment	not modelled	85.5	18	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
38	c5uw8C_	Alignment	not modelled	68.5	15	PDB header: transport protein Chain: C: PDB Molecule: probable phospholipid abc transporter-binding protein mlad; PDBTitle: structure of e. coli mce protein mlad, core mce domain
39	c2nyiB_	Alignment	not modelled	49.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
40	c1m98A_	Alignment	not modelled	30.2	11	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
41	d3bzka5	Alignment	not modelled	25.4	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
42	c3l48B_	Alignment	not modelled	23.3	26	PDB header: transport protein Chain: B: PDB Molecule: outer membrane usher protein papc; PDBTitle: crystal structure of the c-terminal domain of the papc usher
43	c2ysrA_	Alignment	not modelled	17.3	20	PDB header: signaling protein Chain: A: PDB Molecule: dep domain-containing protein 1; PDBTitle: solution structure of the dep domain from human dep domain-2 containing protein 1
44	c3lywA_	Alignment	not modelled	15.2	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ybbr family protein; PDBTitle: crystal structure of ybbr family protein dhaf_0833 from2 desulfitobacterium hafniense dcb-2. northeast structural3 genomics consortium target id dhr29b
45	c6ic4C_	Alignment	not modelled	14.4	17	PDB header: protein transport Chain: C: PDB Molecule: toluene tolerance efflux transporter (abc superfamily, PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
46	c5d5pC_	Alignment	not modelled	13.4	22	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
47	c3k3sG_	Alignment	not modelled	12.9	15	PDB header: hydrolase Chain: G: PDB Molecule: altronate hydrolase; PDBTitle: crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
48	d1znba_	Alignment	not modelled	12.7	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
49	c4oy2D_	Alignment	not modelled	12.7	13	PDB header: transcription Chain: D: PDB Molecule: transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of taf1-taf7, a tfiid subcomplex
50	c3brcA_	Alignment	not modelled	11.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
51	d1w4ma_	Alignment	not modelled	11.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
52	c5kdjA_	Alignment	not modelled	11.1	21	PDB header: hydrolase Chain: A: PDB Molecule: f5/8 type c domain protein; PDBTitle: zmpB metallopeptidase from clostridium perfringens
53	d1fsha_	Alignment	not modelled	9.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
54	c4c9vA_	Alignment	not modelled	9.3	36	PDB header: signaling protein Chain: A: PDB Molecule: rnf43; PDBTitle: xenopus rnf43 ectodomain in complex with xenopus rspo2 fu1-fu2
55	c3lazB_	Alignment	not modelled	9.2	10	PDB header: lyase Chain: B: PDB Molecule: d-galactarate dehydratase; PDBTitle: the crystal structure of the n-terminal domain of d-2

						galactarate dehydratase from escherichia coli cft073
56	d1js8a2	Alignment	not modelled	9.0	26	Fold: C-terminal domain of mollusc hemocyanin Superfamily: C-terminal domain of mollusc hemocyanin Family: C-terminal domain of mollusc hemocyanin
57	c3jrtA	Alignment	not modelled	9.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein vpc_cass2; PDBTitle: structure from the mobile metagenome of v. paracholerae: integron2 cassette protein vpc_cass2
58	d1lnla2	Alignment	not modelled	8.9	22	Fold: C-terminal domain of mollusc hemocyanin Superfamily: C-terminal domain of mollusc hemocyanin Family: C-terminal domain of mollusc hemocyanin
59	d1iq4a	Alignment	not modelled	8.7	17	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
60	c4rgwB	Alignment	not modelled	8.7	27	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of a taf1-taf7 complex in human transcription factor2 iid
61	d1uhwa	Alignment	not modelled	8.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
62	c6d8vA	Alignment	not modelled	7.8	18	PDB header: membrane protein Chain: A: PDB Molecule: probable chemoreceptor (methyl-accepting chemotaxis) PDBTitle: methyl-accepting chemotaxis protein x
63	c5o60F	Alignment	not modelled	7.8	17	PDB header: ribosome Chain: F: PDB Molecule: 50s ribosomal protein l5; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
64	d2zjrd1	Alignment	not modelled	7.4	20	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
65	d1vqod1	Alignment	not modelled	7.4	27	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
66	c6cd2C	Alignment	not modelled	7.4	28	PDB header: membrane protein/chaperone Chain: C: PDB Molecule: outer membrane usher protein papc; PDBTitle: crystal structure of the papc usher bound to the chaperone-adhesin2 papd-papg
67	c6exnc	Alignment	not modelled	6.8	25	PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: post-catalytic p complex spliceosome with 3' splice site docked
68	c1wyla	Alignment	not modelled	6.6	17	PDB header: signaling protein Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: solution structure of the ch domain of human nedd92 interacting protein with calponin homology and lim domains
69	c3ny7A	Alignment	not modelled	6.5	12	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
70	d2z9ia2	Alignment	not modelled	6.5	25	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
71	c5ilaA	Alignment	not modelled	6.4	16	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
72	c6ncxB	Alignment	not modelled	6.4	28	PDB header: hydrolase Chain: B: PDB Molecule: beta-galacturonidase; PDBTitle: crystal structure of gh2 beta-galacturonidase from eisenbergiella tayi2 bound to galacturonate
73	c5z81A	Alignment	not modelled	6.2	13	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
74	c2jysA	Alignment	not modelled	6.1	29	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
75	d1mjia	Alignment	not modelled	6.0	17	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
76	c2ly7A	Alignment	not modelled	6.0	46	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: b-flap domain of rna polymerase (b. subtilis)
77	c2n9zA	Alignment	not modelled	6.0	60	PDB header: toxin Chain: A: PDB Molecule: tau-theraphotoxin-hs1a; PDBTitle: solution structure of k1 lobe of double-knot toxin
78	d1bhga2	Alignment	not modelled	5.9	17	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
79	d1dm9a	Alignment	not modelled	5.9	7	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
80	c1dm9A	Alignment	not modelled	5.9	7	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
81	c5ym0A	Alignment	not modelled	5.8	33	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad

82	d2essa2	Alignment	not modelled	5.8	9	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
83	c6fu4D_	Alignment	not modelled	5.8	6	PDB header: signaling protein Chain: D: PDB Molecule: probable chemotaxis transducer; PDBTitle: ligand binding domain (lbd) of the p. aeruginosa histamine receptor2 tlpq
84	c1b4aA_	Alignment	not modelled	5.7	13	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
85	c6icZ_	Alignment	not modelled	5.7	38	PDB header: splicing Chain: Z: PDB Molecule: pre-mrna-splicing factor slu7; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
86	d1ky9a2	Alignment	not modelled	5.7	28	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
87	c6ecaA_	Alignment	not modelled	5.7	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: lactobacillus rhamnosus beta-glucuronidase
88	d2csoa1	Alignment	not modelled	5.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
89	d1o7fa1	Alignment	not modelled	5.5	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
90	c6n9gB_	Alignment	not modelled	5.5	13	PDB header: signaling protein Chain: B: PDB Molecule: regulator of g-protein signaling 7; PDBTitle: crystal structure of rgs7-gbeta5 dimer
91	c4o2hB_	Alignment	not modelled	5.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein bcam1869; PDBTitle: crystal structure of bcam1869 protein (rsam homolog) from burkholderia2 cenocepacia
92	c3cmgA_	Alignment	not modelled	5.4	22	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
93	c6d4oA_	Alignment	not modelled	5.4	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: eubacterium eligens beta-glucuronidase bound to an amoxapine-2 glucuronide conjugate
94	c6fxdB_	Alignment	not modelled	5.3	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: mupz; PDBTitle: crystal structure of mupz from pseudomonas fluorescens
95	d2o34a1	Alignment	not modelled	5.3	22	Fold: T-fold Superfamily: ApbE-like Family: DVU1097-like
96	c2d89A_	Alignment	not modelled	5.3	17	PDB header: structural protein, protein binding Chain: A: PDB Molecule: ehbp1 protein; PDBTitle: solution structure of the ch domain from human eh domain2 binding protein 1
97	c4jklA_	Alignment	not modelled	5.3	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: crystal structure of streptococcus agalactiae beta-glucuronidase in2 space group p21212
98	c3fn9B_	Alignment	not modelled	5.3	31	PDB header: hydrolase Chain: B: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
99	c4cucA_	Alignment	not modelled	5.3	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: unravelling the multiple functions of the architecturally intricate2 streptococcus pneumoniae beta-galactosidase, bgaa.