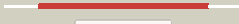



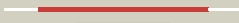






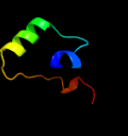



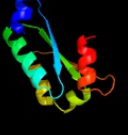






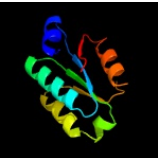
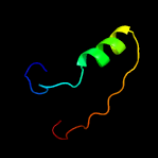
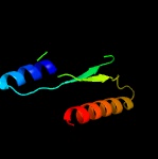
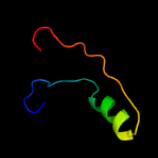

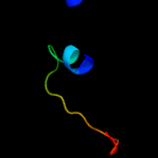
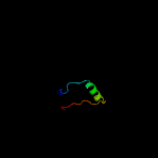
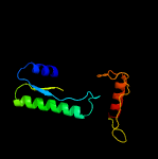



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2611c (-)_2939022_2939972
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	583626bc9cd16f1a

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5knkB_	 Alignment		100.0	17	PDB header: transferase Chain: B; PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
2	c5f34A_	 Alignment		100.0	77	PDB header: transferase Chain: A; PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	c5kymA_	 Alignment		98.8	16	PDB header: transferase Chain: A; PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
4	c4nmnA_	 Alignment		53.6	9	PDB header: replication Chain: A; PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
5	c4p7dA_	 Alignment		45.2	16	PDB header: toxin Chain: A; PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
6	c2j5bA_	 Alignment		43.8	19	PDB header: ligase Chain: A; PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of the tyrosyl trna synthetase from acanthamoeba polyphaga2 mimivirus complexed with tyrosinol
7	c1ltxA_	 Alignment		39.0	14	PDB header: transferase/protein binding Chain: A; PDB Molecule: rab geranylgeranyltransferase alpha subunit; PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
8	d1qopb_	 Alignment		38.6	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
9	d1vlia2	 Alignment		38.4	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
10	d1v8za1	 Alignment		37.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
11	c2zy4F_	 Alignment		36.3	29	PDB header: lyase Chain: F; PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase

12	c4qysA	Alignment		36.0	12	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain 2; PDBTitle: trpb2 enzymes
13	d1r6ta2	Alignment		36.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
14	c3cwcB	Alignment		36.0	14	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
15	c1r6uB	Alignment		35.3	17	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
16	d1v71a1	Alignment		30.8	14	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
17	c3lubE	Alignment		29.4	22	PDB header: hydrolase Chain: E: PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase (yp_211512.1)2 from bacteroides fragilis nctc 9343 at 2.11 a resolution
18	c3kt3D	Alignment		27.5	17	PDB header: ligase Chain: D: PDB Molecule: tryptophanyl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of s. cerevisiae tryptophanyl-trna synthetase in2 complex with trpamp
19	c4wbdA	Alignment		27.0	13	PDB header: ligase Chain: A: PDB Molecule: bshc; PDBTitle: the crystal structure of bshc from bacillus subtilis complexed with2 citrate and adp
20	c2quiB	Alignment		26.8	14	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
21	c3tzeA	Alignment	not modelled	26.1	17	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of a tryptophanyl-trna synthetase from2 encephalitozoon cuniculi bound to tryptophan
22	c3f6tA	Alignment	not modelled	25.7	19	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
23	c6hulB	Alignment	not modelled	24.4	13	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase beta chain 1; PDBTitle: sulfobolus solfataricus tryptophan synthase ab complex
24	c4ix1B	Alignment	not modelled	23.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
25	c3focB	Alignment	not modelled	23.1	20	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
26	c1tdjA	Alignment	not modelled	22.7	15	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
27	c2o2jA	Alignment	not modelled	22.5	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apofrom)
28	c2cycB	Alignment	not modelled	22.0	11	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii

29	c6qeB	Alignment	not modelled	21.6	12	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
30	c5odcD	Alignment	not modelled	21.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: methyl-viologen reducing hydrogenase subunit d; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
31	c1x1qA	Alignment	not modelled	20.8	20	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
32	c2advB	Alignment	not modelled	20.1	38	PDB header: hydrolase Chain: B: PDB Molecule: glutaryl 7- aminocephalosporanic acid acylase; PDBTitle: crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
33	c3no4A	Alignment	not modelled	20.1	18	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
34	c3jxeB	Alignment	not modelled	20.1	20	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
35	d1v7za	Alignment	not modelled	19.9	23	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
36	c6bbmA	Alignment	not modelled	18.7	12	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
37	c6o60A	Alignment	not modelled	18.6	10	PDB header: transferase Chain: A: PDB Molecule: protein prenyltransferase alpha subunit repeat-containing PDBTitle: crystal structure of ggtase3-fbx12-skp1 complex
38	c4j75B	Alignment	not modelled	18.4	20	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of a parasite trna synthetase, product-bound
39	c3hv0A	Alignment	not modelled	18.2	14	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from cryptosporidium parvum
40	c2ip1A	Alignment	not modelled	17.9	17	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
41	c5cvcB	Alignment	not modelled	16.9	11	PDB header: isomerase Chain: B: PDB Molecule: serine racemase; PDBTitle: structure of maize serine racemase
42	c2h1fB	Alignment	not modelled	16.8	11	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
43	c1viiA	Alignment	not modelled	16.7	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
44	c4f4fB	Alignment	not modelled	16.2	18	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
45	d1jcuA	Alignment	not modelled	16.2	7	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
46	d1tuwa	Alignment	not modelled	15.7	18	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Polyketide synthesis cyclase
47	d2obba1	Alignment	not modelled	15.4	20	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
48	c1r6tA	Alignment	not modelled	14.5	21	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of human tryptophanyl-trna synthetase
49	d1k7ja	Alignment	not modelled	14.4	10	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
50	c3h3rD	Alignment	not modelled	14.3	14	PDB header: ligase Chain: D: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase homolog from entamoeba histolytica
51	c3sz8D	Alignment	not modelled	14.2	14	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
52	c5uq2B	Alignment	not modelled	13.3	10	PDB header: transferase/cell cycle Chain: B: PDB Molecule: speedy protein a; PDBTitle: crystal structure of human cdk2-spy1 complex
53	c3h3wD	Alignment	not modelled	13.1	11	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase;

53	c3v9wD_	Alignment	not modelled	13.1	11	PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
54	d2pw6a1	Alignment	not modelled	12.6	18	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
55	c3r0zA_	Alignment	not modelled	12.5	12	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
56	c5kinD_	Alignment	not modelled	12.3	17	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
57	d1hrua_	Alignment	not modelled	12.3	23	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
58	c3iraA_	Alignment	not modelled	12.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
59	c2fyfB_	Alignment	not modelled	11.9	13	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
60	c2pqmA_	Alignment	not modelled	11.7	20	PDB header: lyase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
61	c6ncsB_	Alignment	not modelled	11.7	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminic acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
62	c3i05B_	Alignment	not modelled	11.6	23	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from trypanosoma brucei
63	d2lfba_	Alignment	not modelled	11.5	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
64	c4uaqA_	Alignment	not modelled	11.5	14	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca 2; PDBTitle: crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis
65	c2gn0A_	Alignment	not modelled	10.9	13	PDB header: lyase Chain: A: PDB Molecule: threonine dehydratase catabolic; PDBTitle: crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
66	c2l7kA_	Alignment	not modelled	10.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
67	d1d9ea_	Alignment	not modelled	10.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
68	d1j7ja_	Alignment	not modelled	10.6	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
69	c5iejA_	Alignment	not modelled	10.5	18	PDB header: protein Chain: A: PDB Molecule: sdrG; PDBTitle: solution structure of the bef3-activated conformation of sdrG from2 pseudomonas melonis fr1
70	c5ohxB_	Alignment	not modelled	10.3	18	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
71	d1hgxa_	Alignment	not modelled	10.2	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
72	c3a05A_	Alignment	not modelled	10.1	15	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
73	c6f9oA_	Alignment	not modelled	10.1	19	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
74	c3eywA_	Alignment	not modelled	9.9	9	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
75	c3m8yC_	Alignment	not modelled	9.7	13	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
76	d1tdja1	Alignment	not modelled	9.7	12	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
77	c2kjaA_	Alignment	not modelled	9.6	5	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s6; PDBTitle: solution structure and backbone dynamics of the

						permutant p54-55
78	c2rkbE	Alignment	not modelled	9.5	12	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
79	c2d1fA	Alignment	not modelled	9.3	19	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
80	c2ov3A	Alignment	not modelled	9.0	20	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein component of an abc type zinc PDBTitle: crystal structure of 138-173 znua deletion mutant plus zinc bound
81	c3zfiB	Alignment	not modelled	8.8	21	PDB header: transport protein Chain: B: PDB Molecule: rap1a protein; PDBTitle: rap1a protein (sma2260) from serratia marcescens
82	d1nj8a2	Alignment	not modelled	8.8	22	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
83	d1o60a	Alignment	not modelled	8.6	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
84	c4negA	Alignment	not modelled	8.5	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
85	c2lpmA	Alignment	not modelled	8.5	9	PDB header: transcription regulator Chain: A: PDB Molecule: two-component response regulator; PDBTitle: chemical shift and structure assignments for sma0114
86	c6gtmA	Alignment	not modelled	8.5	13	PDB header: signaling protein Chain: A: PDB Molecule: aldo-keto reductase family protein; PDBTitle: crystal structure of smba in complex with pggpp.
87	c3x43F	Alignment	not modelled	8.3	17	PDB header: transferase Chain: F: PDB Molecule: o-ureido-l-serine synthase; PDBTitle: crystal structure of o-ureido-l-serine synthase
88	c6g1cV	Alignment	not modelled	8.3	5	PDB header: antitoxin Chain: V: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the n-terminal domain of burkholderia2 pseudomallei antitoxin hicb
89	d1iyj4	Alignment	not modelled	8.2	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
90	c4q0mA	Alignment	not modelled	8.1	29	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of pyrococcus furiosus l-asparaginase
91	d1pwha	Alignment	not modelled	8.0	16	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
92	c3v7nA	Alignment	not modelled	8.0	16	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase (thrc) from burkholderia2 thailandensis
93	c2hyij	Alignment	not modelled	8.0	11	PDB header: hydrolase/rna binding protein/rna Chain: J: PDB Molecule: protein casc3; PDBTitle: structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna
94	c3l6cA	Alignment	not modelled	8.0	12	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
95	d1p3qq	Alignment	not modelled	7.9	4	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
96	c3s3tD	Alignment	not modelled	7.9	17	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
97	d1wkva1	Alignment	not modelled	7.9	16	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
98	c4airB	Alignment	not modelled	7.7	21	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: leishmania major cysteine synthase
99	d1d8da	Alignment	not modelled	7.7	10	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase