
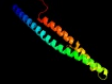
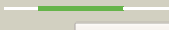






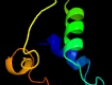
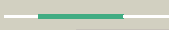
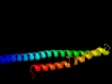









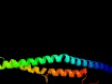
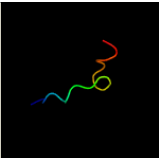
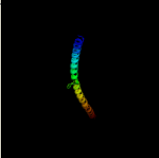

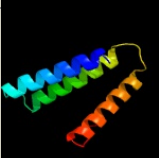
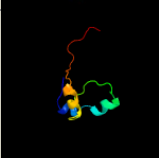
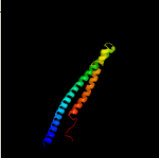
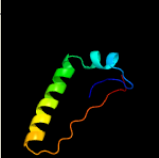
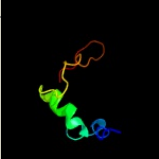
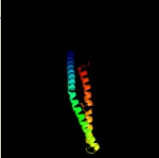


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0739 (-) _830858_831664
Date	Fri Jul 26 01:50:31 BST 2019
Unique Job ID	0f837cacc128f289

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5azpA_	 Alignment		66.1	16	PDB header: membrane protein Chain: A: PDB Molecule: multidrug efflux outer membrane protein oprn; PDBTitle: crystal structure of a membrane protein from pseudomonas aeruginosa
2	c4mt0A_	 Alignment		59.7	19	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: mtre protein; PDBTitle: crystal structure of the open state of the neisseria gonorrhoeae mtre2 outer membrane channel
3	c2g7hA_	 Alignment		51.9	15	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
4	c4p40A_	 Alignment		51.9	9	PDB header: transport protein Chain: A: PDB Molecule: copn; PDBTitle: chlamydia pneumoniae copn
5	c5a48B_	 Alignment		51.3	26	PDB header: protein binding Chain: B: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-240) of drosophila2 oskar in p65
6	c3pikA_	 Alignment		48.6	13	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusc; PDBTitle: outer membrane protein cusc
7	d1kx9b_	 Alignment		44.4	19	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
8	c1wriA_	 Alignment		37.9	13	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
9	c2marA_	 Alignment		31.7	16	PDB header: unknown function Chain: A: PDB Molecule: sxp/ral-2 family protein; PDBTitle: solution structure of ani s 5 anisakis simplex allergen
10	c5azsC_	 Alignment		31.0	19	PDB header: membrane protein Chain: C: PDB Molecule: outer membrane protein oprj; PDBTitle: crystal structure of a membrane protein from pseudomonas aeruginosa
11	d1wplA_	 Alignment		30.8	12	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)

12	c6qviB	Alignment		30.0	53	PDB header: dna binding protein Chain: B: PDB Molecule: comz; PDBTitle: crystal structure of competence-associated pilin comz from thermus2 thermophilus
13	c1d7mA	Alignment		27.9	18	PDB header: contractile protein Chain: A: PDB Molecule: cortexillin i; PDBTitle: coiled-coil dimerization domain from cortexillin i
14	c1gaxB	Alignment		27.1	18	PDB header: ligase/rna Chain: B: PDB Molecule: valyl-trna synthetase; PDBTitle: crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
15	c3lr6A	Alignment		25.8	9	PDB header: structural protein Chain: A: PDB Molecule: major ampullate spidroin 1; PDBTitle: self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
16	c2i3eA	Alignment		25.2	31	PDB header: hydrolase Chain: A: PDB Molecule: g-rich; PDBTitle: solution structure of catalytic domain of goldfish rich2 protein
17	c4mt4C	Alignment		24.8	13	PDB header: transport protein Chain: C: PDB Molecule: cmec; PDBTitle: crystal structure of the campylobacter jejuni cmec outer membrane2 channel
18	c5ah5B	Alignment		23.6	25	PDB header: ligase/rna Chain: B: PDB Molecule: leucine--trna ligase; PDBTitle: crystal structure of the ternary complex of agrobacterium2 radiobacter k84 agnb2 leurs-trna-leuams
19	c4mzvA	Alignment		23.0	22	PDB header: cell adhesion Chain: A: PDB Molecule: epithelial cell adhesion molecule; PDBTitle: crystal structure of extracellular part of human epcam
20	c1yc9A	Alignment		22.4	10	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein; PDBTitle: the crystal structure of the outer membrane protein vcec from the2 bacterial pathogen vibrio cholerae at 1.8 resolution
21	d1xmwa2	Alignment	not modelled	20.7	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
22	c3loeA	Alignment	not modelled	20.6	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (f28a mutant)
23	c3zplE	Alignment	not modelled	20.6	9	PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
24	d1grja1	Alignment	not modelled	20.3	22	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
25	c3lgoA	Alignment	not modelled	18.8	26	PDB header: protein binding Chain: A: PDB Molecule: protein slm4; PDBTitle: structure of gse1p, member of the gse/ego complex
26	c6b3oB	Alignment	not modelled	17.9	12	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
27	c2gvsA	Alignment	not modelled	17.9	19	PDB header: lipid binding protein Chain: A: PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
28	d1n26a1	Alignment	not modelled	17.8	45	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains

29	c4mdvB_	Alignment	not modelled	17.4	13	PDB header: metal binding protein Chain: B: PDB Molecule: annexin; PDBTitle: crystal structure of calcium-bound annexin (sm)1
30	c5aj3j_	Alignment	not modelled	17.1	28	PDB header: ribosome Chain: J: PDB Molecule: mitoribosomal protein us10m, mrps10; PDBTitle: structure of the small subunit of the mammalian mitoribosome
31	c6nzkB_	Alignment	not modelled	16.4	15	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
32	d1n8va_	Alignment	not modelled	16.2	15	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
33	c1sfeA_	Alignment	not modelled	15.9	16	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
34	c3jclC_	Alignment	not modelled	15.2	12	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
35	d1t3ua_	Alignment	not modelled	14.9	19	Fold: Cell division protein ZapA-like Superfamily: Cell division protein ZapA-like Family: Cell division protein ZapA-like
36	c1wkba_	Alignment	not modelled	14.4	20	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
37	c6hcyA_	Alignment	not modelled	14.4	20	PDB header: membrane protein Chain: A: PDB Molecule: metalloreductase steap4; PDBTitle: human steap4 bound to nadp, fad, heme and fe(iii)-nta.
38	d1alaa_	Alignment	not modelled	14.3	16	Fold: Annexin Superfamily: Annexin Family: Annexin
39	c4lb1B_	Alignment	not modelled	13.5	67	PDB header: antimicrobial protein Chain: B: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
40	c4lb1D_	Alignment	not modelled	13.5	67	PDB header: antimicrobial protein Chain: D: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
41	c4lb1E_	Alignment	not modelled	13.5	67	PDB header: antimicrobial protein Chain: E: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
42	c4lb1A_	Alignment	not modelled	13.5	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/f28a mutant
43	c5w7dA_	Alignment	not modelled	13.5	13	PDB header: hydrolase Chain: A: PDB Molecule: acyloxyacyl hydrolase; PDBTitle: murine acyloxyacyl hydrolase (aoah), s262a mutant
44	c3c8zB_	Alignment	not modelled	13.4	11	PDB header: ligase Chain: B: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
45	c3t4aG_	Alignment	not modelled	13.0	21	PDB header: immune system Chain: G: PDB Molecule: fibrinogen-binding protein; PDBTitle: structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
46	c4ariA_	Alignment	not modelled	12.8	25	PDB header: ligase/rna Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: ternary complex of e. coli leucyl-trna synthetase, trna(leu) and the2 benzoxaborole an2679 in the editing conformation
47	c1ileA_	Alignment	not modelled	12.7	20	PDB header: aminoacyl-trna synthetase Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: isoleucyl-trna synthetase
48	c6q8aA_	Alignment	not modelled	12.3	25	PDB header: ligase Chain: A: PDB Molecule: leucine--trna ligase; PDBTitle: neisseria gonorrhoeae leucyl-trna synthetase in complex with 5'-o-(n-2 (l-leucyl)-sulfamoyl)cytidine
49	c6b7nC_	Alignment	not modelled	12.1	11	PDB header: viral protein Chain: C: PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
50	c1obhA_	Alignment	not modelled	11.9	25	PDB header: synthetase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
51	c2w9yA_	Alignment	not modelled	11.8	17	PDB header: lipid transport Chain: A: PDB Molecule: fatty acid/retinol binding protein protein 7, PDBTitle: the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
52	d2fp1a1	Alignment	not modelled	11.8	13	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Secreted chorismate mutase-like
53	c3gfbB_	Alignment	not modelled	11.6	14	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
						PDB header: transferase

54	c5hujB_	Alignment	not modelled	11.3	15	Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nade from streptococcus pyogenes
55	c5nh1A_	Alignment	not modelled	10.9	19	PDB header: immune system Chain: A: PDB Molecule: gasdermin-d; PDBTitle: structure of the c-terminal domain of human gasdermin d
56	c4lb7B_	Alignment	not modelled	10.9	67	PDB header: antimicrobial protein Chain: B: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
57	c4lb7E_	Alignment	not modelled	10.9	67	PDB header: antimicrobial protein Chain: E: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
58	c4lb7D_	Alignment	not modelled	10.9	67	PDB header: antimicrobial protein Chain: D: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
59	c4lb7A_	Alignment	not modelled	10.9	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1) y16a/i20a/i25a/f28a2 mutant.
60	c4akxA_	Alignment	not modelled	10.9	33	PDB header: transport protein Chain: A: PDB Molecule: spsc;u; PDBTitle: structure of the heterodimeric complex exou-spsc from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
61	c6fikA_	Alignment	not modelled	10.6	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
62	c5x5bB_	Alignment	not modelled	10.6	9	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
63	c3t97A_	Alignment	not modelled	10.6	17	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
64	c2bytD_	Alignment	not modelled	10.6	25	PDB header: synthetase Chain: D: PDB Molecule: leucyl-trna synthetase; PDBTitle: thermus thermophilus leucyl-trna synthetase complexed with2 a trnaleu transcript in the post-editing conformation
65	c1wz2B_	Alignment	not modelled	10.4	20	PDB header: ligase/rna Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
66	c6iyoA_	Alignment	not modelled	10.3	21	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
67	c5gxyA_	Alignment	not modelled	10.3	22	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: crystal structure of endoglucanase celq from clostridium thermocellum2 complexed with cellobiose and tris
68	c5w78B_	Alignment	not modelled	10.0	16	PDB header: hydrolase Chain: B: PDB Molecule: acyloxyacyl hydrolase; PDBTitle: human acyloxyacyl hydrolase (aoah), proteolytically processed
69	c6af0P_	Alignment	not modelled	10.0	45	PDB header: transcription Chain: P: PDB Molecule: paf1 protein; PDBTitle: structure of ctr9, paf1 and cdc73 ternary complex from myceliophthora2 thermophila
70	c3tu3A_	Alignment	not modelled	9.9	39	PDB header: toxin/toxin chaperone Chain: A: PDB Molecule: exou chaperone; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
71	c3ziuA_	Alignment	not modelled	9.7	17	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
72	c2jy8A_	Alignment	not modelled	9.6	24	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-binding protein p62; PDBTitle: nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
73	c3a16C_	Alignment	not modelled	9.6	23	PDB header: lyase Chain: C: PDB Molecule: aldoxime dehydratase; PDBTitle: crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
74	c2qffA_	Alignment	not modelled	9.6	22	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of staphylococcal complement inhibitor
75	c2llkA_	Alignment	not modelled	9.4	32	PDB header: cell cycle, transcription Chain: A: PDB Molecule: cyclin-d-binding myb-like transcription factor 1; PDBTitle: solution nmr structure of the n-terminal myb-like 1 domain of the2 human cyclin-d-binding transcription factor 1 (hdmp1), northeast3 structural genomics consortium (nesg) target id hr8011a
76	d2k0bx1	Alignment	not modelled	9.4	39	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
77	c5wrvA_	Alignment	not modelled	9.4	41	PDB header: protein transport Chain: A: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: complex structure of human srp72/srp68
78	c2wuhB_	Alignment	not modelled	9.4	64	PDB header: receptor/peptide Chain: B: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
79	c2wuhC_	Alignment	not modelled	9.4	64	PDB header: receptor/peptide Chain: C: PDB Molecule: collagen peptide;

79	c2w0nc	Alignment	not modelled	9.4	04	PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
80	d1h3na3	Alignment	not modelled	9.4	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
81	c2q25C	Alignment	not modelled	9.3	23	PDB header: virus,hydrolase/rna Chain: C: PDB Molecule: protein alpha; PDBTitle: flock house virus coat protein d75n mutant
82	c6n9oB	Alignment	not modelled	9.2	19	PDB header: immune system Chain: B: PDB Molecule: gasdermin-d; PDBTitle: crystal structure of human gsdmd
83	c2pm4B	Alignment	not modelled	9.0	67	PDB header: antimicrobial protein Chain: B: PDB Molecule: neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha) PDBTitle: human alpha-defensin 1 (multiple arg->lys mutant)
84	c2pm4A	Alignment	not modelled	9.0	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha) PDBTitle: human alpha-defensin 1 (multiple arg->lys mutant)
85	d1nfpA	Alignment	not modelled	8.9	19	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
86	c2k4fA	Alignment	not modelled	8.9	42	PDB header: immune system, signaling protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 epsilon chain; PDBTitle: mouse cd3epsilon cytoplasmic tail
87	c6nb3B	Alignment	not modelled	8.9	8	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
88	c5eqwE	Alignment	not modelled	8.8	35	PDB header: structural protein Chain: E: PDB Molecule: putative major coat protein; PDBTitle: structure of the major structural protein d135 of acidianus tailed2 spindle virus (atsv)
89	c3wo1B	Alignment	not modelled	8.8	27	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
90	c2lrmB	Alignment	not modelled	8.7	19	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein ymgd; PDBTitle: assignment and structure of e coli periplasmic protein ymgd
91	d1fyja	Alignment	not modelled	8.7	26	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: a tRNA synthase domain
92	c3iv1F	Alignment	not modelled	8.6	20	PDB header: hydrolase Chain: F: PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
93	c4q16C	Alignment	not modelled	8.6	15	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
94	c5xlrC	Alignment	not modelled	8.5	9	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
95	c5frgA	Alignment	not modelled	8.4	19	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
96	c4mhlA	Alignment	not modelled	8.0	33	PDB header: protein binding Chain: A: PDB Molecule: interleukin-11; PDBTitle: the crystal structure of human interleukin-11
97	d1kpsb	Alignment	not modelled	7.9	21	Fold: alpha-alpha superhelix Superfamily: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain Family: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain
98	c6n9nB	Alignment	not modelled	7.9	15	PDB header: immune system Chain: B: PDB Molecule: gasdermin-d; PDBTitle: crystal structure of murine gsdmd
99	d2oa5a1	Alignment	not modelled	7.9	19	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like