


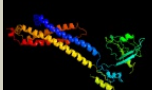






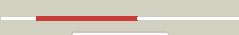


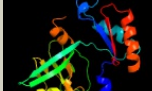







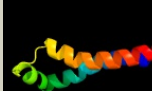


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2563_(-)_2882300_2883349
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	0b42e683bedcfb80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ws4A_	 Alignment		100.0	21	PDB header: membrane protein Chain: A; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
2	c5nikK_	 Alignment		100.0	20	PDB header: transport protein Chain: K; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
3	c5xu1M_	 Alignment		100.0	15	PDB header: transport protein Chain: M; PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
4	c5lj7B_	 Alignment		100.0	18	PDB header: transport protein Chain: B; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
5	c5naaB_	 Alignment		98.3	17	PDB header: protein transport Chain: B; PDB Molecule: lipoprotein-releasing system transmembrane protein lolc; PDBTitle: lipoprotein-releasing system transmembrane protein lolc
6	c5f9qA_	 Alignment		97.8	15	PDB header: membrane protein Chain: A; PDB Molecule: macrolide export atp-binding/permease protein yknz; PDBTitle: crystal structure of the extracellular domain of noncanonic abc-type2 transporter yknz from gram-positive bacteria
7	c5udfB_	 Alignment		97.8	17	PDB header: protein transport Chain: B; PDB Molecule: lipoprotein-releasing system transmembrane protein lolc; PDBTitle: structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lolc from acinetobacter baumannii
8	c3ftjA_	 Alignment		97.4	14	PDB header: hydrolase Chain: A; PDB Molecule: macrolide export atp-binding/permease protein PDBTitle: crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
9	c5c59F_	 Alignment		96.9	21	PDB header: hydrolase Chain: F; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of the periplasmic region of macb from e. coli
10	c5c59G_	 Alignment		94.8	17	PDB header: hydrolase Chain: G; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of the periplasmic region of macb from e. coli
11	c5x5yF_	 Alignment		90.9	22	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex

12	c5I75F_	Alignment		89.9	21	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
13	c5x5yG_	Alignment		87.3	18	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
14	c6mjpG_	Alignment		87.1	19	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
15	c6mjpF_	Alignment		84.9	18	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
16	c5I75G_	Alignment		84.2	19	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
17	c1ciiA_	Alignment		82.8	12	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
18	c2yvxD_	Alignment		76.1	18	PDB header: transport protein Chain: D; PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
19	d1cola_	Alignment		71.2	14	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
20	c3fewX_	Alignment		62.3	11	PDB header: immune system Chain: X; PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain
21	d2yvx3	Alignment	not modelled	46.3	19	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
22	c4aw6B_	Alignment	not modelled	40.1	11	PDB header: hydrolase Chain: B; PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
23	c3is6A_	Alignment	not modelled	39.0	18	PDB header: transport protein Chain: A; PDB Molecule: putative permease protein, abc transporter; PDBTitle: the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a
24	c4ymuC_	Alignment	not modelled	38.9	12	PDB header: protein binding/transport protein Chain: C; PDB Molecule: abc-type amino acid transport system, permease component; PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps
25	c3ltiA_	Alignment	not modelled	37.7	25	PDB header: transferase Chain: A; PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains
26	c6btmD_	Alignment	not modelled	35.2	12	PDB header: membrane protein Chain: D; PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
27	c4av3A_	Alignment	not modelled	26.5	17	PDB header: hydrolase Chain: A; PDB Molecule: k(+)-stimulated pyrophosphate-energized sodium pump; PDBTitle: crystal structure of thermotoga maritima sodium pumping membrane2 integral pyrophosphatase with metal ions in active site PDB header: viral protein

28	c5v2sA_	Alignment	not modelled	22.0	12	Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
29	c4kbmA_	Alignment	not modelled	20.3	25	PDB header: transferase/transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of the mtb card/rnap beta subunit b1-b2 domains complex
30	c2cwbA_	Alignment	not modelled	18.8	4	PDB header: protein binding Chain: A: PDB Molecule: chimera of immunoglobulin g binding protein g PDBTitle: solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
31	c1wr1B_	Alignment	not modelled	17.7	4	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like protein dsk2; PDBTitle: the complex structure of dsk2p uba with ubiquitin
32	d2bwba1	Alignment	not modelled	16.7	4	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
33	d2dnaa1	Alignment	not modelled	16.6	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
34	d2r6gg1	Alignment	not modelled	16.4	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
35	c2dahA_	Alignment	not modelled	16.3	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-3; PDBTitle: solution structure of the c-terminal uba domain in the2 human ubiquilin 3
36	c2dnaA_	Alignment	not modelled	15.2	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
37	d1veja1	Alignment	not modelled	14.9	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
38	d2daha1	Alignment	not modelled	14.7	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
39	c6f0kD_	Alignment	not modelled	13.6	12	PDB header: membrane protein Chain: D: PDB Molecule: actcd; PDBTitle: alternative complex iii
40	c5a43B_	Alignment	not modelled	13.2	19	PDB header: transport protein Chain: B: PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
41	c1a87A_	Alignment	not modelled	12.5	20	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
42	d1a87a_	Alignment	not modelled	12.5	20	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
43	c2jy5A_	Alignment	not modelled	12.1	12	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
44	c4r4eA_	Alignment	not modelled	11.3	21	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
45	c2i88A_	Alignment	not modelled	11.2	12	PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin e1
46	c5a40C_	Alignment	not modelled	11.1	16	PDB header: transport protein Chain: C: PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
47	c2v50A_	Alignment	not modelled	11.0	17	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
48	c5xjyA_	Alignment	not modelled	10.9	14	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
49	c5jefA_	Alignment	not modelled	10.3	15	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
50	d1dv0a_	Alignment	not modelled	9.9	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
51	d1rh1a2	Alignment	not modelled	9.9	13	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
52	d1q08a_	Alignment	not modelled	9.7	29	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
53	c2ndjA_	Alignment	not modelled	9.0	21	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
54	c5klbB_	Alignment	not modelled	8.5	6	PDB header: transport protein Chain: B: PDB Molecule: ion transport protein; PDBTitle: crystal structure of the cavab voltage-gated calcium

						channel(wild-2 type, 2.7a)
55	c6owsB_	Alignment	not modelled	8.4	17	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
56	c6csxA_	Alignment	not modelled	8.3	20	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
57	d1ciaa1	Alignment	not modelled	8.2	16	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
58	c5oy0M_	Alignment	not modelled	8.1	5	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
59	c5oy09_	Alignment	not modelled	8.1	5	PDB header: photosynthesis Chain: 9: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
60	c4l6v7_	Alignment	not modelled	8.1	5	PDB header: electron transport Chain: 7: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
61	c6hqbm_	Alignment	not modelled	8.1	5	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: monomeric cyanobacterial photosystem i
62	c5oy0m_	Alignment	not modelled	8.1	5	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
63	c4l6vM_	Alignment	not modelled	8.1	5	PDB header: electron transport Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
64	c2jpcA_	Alignment	not modelled	8.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
65	c2k29A_	Alignment	not modelled	7.9	19	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
66	c5mg3D_	Alignment	not modelled	7.9	14	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secD; PDBTitle: em fitted model of bacterial holo-translocon
67	c4il3B_	Alignment	not modelled	7.8	14	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
68	c2k21A_	Alignment	not modelled	7.7	0	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
69	c6c90B_	Alignment	not modelled	7.7	13	PDB header: hydrolase/rna binding protein Chain: B: PDB Molecule: zinc finger cchc domain-containing protein 8; PDBTitle: human mtr4 helicase in complex with zchc8-ctd
70	c4r24B_	Alignment	not modelled	7.7	41	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
71	c5gasN_	Alignment	not modelled	7.6	12	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
72	c4fxeB_	Alignment	not modelled	7.5	19	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
73	d2i76a1	Alignment	not modelled	7.5	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
74	d1oqya2	Alignment	not modelled	7.4	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
75	c6ic4H_	Alignment	not modelled	7.4	20	PDB header: protein transport Chain: H: PDB Molecule: abc transporter permease; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
76	c3idwA_	Alignment	not modelled	7.2	13	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
77	c2lorA_	Alignment	not modelled	7.1	12	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 141; PDBTitle: backbone structure of human membrane protein tmem141
78	c3gp4B_	Alignment	not modelled	7.1	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
79	c3sztB_	Alignment	not modelled	7.0	22	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
80	c2jnhA_	Alignment	not modelled	6.8	14	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of the uba domain from cbl-b

81	c2ksfA	Alignment	not modelled	6.7	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein kdpd; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor kdpd, center for structures of membrane proteins (csm)3 target 4312c
82	c3vw4B	Alignment	not modelled	6.5	17	PDB header: dna binding protein/dna Chain: B: PDB Molecule: rep; PDBTitle: crystal structure of the dna-binding domain of cole2-p9 rep in complex2 with the replication origin
83	c5fgnA	Alignment	not modelled	6.4	11	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
84	c5zazA	Alignment	not modelled	6.3	29	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
85	c4ev6E	Alignment	not modelled	6.3	15	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
86	c6ithA	Alignment	not modelled	6.2	16	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
87	c1hjpA	Alignment	not modelled	6.2	17	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
88	c2krfB	Alignment	not modelled	6.2	17	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
89	d1cuka1	Alignment	not modelled	6.2	14	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
90	c2kncA	Alignment	not modelled	6.1	9	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
91	c6jqsA	Alignment	not modelled	6.1	22	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
92	c4q2uM	Alignment	not modelled	6.1	7	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
93	c2m0qA	Alignment	not modelled	6.1	6	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
94	c2kncB	Alignment	not modelled	6.1	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
95	d1yioa1	Alignment	not modelled	5.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
96	c5tw1C	Alignment	not modelled	5.9	19	PDB header: transcription activator/transferase/dna Chain: C: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
97	d1l3a1	Alignment	not modelled	5.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
98	d1fsea	Alignment	not modelled	5.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
99	c5crlA	Alignment	not modelled	5.8	21	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 mer in complex2 with mercury (ii)