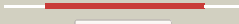



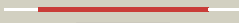





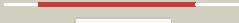

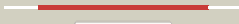











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3063_(cstA)_3427240_3429516
Date	Thu Aug 8 16:20:24 BST 2019
Unique Job ID	0b0c3ceb7b88f4cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wgvC_	 Alignment		98.7	13	PDB header: transport protein Chain: C; PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
2	c4wgvA_	 Alignment		98.7	13	PDB header: transport protein Chain: A; PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
3	c3giaA_	 Alignment		97.5	16	PDB header: transport protein Chain: A; PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
4	c2jlnA_	 Alignment		97.4	12	PDB header: membrane protein Chain: A; PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
5	c5oqtA_	 Alignment		97.2	14	PDB header: transport protein Chain: A; PDB Molecule: amino acid transporter; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
6	c6csfC_	 Alignment		97.0	19	PDB header: membrane protein Chain: C; PDB Molecule: sodium/alanine symporter agcs; PDBTitle: crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
7	c2xq2A_	 Alignment		96.6	14	PDB header: transport protein Chain: A; PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
8	c5nvaA_	 Alignment		96.4	10	PDB header: membrane protein Chain: A; PDB Molecule: putative sodium:solute symporter; PDBTitle: substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
9	c5m87A_	 Alignment		96.1	12	PDB header: transport protein Chain: A; PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
10	c6irtB_	 Alignment		95.9	12	PDB header: membrane protein Chain: B; PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch
11	c3lrcC_	 Alignment		94.5	14	PDB header: transport protein Chain: C; PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)

12	c6f2wA_	Alignment		94.2	14	PDB header: transport protein Chain: A: PDB Molecule: putative amino acid/polyamine transport protein; PDBTitle: bacterial asc transporter crystal structure in open to in conformation
13	c3dh4A_	Alignment		94.0	13	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
14	c6jmqa_	Alignment		92.4	11	PDB header: membrane protein/immune system Chain: A: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: lat1-cd98hc complex bound to mem-108 fab
15	c5kteA_	Alignment		84.0	16	PDB header: transport protein/immune system Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
16	c4px7A_	Alignment		57.5	8	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pgpb
17	c6c08C_	Alignment		49.6	11	PDB header: membrane protein Chain: C: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
18	c4g29A_	Alignment		44.4	38	PDB header: protein binding Chain: A: PDB Molecule: secreted effector protein ssei; PDBTitle: structure of the catalytic domain of the salmonella virulence factor2 ssei
19	c6nplA_	Alignment		42.8	13	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride) PDBTitle: cryo-em structure of nkcc1
20	c4djiA_	Alignment		40.5	12	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
21	c5mrwA_	Alignment	not modelled	39.2	10	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase potassium-binding subunit; PDBTitle: structure of the kdpfabc complex
22	c6btmD_	Alignment	not modelled	35.5	14	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
23	c3a8qB_	Alignment	not modelled	33.4	70	PDB header: signaling protein Chain: B: PDB Molecule: t-lymphoma invasion and metastasis-inducing PDBTitle: low-resolution crystal structure of the tiam2 phcccx domain
24	c6hwhX_	Alignment	not modelled	33.4	23	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
25	c3a8nA_	Alignment	not modelled	30.3	50	PDB header: signaling protein Chain: A: PDB Molecule: t-lymphoma invasion and metastasis-inducing PDBTitle: crystal structure of the tiam1 phcccx domain
26	c6btmC_	Alignment	not modelled	30.1	17	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
27	c2k9pA_	Alignment	not modelled	29.0	26	PDB header: membrane protein Chain: A: PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles
28	c6c08F_	Alignment	not modelled	25.5	10	PDB header: membrane protein Chain: F: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state

29	c2bbjB	Alignment	not modelled	24.7	14	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
30	c3pl0B	Alignment	not modelled	24.6	33	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
31	d1rh5a	Alignment	not modelled	24.4	15	Fold: Preprotein translocase SecY subunit Superfamily: Preprotein translocase SecY subunit Family: Preprotein translocase SecY subunit
32	c3hd6A	Alignment	not modelled	23.8	23	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
33	c4o65A	Alignment	not modelled	23.7	47	PDB header: oxidoreductase Chain: A: PDB Molecule: putative archaeal ammonia monooxygenase subunit b; PDBTitle: crystal structure of the cupredoxin domain of amob from nitrosocaldus2 yellowstonii
34	c3zy6A	Alignment	not modelled	22.7	27	PDB header: transferase Chain: A: PDB Molecule: putative gdp-fucose protein o-fucosyltransferase 1; PDBTitle: crystal structure of pofut1 in complex with gdp-fucose (crystal-form-2 ii)
35	c5nikK	Alignment	not modelled	21.1	19	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
36	c2wwbA	Alignment	not modelled	20.4	16	PDB header: ribosome Chain: A: PDB Molecule: protein transport protein sec61 subunit alpha isoform 1; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
37	d1rp4a	Alignment	not modelled	19.6	30	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
38	c2wwaA	Alignment	not modelled	19.4	19	PDB header: ribosome Chain: A: PDB Molecule: sec sixty-one protein homolog; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
39	c6n3qA	Alignment	not modelled	18.5	15	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec61; PDBTitle: cryo-em structure of the yeast sec complex
40	c5jnoA	Alignment	not modelled	18.5	12	PDB header: cell cycle Chain: A: PDB Molecule: ben domain-containing protein 3; PDBTitle: crystal structure of the bd1-ntrp complex from bend3 and pich
41	c3b9yA	Alignment	not modelled	18.4	31	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
42	c5ws4A	Alignment	not modelled	18.1	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
43	c4p6vB	Alignment	not modelled	18.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit b; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
44	c2jo1A	Alignment	not modelled	17.8	17	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
45	c4atbB	Alignment	not modelled	16.9	21	PDB header: immune system Chain: B: PDB Molecule: interleukin enhancer-binding factor 3; PDBTitle: crystal structure of the nf90-nf45 dimerisation domain2 complex with ctp
46	c5o4uK	Alignment	not modelled	16.8	24	PDB header: cell adhesion Chain: K: PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus
47	d2bfdb2	Alignment	not modelled	16.1	4	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
48	c4p6vC	Alignment	not modelled	16.1	11	PDB header: oxidoreductase Chain: C: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit c; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
49	c5z1lL	Alignment	not modelled	15.2	24	PDB header: protein fibril Chain: L: PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanococcus maripaludis archaeillum
50	c2l8sA	Alignment	not modelled	14.0	23	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
51	d1qs0b2	Alignment	not modelled	13.6	19	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
52	d1s6la1	Alignment	not modelled	13.5	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
53	c5yu1M	Alignment	not modelled	13.4	22	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae;

53	c3x01M_	Alignment	not modelled	13.4	23	PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
54	d1oqja_	Alignment	not modelled	13.4	27	Fold: SAND domain-like Superfamily: SAND domain-like Family: SAND domain
55	c2vy2A_	Alignment	not modelled	13.3	21	PDB header: transcription Chain: A: PDB Molecule: protein leafy; PDBTitle: structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
56	c5w6yB_	Alignment	not modelled	13.3	8	PDB header: biosynthetic protein,isomerase Chain: B: PDB Molecule: chorismate mutase; PDBTitle: physcomitrella patens chorismate mutase
57	c1yewl_	Alignment	not modelled	13.2	40	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
58	d1fasa_	Alignment	not modelled	13.1	40	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
59	d2fug6l	Alignment	not modelled	13.1	36	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nqo6-like
60	d1h5pa_	Alignment	not modelled	13.0	27	Fold: SAND domain-like Superfamily: SAND domain-like Family: SAND domain
61	c3eamB_	Alignment	not modelled	13.0	17	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: glr4197 protein; PDBTitle: an open-pore structure of a bacterial pentameric ligand-2 gated ion channel
62	c3a0hj_	Alignment	not modelled	12.9	36	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
63	d2axtj1	Alignment	not modelled	12.9	36	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
64	d1afra_	Alignment	not modelled	12.8	30	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
65	c5tfyl_	Alignment	not modelled	12.7	24	PDB header: cell adhesion Chain: J: PDB Molecule: flagellin; PDBTitle: the archaeal flagellum of methanospirillum hungatei strain jf1.
66	c4wepA_	Alignment	not modelled	12.6	17	PDB header: transport protein Chain: A: PDB Molecule: putative osmoprotectant uptake system substrate-binding PDBTitle: apo yehz from escherichia coli
67	c3rfri_	Alignment	not modelled	12.5	40	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
68	d1ufna_	Alignment	not modelled	12.4	20	Fold: SAND domain-like Superfamily: SAND domain-like Family: SAND domain
69	c3iymA_	Alignment	not modelled	12.4	23	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: backbone trace of the capsid protein dimer of a fungal partitivirus2 from electron cryomicroscopy and homology modeling
70	c2m0qA_	Alignment	not modelled	12.4	12	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
71	d1v54c_	Alignment	not modelled	12.3	14	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
72	d2axtc1	Alignment	not modelled	12.0	18	Fold: Photosystem II antenna protein-like Superfamily: Photosystem II antenna protein-like Family: Photosystem II antenna protein-like
73	c2axtc_	Alignment	not modelled	12.0	18	PDB header: electron transport Chain: C: PDB Molecule: photosystem ii cp43 protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
74	c5lj7B_	Alignment	not modelled	11.8	19	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)
75	c2ktlA_	Alignment	not modelled	11.3	20	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mtyrrs of a. nidulans
76	d1lk6a2	Alignment	not modelled	11.1	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
77	c3jadC_	Alignment	not modelled	11.0	17	PDB header: signaling protein/antagonist Chain: C: PDB Molecule: glycine receptor subunit alphaz1; PDBTitle: structure of alpha-1 glycine receptor by single particle electron2 cryo-microscopy, strychnine-bound state
78	c3chxE_	Alignment	not modelled	10.9	40	PDB header: membrane protein Chain: E: PDB Molecule: pmob; PDBTitle: crystal structure of methyloinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
79	c2kncA_	Alignment	not modelled	10.8	55	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaiiB-beta3 transmembrane-

						cytoplasmic2 heterocomplex
80	c3ahrA_	Alignment	not modelled	10.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
81	c3v69A_	Alignment	not modelled	10.7	8	PDB header: protein binding Chain: A: PDB Molecule: protein filia; PDBTitle: filia-n crystal structure
82	c3rgbA_	Alignment	not modelled	10.4	40	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
83	c4n7wA_	Alignment	not modelled	10.2	11	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
84	c2ndjA_	Alignment	not modelled	10.1	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
85	d5csma_	Alignment	not modelled	9.9	8	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Allosteric chorismate mutase
86	d1nekd_	Alignment	not modelled	9.7	20	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
87	d2ozlb2_	Alignment	not modelled	9.7	14	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
88	c6hwhb_	Alignment	not modelled	9.7	12	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
89	c5mdxX_	Alignment	not modelled	9.6	20	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
90	c5mdxx_	Alignment	not modelled	9.6	20	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
91	c4wala_	Alignment	not modelled	9.5	21	PDB header: protein binding/rna Chain: A: PDB Molecule: branchpoint-bridging protein; PDBTitle: crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
92	c6h3pB_	Alignment	not modelled	9.4	4	PDB header: plant protein Chain: B: PDB Molecule: chorismate mutase; PDBTitle: crystal structure of the cytoplasmic chorismate mutase from zea mays
93	c4kmfA_	Alignment	not modelled	9.4	29	PDB header: transferase/dna Chain: A: PDB Molecule: interferon-inducible and double-stranded-dependent eif- PDBTitle: crystal structure of zalpha domain from carassius auratus pkz in2 complex with z-dna
94	c2lnhA_	Alignment	not modelled	9.2	20	PDB header: signaling protein/protein binding Chain: A: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
95	c4jkvA_	Alignment	not modelled	9.2	9	PDB header: membrane protein Chain: A: PDB Molecule: soluble cytochrome b562, smoothed homolog; PDBTitle: structure of the human smoothed 7tm receptor in complex with an2 antitumor agent
96	c4ppuA_	Alignment	not modelled	9.1	12	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase 1, chloroplastic; PDBTitle: crystal structure of atcm1 with tyrosine bound in allosteric site
97	c2k21A_	Alignment	not modelled	9.0	15	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
98	d2yrka1_	Alignment	not modelled	8.9	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
99	c5y9pA_	Alignment	not modelled	8.8	67	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: staphylococcus aureus rnase hii