

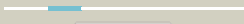









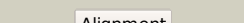







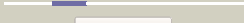



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2571c_(-) _2894903_2895970
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	a5688d70f55e3b4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5nvaA_	 Alignment		60.3	14	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
2	c6drhC_	 Alignment		37.8	17	PDB header: toxin Chain: C: PDB Molecule: adp-ribosyl-(dinitrogen reductase) hydrolase; PDBTitle: adp-ribosyltransferase toxin/immunity pair
3	c5khnB_	 Alignment		30.3	13	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
4	c3hfwA_	 Alignment		29.3	11	PDB header: hydrolase Chain: A: PDB Molecule: protein adp-ribosylarginine hydrolase; PDBTitle: crystal structure of human adp-ribosylhydrolase 1 (harh1)
5	d1otsa_	 Alignment		28.3	13	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
6	c2ht2B_	 Alignment		26.4	13	PDB header: membrane protein Chain: B: PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
7	c6ithA_	 Alignment		22.1	25	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
8	c6ajjA_	 Alignment		20.1	17	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
9	c2l35B_	 Alignment		19.8	50	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
10	c2l34A_	 Alignment		19.4	50	PDB header: protein binding Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
11	c4wo1A_	 Alignment		19.4	50	PDB header: signaling protein Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase

12	c2l34B_	Alignment		19.4	50	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
13	c4wo1D_	Alignment		18.4	50	PDB header: signaling protein Chain: D: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
14	c4wo1A_	Alignment		18.4	50	PDB header: signaling protein Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
15	c4wo1B_	Alignment		18.4	50	PDB header: signaling protein Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
16	c4wo1C_	Alignment		18.4	50	PDB header: signaling protein Chain: C: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
17	c6csxA_	Alignment		18.4	16	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
18	c6g1qA_	Alignment		18.3	22	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribosylhydrolase like 2; PDBTitle: adp-ribosylserine hydrolase arh3 of latimeria chalumnae in complex2 with adp-ribose
19	c4wo1C_	Alignment		18.0	50	PDB header: signaling protein Chain: C: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
20	c4wo1B_	Alignment		18.0	50	PDB header: signaling protein Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
21	c2yvxD_	Alignment	not modelled	17.5	19	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
22	c3g9dB_	Alignment	not modelled	15.2	28	PDB header: hydrolase Chain: B: PDB Molecule: dinitrogenase reductase activating PDBTitle: crystal structure glycohydrolase
23	c2wocA_	Alignment	not modelled	14.3	28	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribosyl-[dinitrogen reductase] glycohydrolase; PDBTitle: crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
24	c3nd0A_	Alignment	not modelled	13.4	14	PDB header: transport protein Chain: A: PDB Molecule: sll0855 protein; PDBTitle: x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
25	c2qyB_	Alignment	not modelled	12.6	27	PDB header: hydrolase Chain: B: PDB Molecule: poly(adp-ribose) glycohydrolase arh3; PDBTitle: crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
26	c6iu3A_	Alignment	not modelled	12.5	11	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
27	d1j4na_	Alignment	not modelled	12.4	10	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
28	c2yzwA_	Alignment	not modelled	12.0	26	PDB header: hydrolase Chain: A: PDB Molecule: adp-ribosylglycohydrolase; PDBTitle: adp-ribosylglycohydrolase-related protein complex

29	d1fx8a_	Alignment	not modelled	11.7	17	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
30	c1ldaA_	Alignment	not modelled	11.7	17	PDB header: transport protein Chain: A: PDB Molecule: glycerol uptake facilitator protein; PDBTitle: crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
31	c4px7A_	Alignment	not modelled	11.5	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pggb
32	d2f1ka1	Alignment	not modelled	11.5	14	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
33	c2b6pA_	Alignment	not modelled	11.4	12	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like PDB header: transferase Chain: A: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles
34	d2g5ca1	Alignment	not modelled	11.3	5	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like PDB header: transferase Chain: B: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles
35	c2n90A_	Alignment	not modelled	11.2	22	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
36	c2n90B_	Alignment	not modelled	11.2	22	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
37	c2mpnB_	Alignment	not modelled	10.8	23	PDB header: phosphate-binding protein Chain: A: PDB Molecule: putative phou-like phosphate regulatory protein; PDBTitle: crystal structure of putative phou-like phosphate regulatory protein2 (bt4638) from bacteroides thetaiotaomicron vpi-5482 at 1.93 a3 resolution
38	c2mpnA_	Alignment	not modelled	10.8	23	PDB header: proton transport Chain: Q: PDB Molecule: proton-translocating nadh-quinone dehydrogenase subunit q PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
39	c3l39A_	Alignment	not modelled	10.8	7	Fold: ADP-ribosylglycohydrolase Superfamily: ADP-ribosylglycohydrolase Family: ADP-ribosylglycohydrolase
40	c6humQ_	Alignment	not modelled	10.8	19	PDB header: membrane protein Chain: A: PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2
41	d1t5ja_	Alignment	not modelled	10.7	29	PDB header: protein binding Chain: A: PDB Molecule: dap12-nkg2c_tm; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
42	c6gctA_	Alignment	not modelled	10.5	15	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
43	c2l35A_	Alignment	not modelled	9.9	50	PDB header: membrane protein Chain: D: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
44	c4mt1A_	Alignment	not modelled	9.1	13	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
45	c6cfwD_	Alignment	not modelled	9.0	17	PDB header: transport protein Chain: A: PDB Molecule: aquaporin-10; PDBTitle: crystal structure of human aqp10
46	c3zq6D_	Alignment	not modelled	9.0	23	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
47	c6f7hA_	Alignment	not modelled	8.9	19	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
48	d1oqwa_	Alignment	not modelled	8.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	c2xq2A_	Alignment	not modelled	8.8	16	PDB header: apoptosis Chain: B: PDB Molecule: df4; PDBTitle: human bfl-1 in complex with the designed peptide df4
50	d1ihua1	Alignment	not modelled	8.8	31	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
51	c6mbcB_	Alignment	not modelled	8.6	13	PDB header: unknown function Chain: A: PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
52	d1y0ya2	Alignment	not modelled	8.6	47	PDB header: unknown function Chain: A: PDB Molecule: rpfr; PDBTitle: cronobacter turicensis rpfr quorum-sensing receptor rpff
53	c6bs3A_	Alignment	not modelled	8.5	31	
54	c6dgaA_	Alignment	not modelled	8.5	9	

						interaction2 domain
55	d1kpla_	Alignment	not modelled	8.3	10	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
56	c3kqjB_	Alignment	not modelled	8.2	38	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
57	c6eikE_	Alignment	not modelled	8.1	17	PDB header: de novo protein Chain: E: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
58	d1ihua2	Alignment	not modelled	8.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
59	c1p58F_	Alignment	not modelled	7.9	10	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
60	c1p58E_	Alignment	not modelled	7.9	10	PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
61	c6eznE_	Alignment	not modelled	7.8	29	PDB header: membrane protein Chain: E: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
62	c2wooC_	Alignment	not modelled	7.8	23	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
63	c4pfsA_	Alignment	not modelled	7.7	36	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from 2 mycobacterium smegmatis
64	c4q25B_	Alignment	not modelled	7.7	11	PDB header: unknown function Chain: B: PDB Molecule: phosphate-specific transport system accessory protein phou PDBTitle: crystal structure of phou from pseudomonas aeruginosa
65	d2i9ca1	Alignment	not modelled	7.6	22	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: RPA1889-like
66	c6eikA_	Alignment	not modelled	7.6	17	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
67	c6eikC_	Alignment	not modelled	7.6	17	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
68	c6eikB_	Alignment	not modelled	7.6	17	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
69	c6eikG_	Alignment	not modelled	7.6	17	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
70	c6eikD_	Alignment	not modelled	7.6	17	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
71	c6eikF_	Alignment	not modelled	7.6	17	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
72	c3sokB_	Alignment	not modelled	7.6	9	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
73	c6bs5B_	Alignment	not modelled	7.5	31	PDB header: unknown function Chain: B: PDB Molecule: anion transporter; PDBTitle: crystal structure of amp-pnp-bound bacterial get3-like a and b in 2 mycobacterium tuberculosis
74	d2pila_	Alignment	not modelled	7.4	4	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
75	c2lzsE_	Alignment	not modelled	7.4	14	PDB header: protein transport Chain: E: PDB Molecule: sec-independent protein translocase protein tata; PDBTitle: tata oligomer
76	c3endA_	Alignment	not modelled	7.4	7	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the 4 nitrogenase fe protein
77	c3ug7D_	Alignment	not modelled	7.3	29	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
78	c6nhwD_	Alignment	not modelled	7.3	37	PDB header: immune system Chain: D: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
79	c3ibgF_	Alignment	not modelled	7.2	31	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
80	d2yvxa3	Alignment	not modelled	7.2	19	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like

81	c3jd8A_	Alignment	not modelled	7.1	16	PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
82	c2m7gA_	Alignment	not modelled	7.0	14	PDB header: cell adhesion, structural protein, elect Chain: A: PDB Molecule: geopilin domain 1 protein; PDBTitle: structure of the type iva major pilin from the electrically conductive2 bacterial nanowires of geobacter sulfurreducens
83	c4k0eA_	Alignment	not modelled	7.0	18	PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
84	c5cukA_	Alignment	not modelled	6.9	17	PDB header: cell invasion Chain: A: PDB Molecule: ruler protein; PDBTitle: crystal structure of the pscp ss domain
85	c2wojD_	Alignment	not modelled	6.9	15	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
86	c5jkiA_	Alignment	not modelled	6.8	15	PDB header: hydrolase Chain: A: PDB Molecule: putative lipid phosphate phosphatase yodm; PDBTitle: crystal structure of the first transmembrane pap2 type2 phosphatidylglycerolphosphate phosphatase from bacillus subtilis
87	c4b03D_	Alignment	not modelled	6.8	10	PDB header: virus Chain: D: PDB Molecule: dengue virus 1 prm protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
88	c4k0eC_	Alignment	not modelled	6.8	16	PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
89	d1ymga1	Alignment	not modelled	6.7	13	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
90	c1ymgA_	Alignment	not modelled	6.7	13	PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: the channel architecture of aquaporin o at 2.2 angstrom resolution
91	c2ph1A_	Alignment	not modelled	6.7	29	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
92	d1k8ib2	Alignment	not modelled	6.6	30	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
93	c3dh4A_	Alignment	not modelled	6.6	14	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
94	c6akmB_	Alignment	not modelled	6.6	18	PDB header: protein binding Chain: B: PDB Molecule: sarcolemmal membrane-associated protein; PDBTitle: crystal structure of slmap-sike1 complex
95	c2ki9A_	Alignment	not modelled	6.6	27	PDB header: membrane protein Chain: A: PDB Molecule: cannabinoid receptor 2; PDBTitle: human cannabinoid receptor-2 helix 6
96	c5xj6A_	Alignment	not modelled	6.4	10	PDB header: transferase Chain: A: PDB Molecule: glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of psls (ygih), an integral membrane glycerol 3-2 phosphate acyltransferase - the glycerol 3-phosphate form
97	c5ireD_	Alignment	not modelled	6.3	24	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus
98	c1ijjA_	Alignment	not modelled	6.3	21	PDB header: signaling protein Chain: A: PDB Molecule: erbB-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbB-2 membrane spanning2 segment
99	c2oltB_	Alignment	not modelled	6.3	9	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a phou-like protein (so_3770) from shewanella2 oneidensis mr-1 at 2.00 a resolution