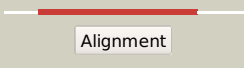

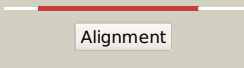
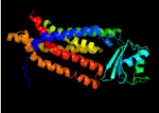
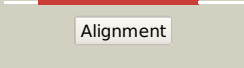

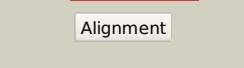
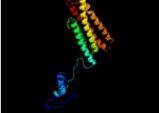
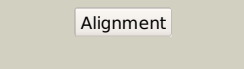

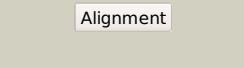

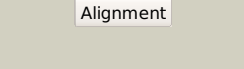

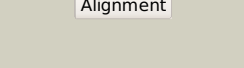

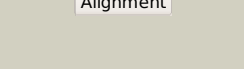

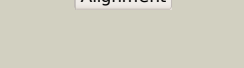

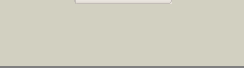


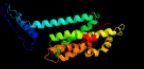







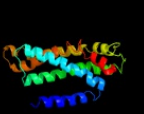

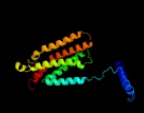

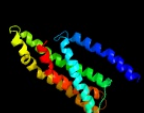







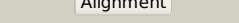
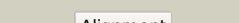

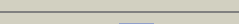



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2586c_(secF)_2912693_2914021
Date	Wed Aug 7 12:50:22 BST 2019
Unique Job ID	d07e601fbcc864d0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mg3F_	 Alignment		100.0	25	PDB header: chaperone Chain: F; PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
2	c3aqpB_	 Alignment		100.0	29	PDB header: membrane protein Chain: B; PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus
3	c5xamA_	 Alignment		100.0	27	PDB header: membrane protein Chain: A; PDB Molecule: protein translocase subunit secd; PDBTitle: crystal structure of secdf in i form at 4 a resolution
4	c5mg3D_	 Alignment		99.9	15	PDB header: chaperone Chain: D; PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
5	c5lq3F_	 Alignment		99.9	15	PDB header: transport protein Chain: F; PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
6	c2v50A_	 Alignment		99.9	14	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
7	c6owsB_	 Alignment		99.9	14	PDB header: membrane protein Chain: B; PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
8	c6ajjA_	 Alignment		99.8	16	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	c4mt1A_	 Alignment		99.8	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
10	c3k07A_	 Alignment		99.8	11	PDB header: transport protein Chain: A; PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
11	c4k0eA_	 Alignment		99.8	12	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

12	c6csxA	 Alignment		99.8	15	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
13	c1oy8A	 Alignment		99.8	15	PDB header: membrane protein Chain: A; PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
14	c5khnB	 Alignment		99.8	17	PDB header: membrane protein Chain: B; PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
15	d1iwga7	 Alignment		99.8	16	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
16	d1iwga8	 Alignment		99.8	20	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
17	c6dmoA	 Alignment		99.7	16	PDB header: protein binding Chain: A; PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
18	c4k0eC	 Alignment		99.7	17	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
19	c3jd8A	 Alignment		99.6	13	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
20	c2rrnA	 Alignment		99.5	18	PDB header: protein transport Chain: A; PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4
21	c5oonA	 Alignment	not modelled	82.0	15	PDB header: membrane protein Chain: A; PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca
22	c4a01B	 Alignment	not modelled	63.2	14	PDB header: hydrolase Chain: B; PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
23	c2bpa3	 Alignment	not modelled	38.6	46	PDB header: virus/dna Chain: 3; PDB Molecule: protein (subunit of bacteriophage phix174); PDBTitle: atomic structure of single-stranded dna bacteriophage2 phix174 and its functional implications
24	c6b2zf	 Alignment	not modelled	30.2	12	PDB header: membrane protein Chain: F; PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
25	c4hydA	 Alignment	not modelled	28.6	24	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a presenilin family intramembrane aspartate protease in2 c2221 space group
26	c6b8ht	 Alignment	not modelled	26.7	12	PDB header: membrane protein Chain: T; PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
27	c5xj6A	 Alignment	not modelled	26.2	20	PDB header: transferase Chain: A; PDB Molecule: glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of plsy (ygih), an integral membrane glycerol 3-2 phosphate acyltransferase - the glycerol 3-phosphate form
28	c1ciiA	 Alianment	not modelled	18.5	14	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia;

						PDBTitle: colicin ia
29	c3uz0A_	Alignment	not modelled	16.5	14	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiah and spoiiq complex
30	d1bg3a1	Alignment	not modelled	16.2	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
31	c6ib1B_	Alignment	not modelled	15.4	14	PDB header: immune system Chain: B: PDB Molecule: thioredoxin 1,beta-1 adrenergic receptor; PDBTitle: activated turkey beta1 adrenoceptor with bound agonist formoterol and2 nanobody nb80
32	c4yzfA_	Alignment	not modelled	14.5	11	PDB header: immune system Chain: A: PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the anion exchanger domain of human erythrocyte2 band 3
33	c3f1jA_	Alignment	not modelled	14.2	55	PDB header: viral protein Chain: A: PDB Molecule: matrix protein; PDBTitle: crystal structure of the borna disease virus matrix protein2 (bdv-m) reveals rna binding properties
34	c1w8xP_	Alignment	not modelled	13.9	20	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
35	c3tufA_	Alignment	not modelled	12.5	12	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
36	d1cola_	Alignment	not modelled	12.4	18	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
37	c4bj5A_	Alignment	not modelled	11.2	30	PDB header: transcription Chain: A: PDB Molecule: protein rif2; PDBTitle: crystal structure of rif2 in complex with the c-terminal domain of2 rap1 (rap1-rct)
38	c3fewX_	Alignment	not modelled	10.7	17	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
39	c2lx0A_	Alignment	not modelled	10.4	9	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
40	c4hitD_	Alignment	not modelled	10.1	67	PDB header: viral protein Chain: D: PDB Molecule: matrix protein; PDBTitle: crystal structure of h112w mutant of borna disease virus matrix2 protein
41	c5l22B_	Alignment	not modelled	10.1	9	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtd t1ss abc transporter
42	c3dl8D_	Alignment	not modelled	9.7	26	PDB header: protein transport Chain: D: PDB Molecule: sece; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
43	c3dl8C_	Alignment	not modelled	9.7	26	PDB header: protein transport Chain: C: PDB Molecule: sece; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
44	c5sv9B_	Alignment	not modelled	9.3	13	PDB header: transport protein Chain: B: PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
45	d1pgya_	Alignment	not modelled	8.7	25	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
46	d1o75a2	Alignment	not modelled	8.7	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Tp47 lipoprotein, middle and C-terminal domains Family: Tp47 lipoprotein, middle and C-terminal domains
47	c6k1hF_	Alignment	not modelled	8.7	25	PDB header: protein transport Chain: F: PDB Molecule: pts system mannose-specific eiid component; PDBTitle: structure of membrane protein
48	c2n1pA_	Alignment	not modelled	8.7	23	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
49	c6fkip_	Alignment	not modelled	8.4	17	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
50	c2mkaA_	Alignment	not modelled	8.2	14	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
51	c2mkaB_	Alignment	not modelled	8.2	14	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
52	c2mk9B_	Alignment	not modelled	8.2	14	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
53	c2mkaC_	Alignment	not modelled	8.2	14	PDB header: immune system Chain: C: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
54	c2mk9A_	Alignment	not modelled	8.2	14	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3;

54	c2mk9A	Alignment	not modelled	6.2	14	PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
55	c5fshA	Alignment	not modelled	7.8	43	PDB header: hydrolase Chain: A: PDB Molecule: csm6; PDBTitle: crystal structure of thermus thermophilus csm6
56	d1wh9a	Alignment	not modelled	7.6	8	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
57	c3qf4B	Alignment	not modelled	7.4	9	PDB header: transport protein Chain: B: PDB Molecule: uncharacterized abc transporter atp-binding protein PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
58	c5mkkB	Alignment	not modelled	7.3	13	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
59	c5u1dB	Alignment	not modelled	7.3	8	PDB header: transport protein Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
60	c5lj7B	Alignment	not modelled	7.3	8	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)
61	c4bhqA	Alignment	not modelled	7.3	30	PDB header: cell adhesion Chain: A: PDB Molecule: competence protein piln; PDBTitle: structure of the periplasmic domain of the piln type iv2 pilus biogenesis protein from thermus thermophilus
62	c3i0pA	Alignment	not modelled	7.2	26	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from entamoeba histolytica
63	c3k3gA	Alignment	not modelled	7.1	14	PDB header: transport protein Chain: A: PDB Molecule: urea transporter; PDBTitle: crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
64	c3aqaD	Alignment	not modelled	7.1	14	PDB header: membrane protein Chain: D: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export
65	d1ehkb2	Alignment	not modelled	7.0	28	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
66	c3qf4A	Alignment	not modelled	6.9	8	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
67	c6c14A	Alignment	not modelled	6.8	13	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
68	d1rh1a2	Alignment	not modelled	6.8	16	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
69	d1lgha	Alignment	not modelled	6.8	25	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
70	c5fgnA	Alignment	not modelled	6.6	7	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
71	d1txka1	Alignment	not modelled	6.6	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
72	c4y7jE	Alignment	not modelled	6.6	12	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
73	c1z2iA	Alignment	not modelled	6.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
74	c3mk7F	Alignment	not modelled	6.5	5	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
75	c5t4oj	Alignment	not modelled	6.5	9	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
76	c5sxpF	Alignment	not modelled	6.4	44	PDB header: signaling protein/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
77	c5nikK	Alignment	not modelled	6.4	14	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
78	c6rdu9	Alignment	not modelled	6.4	28	PDB header: proton transport Chain: 9: PDB Molecule: asa-9: polytomella f-atp synthase associated subunit 9;

						PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
79	d1uc8a1	Alignment	not modelled	6.3	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
80	c2bbjB_	Alignment	not modelled	6.3	12	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
81	c2kluA_	Alignment	not modelled	6.2	33	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
82	c2g8yB_	Alignment	not modelled	6.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
83	c5xyiG_	Alignment	not modelled	6.1	19	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6; PDBTitle: small subunit of trichomonas vaginalis ribosome
84	c1wtjB_	Alignment	not modelled	6.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: ureidoglycolate dehydrogenase; PDBTitle: crystal structure of delta1-piperidine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
85	d1pama3	Alignment	not modelled	6.0	20	Fold: Glycosyl hydrolase syring Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
86	c1pi8A_	Alignment	not modelled	5.9	32	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
87	c2gohA_	Alignment	not modelled	5.9	32	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
88	c1pi7A_	Alignment	not modelled	5.9	32	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
89	c2gofA_	Alignment	not modelled	5.9	32	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
90	c1pjeA_	Alignment	not modelled	5.9	32	PDB header: viral protein Chain: A: PDB Molecule: vpu protein; PDBTitle: structure of the channel-forming trans-membrane domain of2 virus protein "u"(vpu) from hiv-1
91	d1hkya_	Alignment	not modelled	5.9	45	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Pan module (APPLE domain)
92	c5sxpG_	Alignment	not modelled	5.8	44	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
93	c2jo1A_	Alignment	not modelled	5.8	21	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
94	c5hg1A_	Alignment	not modelled	5.8	31	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hexokinase-2; PDBTitle: crystal structure of human hexokinase 2 with cmpd 1, a c-2-substituted2 glucosamine
95	c1v9nA_	Alignment	not modelled	5.8	29	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structure of malate dehydrogenase from pyrococcus horikoshii ot3
96	d1czan3	Alignment	not modelled	5.8	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
97	d1jcb2	Alignment	not modelled	5.6	25	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
98	c1alga_	Alignment	not modelled	5.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: p11; PDBTitle: solution structure of an hgr inhibitor, nmr, 10 structures
99	c1yg0A_	Alignment	not modelled	5.6	8	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori