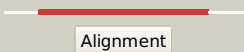

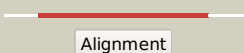

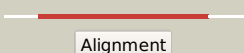

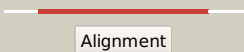




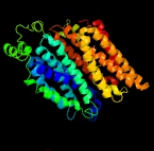
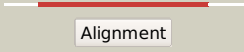
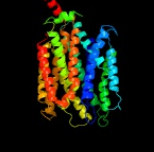
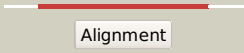



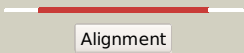

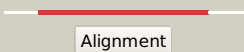



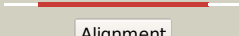


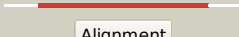


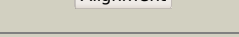


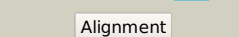
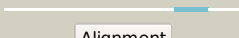
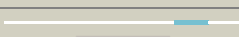

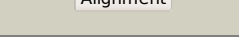
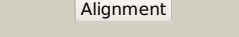

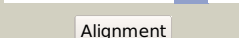

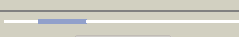

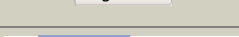
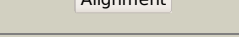

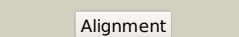

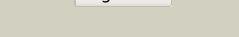
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3331_(sugl)_3717261_3718769
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	36fa95c6ae37174e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h7dA_	 Alignment		100.0	26	PDB header: membrane protein Chain: A: PDB Molecule: sugar transport protein 10; PDBTitle: crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
2	c4ybgB_	 Alignment		100.0	25	PDB header: transport protein/immune system Chain: B: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: rat glut5 with fv in the outward-open form
3	c5c65A_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: structure of the human glucose transporter glut3 / slc2a3
4	c4gbzA_	 Alignment		100.0	20	PDB header: transport protein Chain: A: PDB Molecule: d-xylose-proton symporter; PDBTitle: the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
5	c4ldsB_	 Alignment		100.0	30	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: bicyclomycin resistance protein tcb; PDBTitle: the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
6	c4pypA_	 Alignment		100.0	25	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 2, facilitated glucose transporter PDBTitle: crystal structure of the human glucose transporter glut1
7	c4j05A_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: phosphate transporter; PDBTitle: crystal structure of a eukaryotic phosphate transporter
8	c6e9oA_	 Alignment		100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: d-galactonate transport; PDBTitle: e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
9	d1pw4a_	 Alignment		100.0	15	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
10	c4zp0A_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: multidrug transporter mdfa; PDBTitle: crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
11	c6gs7A_	 Alignment		100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer

12	c6exsA_	Alignment		100.0	11	PDB header: membrane protein Chain: A: PDB Molecule: peptide abc transporter permease; PDBTitle: crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
13	c4cl5B_	Alignment		100.0	13	PDB header: transport protein Chain: B: PDB Molecule: nitrate transporter 1.1; PDBTitle: crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
14	c4w6vA_	Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: di-/tripeptide transporter; PDBTitle: crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
15	c4ikyA_	Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: di-tripeptide abc transporter (permease); PDBTitle: crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
16	c3wdoA_	Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
17	c4apsB_	Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: di-or tripeptide h+ symporter; PDBTitle: crystal structure of a pot family peptide transporter in an inward2 open conformation.
18	c6g9xB_	Alignment		100.0	15	PDB header: membrane protein Chain: B: PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstrom resolution
19	c3o7pA_	Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
20	c4lepB_	Alignment		100.0	13	PDB header: membrane protein, tranport protein Chain: B: PDB Molecule: proton:oligopeptide symporter pot family; PDBTitle: structural insights into substrate recognition in proton dependent2 oligopeptide transporters
21	c6ei3A_	Alignment	not modelled	100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter
22	c4iu8A_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
23	d1pv7a_	Alignment	not modelled	100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
24	c1pv7B_	Alignment	not modelled	100.0	12	PDB header: transport protein Chain: B: PDB Molecule: lactose permease; PDBTitle: crystal structure of lactose permease with tdg
25	c2xutC_	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
26	c2gfpA_	Alignment	not modelled	100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
27	c4q65A_	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: A: PDB Molecule: dipeptide permease d; PDBTitle: structure of the e. coli peptide transporter ybgh
28	c4iu9A_	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter

29	c5aynA_	 Alignment	not modelled	99.9	14	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
30	c5aymA_	 Alignment	not modelled	99.8	13	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
31	c4m64D_	 Alignment	not modelled	99.7	12	PDB header: transport protein Chain: D: PDB Molecule: melibiose carrier protein; PDBTitle: 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
32	c6ob7A_	 Alignment	not modelled	99.4	11	PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound
33	c2b6pA_	 Alignment	not modelled	81.5	11	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
34	c4djiA_	 Alignment	not modelled	77.3	11	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
35	c5xjIA_	 Alignment	not modelled	38.0	11	PDB header: transport protein Chain: A: PDB Molecule: multi drug efflux transporter; PDBTitle: crystal structure of a mate family protein
36	c3b9yA_	 Alignment	not modelled	37.7	10	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
37	d2j85a1	 Alignment	not modelled	36.1	25	Fold: STIV B116-like Superfamily: STIV B116-like Family: STIV B116-like
38	c3ff5B_	 Alignment	not modelled	36.0	31	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
39	c5aonB_	 Alignment	not modelled	34.7	31	PDB header: signaling protein Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
40	c5i87A_	 Alignment	not modelled	32.5	31	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
41	d1fs1b1	 Alignment	not modelled	27.8	46	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
42	c2w85A_	 Alignment	not modelled	26.2	31	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
43	c3c9pA_	 Alignment	not modelled	25.7	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sp1917; PDBTitle: crystal structure of uncharacterized protein sp1917
44	c5i6xA_	 Alignment	not modelled	22.0	10	PDB header: membrane protein Chain: A: PDB Molecule: sodium-dependent serotonin transporter; PDBTitle: x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
45	c4kppA_	 Alignment	not modelled	21.4	14	PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
46	c5aexI_	 Alignment	not modelled	20.4	14	PDB header: membrane protein Chain: J: PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
47	c6eu6A_	 Alignment	not modelled	20.2	13	PDB header: membrane protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: sensor amt protein
48	d1rhzb_	 Alignment	not modelled	18.6	30	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
49	c3oc5A_	 Alignment	not modelled	18.1	23	PDB header: cell adhesion Chain: A: PDB Molecule: toxin coregulated pilus biosynthesis protein f; PDBTitle: crystal structure of the vibrio cholerae secreted colonization factor2 tcpf
50	c3mkuB_	 Alignment	not modelled	17.3	10	PDB header: transport protein Chain: B: PDB Molecule: multi antimicrobial extrusion protein (na(+))/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
51	c2f9jP_	 Alignment	not modelled	15.0	28	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
52	d1ov9a_	 Alignment	not modelled	14.6	13	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
53	d1xjsa_	 Alignment	not modelled	14.5	7	Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
54	d1fs2b1	 Alignment	not modelled	14.2	50	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like

							Family: Skp1 dimerisation domain-like
55	c2g9pA_	Alignment	not modelled	13.8	36		PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide laticarin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, laticarin 2a,2 from spider (lachesana tarabaevi) venom
56	d1ni8a_	Alignment	not modelled	13.8	22		Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
57	c2fhoA_	Alignment	not modelled	13.0	29		PDB header: rna binding protein Chain: A: PDB Molecule: spliceosomal protein sf3b155; PDBTitle: nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
58	d1ofcx1	Alignment	not modelled	12.3	20		Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
59	c4k1cA_	Alignment	not modelled	12.2	12		PDB header: membrane protein/metal transport Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
60	c3hd6A_	Alignment	not modelled	12.1	10		PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
61	d1nexa1	Alignment	not modelled	11.6	46		Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
62	c3qnqD_	Alignment	not modelled	11.1	15		PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
63	d2csba1	Alignment	not modelled	10.8	46		Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
64	c5tgyA_	Alignment	not modelled	10.4	35		PDB header: unknown function Chain: A: PDB Molecule: ps1; PDBTitle: nmr structure of holo-ps1
65	c5uftA_	Alignment	not modelled	10.2	18		PDB header: metal binding protein Chain: A: PDB Molecule: nitrogen-fixing nifu-like, n-terminal; PDBTitle: crystal structure of a nitrogen-fixing nifu-like protein (n-terminal)2 from brucella abortus
66	c6adqP_	Alignment	not modelled	9.8	10		PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
67	c2wwbB_	Alignment	not modelled	9.4	17		PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
68	d1su0b_	Alignment	not modelled	9.4	9		Fold: SufE/NifU Superfamily: SufE/NifU Family: NifU/IscU domain
69	c3h1cD_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: D: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
70	c3h1cS_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: S: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
71	c3h1cH_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: H: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
72	c3h1cU_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: U: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
73	c3h1cN_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: N: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
74	c3gcmF_	Alignment	not modelled	9.2	36		PDB header: transferase / protein binding Chain: F: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of e. coli polynucleotide phosphorylase2 bound to rna and rnase e
75	c3gcmD_	Alignment	not modelled	9.2	36		PDB header: transferase / protein binding Chain: D: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of e. coli polynucleotide phosphorylase2 bound to rna and rnase e
76	c3gmeD_	Alignment	not modelled	9.2	36		PDB header: transferase / protein binding Chain: D: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase in complex2 with rnase e and manganese
77	c3h1cY_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: Y: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
78	c3h1cF_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: F: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate
79	c3h1cP_	Alignment	not modelled	9.2	36		PDB header: transferase Chain: P: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnpase)2 core bound to rnase e and tungstate

80	c3h1cW_	Alignment	not modelled	9.2	36	PDB header: transferase Chain: W: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnase)2 core bound to rnase e and tungstate
81	c3h1cL_	Alignment	not modelled	9.2	36	PDB header: transferase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnase)2 core bound to rnase e and tungstate
82	c3h1cE_	Alignment	not modelled	9.2	36	PDB header: transferase Chain: E: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnase)2 core bound to rnase e and tungstate
83	c3h1cJ_	Alignment	not modelled	9.2	36	PDB header: transferase Chain: J: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of polynucleotide phosphorylase (pnase)2 core bound to rnase e and tungstate
84	c3gcmE_	Alignment	not modelled	9.1	36	PDB header: transferase / protein binding Chain: E: PDB Molecule: ribonuclease e; PDBTitle: crystal structure of e. coli polynucleotide phosphorylase2 bound to rna and rnase e
85	d2ovra1	Alignment	not modelled	9.0	50	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
86	d3proc1	Alignment	not modelled	8.4	7	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
87	c5vf3Z_	Alignment	not modelled	8.4	33	PDB header: virus Chain: Z: PDB Molecule: highly immunogenic outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
88	c2vpzG_	Alignment	not modelled	8.3	23	PDB header: oxidoreductase Chain: G: PDB Molecule: hypothetical membrane spanning protein; PDBTitle: polysulfide reductase native structure
89	c3mmyF_	Alignment	not modelled	8.1	31	PDB header: nuclear protein Chain: F: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
90	d1xta2	Alignment	not modelled	8.1	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
91	c2mkvA_	Alignment	not modelled	8.1	17	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
92	c1y7oE_	Alignment	not modelled	8.0	20	PDB header: hydrolase Chain: E: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: the structure of streptococcus pneumoniae a153p clpp
93	c3ervA_	Alignment	not modelled	8.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative c39-like peptidase; PDBTitle: crystal structure of an putative c39-like peptidase from bacillus2 anthracis
94	c3t7vA_	Alignment	not modelled	8.0	24	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
95	c2lr8A_	Alignment	not modelled	7.8	0	PDB header: apoptosis Chain: A: PDB Molecule: casp8-associated protein 2; PDBTitle: solution nmr structure of casp8-associated protein 2 from homo2 sapiens, northeast structural genomics consortium (nesg) target3 hr8150a
96	d1xeqa1	Alignment	not modelled	7.7	27	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: N-terminal, RNA-binding domain of nonstructural protein NS1
97	d1w7ca3	Alignment	not modelled	7.6	8	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
98	c4jigB_	Alignment	not modelled	7.6	35	PDB header: oxidoreductase Chain: B: PDB Molecule: 5,10-methenyltetrahydromethanopterin hydrogenase; PDBTitle: crystal structure of fe-hydrogenase from methanothermobacter2 marburgensis in complex with toluenesulfonylmethylisocyanide
99	d1nh2d1	Alignment	not modelled	7.6	19	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain