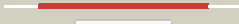


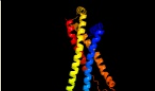
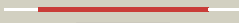


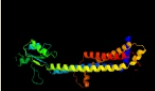

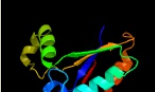












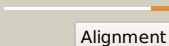

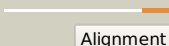
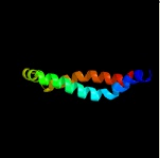
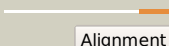
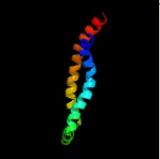
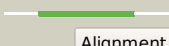
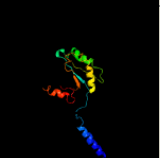
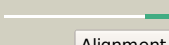
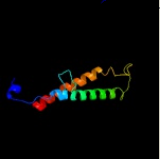
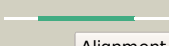
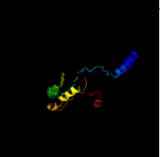
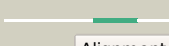
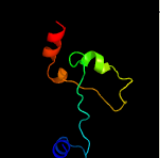

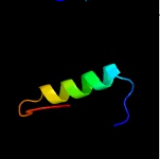

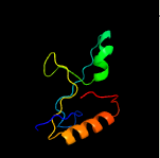

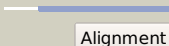
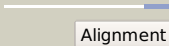
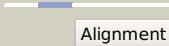
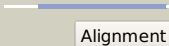
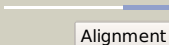



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3101c_(ftsX)_3469783_3470676
 Date Thu Aug 8 16:20:28 BST 2019
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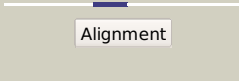
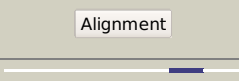
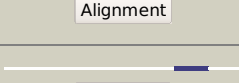
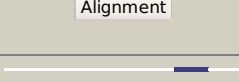
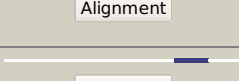
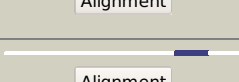
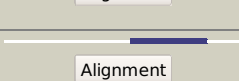
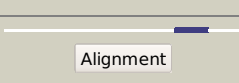
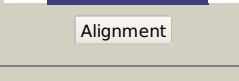
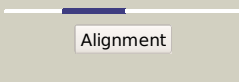
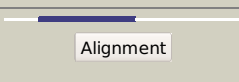

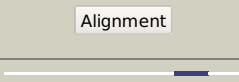
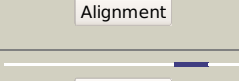
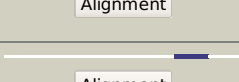
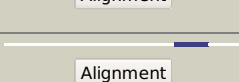
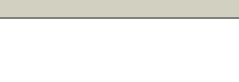

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xu1M_	 Alignment		100.0	15	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus pneumoniae r6
2	c5nikK_	 Alignment		100.0	17	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
3	c5ws4A_	 Alignment		100.0	18	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
4	c5lj7B_	 Alignment		100.0	15	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
5	c4n8oA_	 Alignment		99.5	100	PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: crystal structure of mycobacterial ftsx extracellular domain, bromide2 derivative
6	c6mk7A_	 Alignment		99.3	19	PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: solution structure of the large extracellular loop of ftsx in2 streptococcus pneumoniae
7	c5x5yF_	 Alignment		93.0	14	PDB header: membrane protein Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
8	c1ciiA_	 Alignment		92.1	9	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
9	c6mjpF_	 Alignment		91.7	15	PDB header: lipid transport Chain: F: PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
10	c5l75F_	 Alignment		91.4	11	PDB header: transport protein Chain: F: PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
11	c6ic4H_	 Alignment		89.8	12	PDB header: protein transport Chain: H: PDB Molecule: abc transporter permease; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution

12	c5I75G_	 Alignment		88.0	15	PDB header: transport protein Chain: G: PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
13	c6mjpG_	 Alignment		87.5	14	PDB header: lipid transport Chain: G: PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
14	c5x5yG_	 Alignment		86.0	12	PDB header: membrane protein Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
15	c1oy8A_	 Alignment		55.4	13	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
16	c6btmD_	 Alignment		49.5	8	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
17	c4k0eC_	 Alignment		42.0	12	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
18	c5naaB_	 Alignment		40.7	11	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein-releasing system transmembrane protein lolc; PDBTitle: lipoprotein-releasing system transmembrane protein lolc
19	c3ibwA_	 Alignment		38.4	14	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
20	d2cyya2	 Alignment		31.2	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
21	c3ftjA_	 Alignment	not modelled	30.1	10	PDB header: hydrolase Chain: A: PDB Molecule: macrolide export atp-binding/permease protein PDBTitle: crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
22	c6ajjA_	 Alignment	not modelled	29.1	12	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
23	c6f0kD_	 Alignment	not modelled	28.9	15	PDB header: membrane protein Chain: D: PDB Molecule: actd; PDBTitle: alternative complex iii
24	c5njgB_	 Alignment	not modelled	27.4	16	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: part of the structure that could be2 built de novo
25	c5jefA_	 Alignment	not modelled	25.2	7	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
26	c4ymuC_	 Alignment	not modelled	25.2	7	PDB header: protein binding/transport protein Chain: C: PDB Molecule: abc-type amino acid transport system, permease component; PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps
27	c2zbcH_	 Alignment	not modelled	23.8	20	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii

						strain7.
28	dli1ga2	Alignment	not modelled	22.6	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
29	c5gasN	Alignment	not modelled	19.1	8	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
30	c2e1aD	Alignment	not modelled	17.3	14	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
31	d2cg4a2	Alignment	not modelled	16.6	7	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
32	c6n3qA	Alignment	not modelled	13.0	23	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec61; PDBTitle: cryo-em structure of the yeast sec complex
33	c5udfB	Alignment	not modelled	12.8	5	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein-releasing system transmembrane protein lole; PDBTitle: structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lole from acinetobacter baumannii
34	c2cwba	Alignment	not modelled	12.6	16	PDB header: protein binding Chain: A: PDB Molecule: chimera of immunoglobulin g binding protein g PDBTitle: solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
35	c1wr1B	Alignment	not modelled	12.5	8	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like protein dsk2; PDBTitle: the complex sturcture of dsk2p uba with ubiquitin
36	c2wwbA	Alignment	not modelled	11.6	13	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	d1veja1	Alignment	not modelled	11.0	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
38	d2bwba1	Alignment	not modelled	10.8	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
39	c5a43B	Alignment	not modelled	10.7	14	PDB header: transport protein Chain: B: PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
40	c3i4pA	Alignment	not modelled	10.5	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
41	d2dnaa1	Alignment	not modelled	10.5	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
42	c3ltiA	Alignment	not modelled	10.5	19	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains
43	c2dahA	Alignment	not modelled	9.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-3; PDBTitle: solution structure of the c-terminal uba domain in the2 human ubiquilin 3
44	d2daha1	Alignment	not modelled	9.6	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
45	c2dnaA	Alignment	not modelled	9.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
46	c2ec1A	Alignment	not modelled	8.2	7	PDB header: transport protein Chain: A: PDB Molecule: nucleoporin 50 kda; PDBTitle: solution structure of the ranbd1 domain from human2 nucleoporin 50 kda
47	c2mv6A	Alignment	not modelled	8.2	14	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: solution structure of the transmembrane domain and the juxta-membrane2 domain of the erythropoietin receptor in micelles
48	c5zazA	Alignment	not modelled	8.1	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
49	c2jy5A	Alignment	not modelled	7.9	12	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
50	c1vx11	Alignment	not modelled	7.9	13	PDB header: ribosome Chain: 1: PDB Molecule: sec61 alpha subunit; PDBTitle: structure of the translating mammalian ribosome-sec61 complex. this2 entry contains the large subunit ribosomal proteins.
51	c1i1gA	Alignment	not modelled	7.8	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
52	c2mxbA	Alignment	not modelled	7.4	26	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: structure of the transmembrane domain of the mouse erythropoietin2 receptor
						PDB header: transport protein

53	c5xjyA_	Alignment	not modelled	7.4	17	Chain: A; PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
54	c6raoI_	Alignment	not modelled	7.3	11	PDB header: virus like particle Chain: I; PDB Molecule: afp11; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
55	c5wtqB_	Alignment	not modelled	7.1	16	PDB header: chaperone Chain: B; PDB Molecule: proteasome assembly chaperone 4; PDBTitle: crystal structure of human proteasome-assembling chaperone pac4
56	c2ksfA_	Alignment	not modelled	7.0	15	PDB header: transferase Chain: A; PDB Molecule: sensor protein kdpd; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor kdpd, center for structures of membrane proteins (csm)3 target 4312c
57	d1m56d_	Alignment	not modelled	6.9	9	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
58	d1f06a2	Alignment	not modelled	6.9	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehide-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
59	c4kbmA_	Alignment	not modelled	6.7	13	PDB header: transferase/transcription Chain: A; PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of the mtb card/rnap beta subunit b1-b2 domains complex
60	c1rwuA_	Alignment	not modelled	6.7	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical uf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
61	d1rwua_	Alignment	not modelled	6.7	14	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
62	c6ithA_	Alignment	not modelled	6.6	18	PDB header: membrane protein Chain: A; PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
63	c2kncB_	Alignment	not modelled	6.6	15	PDB header: cell adhesion Chain: B; PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
64	c2e7xA_	Alignment	not modelled	6.4	18	PDB header: transcription regulator Chain: A; PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
65	c4a01B_	Alignment	not modelled	6.4	15	PDB header: hydrolase Chain: B; PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
66	c4j29A_	Alignment	not modelled	6.3	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: engineered protein or258; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or258.
67	c2lvwA_	Alignment	not modelled	6.3	11	PDB header: transferase Chain: A; PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
68	d1tc3c_	Alignment	not modelled	6.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
69	d1dv0a_	Alignment	not modelled	6.1	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
70	d2joqa1	Alignment	not modelled	6.1	6	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
71	c5a40C_	Alignment	not modelled	6.1	16	PDB header: transport protein Chain: C; PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
72	d3dhwa1	Alignment	not modelled	6.0	10	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
73	c4gn0D_	Alignment	not modelled	6.0	7	PDB header: signaling protein Chain: D; PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
74	c2jxsA_	Alignment	not modelled	6.0	27	PDB header: chaperone Chain: A; PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
75	c3n7cB_	Alignment	not modelled	5.9	15	PDB header: protein transport Chain: B; PDB Molecule: abr034wp; PDBTitle: crystal structure of the ran binding domain from the nuclear pore2 complex component nup2 from ashbya gossypii
76	d2cfxa2	Alignment	not modelled	5.8	6	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
77	d1ygya3	Alignment	not modelled	5.7	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
78	c3hd7A_	Alignment	not modelled	5.6	7	PDB header: exocytosis Chain: A; PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1

79	c4l6eA_	 Alignment	not modelled	5.5	11	PDB header: ligase, isomerase Chain: A: PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: crystal structure of the ranbd1 fourth domain of e3 sumo-protein2 ligase ranbp2. northeast structural genomics consortium (nesg) target3 hr9193b
80	c1ib8A_	 Alignment	not modelled	5.5	18	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: conserved protein sp14.3; PDBTitle: solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
81	d1uj4a2	 Alignment	not modelled	5.4	15	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
82	c6c6lN_	 Alignment	not modelled	5.4	15	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
83	c6hrbD_	 Alignment	not modelled	5.4	17	PDB header: membrane protein Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)
84	c5mrwD_	 Alignment	not modelled	5.4	17	PDB header: hydrolase Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
85	c5mrwL_	 Alignment	not modelled	5.4	17	PDB header: hydrolase Chain: L: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
86	c5mrwH_	 Alignment	not modelled	5.4	17	PDB header: hydrolase Chain: H: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
87	c5sv0C_	 Alignment	not modelled	5.3	19	PDB header: transport protein Chain: C: PDB Molecule: biopolymer transport protein exbb; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 7.0
88	c2rmzA_	 Alignment	not modelled	5.3	15	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
89	d1ib8a2	 Alignment	not modelled	5.3	18	Fold: Alpha-lytic protease prodomain-like Superfamily: YhbC-like, N-terminal domain Family: YhbC-like, N-terminal domain
90	c3k07A_	 Alignment	not modelled	5.2	16	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
91	c4czdA_	 Alignment	not modelled	5.2	14	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
92	c6elhA_	 Alignment	not modelled	5.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
93	d1m0sa2	 Alignment	not modelled	5.1	11	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
94	c4l6vM_	 Alignment	not modelled	5.1	29	PDB header: electron transport Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
95	c4l6v7_	 Alignment	not modelled	5.1	29	PDB header: electron transport Chain: 7: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
96	c5oy0m_	 Alignment	not modelled	5.1	29	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
97	c5oy0M_	 Alignment	not modelled	5.1	29	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
98	c6hqbM_	 Alignment	not modelled	5.1	29	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: monomeric cyanobacterial photosystem i