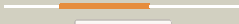
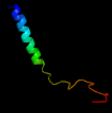
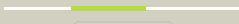
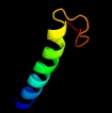
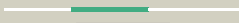
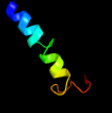











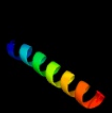



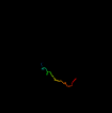


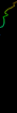
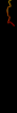







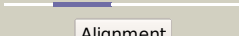
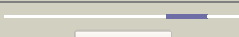
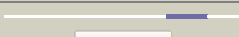


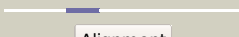



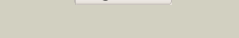




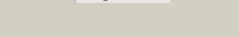

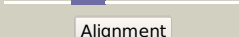


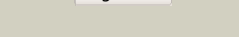
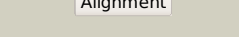
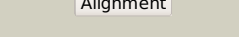
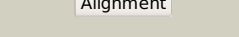
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3706c_(-)_4149769_4150089
Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	905f5602a13d7245

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k74A_	 Alignment		81.3	20	PDB header: membrane protein, oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
2	c2m6iC_	 Alignment		61.2	21	PDB header: membrane protein Chain: C: PDB Molecule: full-length transmembrane domains of human glycine receptor PDBTitle: putative pentameric open-channel structure of full-length2 transmembrane domains of human glycine receptor alpha1 subunit
3	c2l9uB_	 Alignment		43.0	41	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain
4	c2l9uA_	 Alignment		36.6	41	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain
5	c3vu1A_	 Alignment		36.0	29	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein ph0242; PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (phaglb-l, o74088_pyrho) from pyrococcus3 horikoshii
6	c3ctwB_	 Alignment		33.6	25	PDB header: protein binding Chain: B: PDB Molecule: rcda; PDBTitle: crystal structure of rcda from caulobacter crescentus cb15
7	c6a69B_	 Alignment		29.7	24	PDB header: structural protein Chain: B: PDB Molecule: neuroplastin; PDBTitle: cryo-em structure of a p-type atpase
8	c6ffvA_	 Alignment		29.1	34	PDB header: transport protein Chain: A: PDB Molecule: btum; PDBTitle: the crystal structure of btum cobalamin transporter
9	c6c14B_	 Alignment		29.1	29	PDB header: membrane protein, metal transport Chain: B: PDB Molecule: lhfp1 tetraspan subfamily member 5 protein; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
10	c2k1vB_	 Alignment		25.8	62	PDB header: hormone Chain: B: PDB Molecule: relaxin-3; PDBTitle: r3/i5 relaxin chimera
11	c6a0aA_	 Alignment		23.7	43	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii

12	c2k1aA_	Alignment		22.4	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
13	c1x1kF_	Alignment		22.2	80	PDB header: structural protein Chain: F: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)4 PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
14	c6a0aC_	Alignment		21.7	43	PDB header: structural protein Chain: C: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
15	c6a0aB_	Alignment		21.7	43	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
16	c2k1IA_	Alignment		20.8	86	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
17	c2k1IB_	Alignment		20.8	86	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
18	c2k1kB_	Alignment		20.8	86	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
19	c2k1kA_	Alignment		20.8	86	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
20	c4yzfA_	Alignment		20.0	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
21	c2hacB_	Alignment	not modelled	19.5	26	PDB header: membrane protein Chain: B: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
22	c2hacA_	Alignment	not modelled	19.5	26	PDB header: membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
23	c2n8rC_	Alignment	not modelled	18.5	48	PDB header: hydrolase/structural protein Chain: C: PDB Molecule: collagen triple helix repeat family protein; PDBTitle: productive complex between mmp-12 and synthetic triple-helical2 collagen, revealed through paramagnetic nmr
24	c2n8rD_	Alignment	not modelled	18.5	48	PDB header: hydrolase/structural protein Chain: D: PDB Molecule: collagen triple helix repeat family protein; PDBTitle: productive complex between mmp-12 and synthetic triple-helical2 collagen, revealed through paramagnetic nmr
25	c2n8rB_	Alignment	not modelled	18.5	48	PDB header: hydrolase/structural protein Chain: B: PDB Molecule: collagen triple helix repeat family protein; PDBTitle: productive complex between mmp-12 and synthetic triple-helical2 collagen, revealed through paramagnetic nmr
26	c6ajjA_	Alignment	not modelled	18.3	50	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
27	c5xnmj_	Alignment	not modelled	18.2	32	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
28	c3jcu_	Alignment	not modelled	16.9	36	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution

29	c6caaA	 Alignment	not modelled	16.8	7	PDB header: transport protein Chain: A: PDB Molecule: electrogenic sodium bicarbonate cotransporter 1; PDBTitle: cryoem structure of human slc4a4 sodium-coupled acid-base transporter2 nbce1
30	c3a0aE	 Alignment	not modelled	16.2	79	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
31	c3a0aF	 Alignment	not modelled	15.5	79	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
32	c3a0aD	 Alignment	not modelled	15.5	79	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
33	d1fzda	 Alignment	not modelled	14.5	33	Fold: Fibrinogen C-terminal domain-like Superfamily: Fibrinogen C-terminal domain-like Family: Fibrinogen C-terminal domain-like
34	c2kncA	 Alignment	not modelled	14.3	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
35	c3a0aA	 Alignment	not modelled	14.1	79	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
36	c2lnbA	 Alignment	not modelled	13.9	46	PDB header: immune system Chain: A: PDB Molecule: z-dna-binding protein 1; PDBTitle: solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a.
37	c6nhwD	 Alignment	not modelled	13.4	55	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
38	c6nhwA	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
39	c6nhwE	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: E: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
40	c6nhwB	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
41	c6nhwF	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
42	c6nhwC	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
43	c6nhyC	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only
44	c6nhyB	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only
45	c6nhyA	 Alignment	not modelled	13.4	55	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 mutant2 (g217y) - trimer only
46	c4h44E	 Alignment	not modelled	12.9	50	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
47	c4ogqE	 Alignment	not modelled	12.9	50	PDB header: electron transport Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
48	c2zt9E	 Alignment	not modelled	12.9	50	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
49	c3zljC	 Alignment	not modelled	12.6	38	PDB header: dna binding protein/dna Chain: C: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
50	c3a0aC	 Alignment	not modelled	12.3	79	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
51	c2m0qA	 Alignment	not modelled	12.3	13	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent

						micelles2 demonstrate a straight transmembrane helix
52	c3zljD_	Alignment	not modelled	12.1	38	PDB header: dna binding protein/dna Chain: D: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
53	c2zxeG_	Alignment	not modelled	11.3	25	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
54	c5sv9B_	Alignment	not modelled	11.1	8	PDB header: transport protein Chain: B: PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
55	c2mkvA_	Alignment	not modelled	11.1	50	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
56	c3a0aB_	Alignment	not modelled	11.0	58	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
57	c2jo1A_	Alignment	not modelled	11.0	33	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
58	c6irtA_	Alignment	not modelled	10.9	31	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
59	c3kdpG_	Alignment	not modelled	10.7	43	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
60	c3kdpH_	Alignment	not modelled	10.7	43	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
61	c6ef3s_	Alignment	not modelled	10.2	40	PDB header: motor protein Chain: S: PDB Molecule: PDBTitle: yeast 26s proteasome bound to ubiquitinated substrate (4d motor state)
62	c4hqjG_	Alignment	not modelled	10.2	43	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
63	c3jcul_	Alignment	not modelled	10.2	31	PDB header: membrane protein Chain: L: PDB Molecule: protein photosystem ii reaction center protein l; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
64	c2lieA_	Alignment	not modelled	10.1	38	PDB header: sugar binding protein Chain: A: PDB Molecule: ccl2 lectin; PDBTitle: nmr structure of the lectin ccl2
65	c2mfrA_	Alignment	not modelled	10.0	31	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
66	c3n23E_	Alignment	not modelled	9.9	50	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
67	c2drtB_	Alignment	not modelled	9.8	83	PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
68	c2drtA_	Alignment	not modelled	9.8	83	PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
69	c2lkgA_	Alignment	not modelled	9.6	50	PDB header: signaling protein Chain: A: PDB Molecule: acetylcholine receptor; PDBTitle: wsa major conformation
70	c4l0eA_	Alignment	not modelled	9.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: p450 monooxygenase; PDBTitle: structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis (heme-coordinated expression tag)
71	c2drtC_	Alignment	not modelled	9.6	83	PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
72	c2v53D_	Alignment	not modelled	9.4	88	PDB header: cell adhesion Chain: D: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparc-collagen complex
73	c2v53B_	Alignment	not modelled	9.4	88	PDB header: cell adhesion Chain: B: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparc-collagen complex
74	c2v53C_	Alignment	not modelled	9.4	88	PDB header: cell adhesion Chain: C: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparc-collagen complex
75	c4hqjE_	Alignment	not modelled	9.3	43	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
76	c2d3fB_	Alignment	not modelled	9.3	79	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
						PDB header: structural protein

77	c1x1kE_	Alignment	not modelled	9.3	79	Chain: E; PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
78	c2d3fC_	Alignment	not modelled	9.3	79	PDB header: structural protein Chain: C; PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
79	c2d3fA_	Alignment	not modelled	9.3	79	PDB header: structural protein Chain: A; PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
80	c6adqP_	Alignment	not modelled	9.0	29	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
81	c2k21A_	Alignment	not modelled	9.0	19	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and 2 40 degree c
82	c2lm4A_	Alignment	not modelled	8.8	33	PDB header: protein binding Chain: A; PDB Molecule: succinate dehydrogenase assembly factor 2, mitochondrial; PDBTitle: solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a
83	c4pj0L_	Alignment	not modelled	8.4	15	PDB header: oxidoreductase, electron transport Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
84	c4pj0L_	Alignment	not modelled	8.4	15	PDB header: oxidoreductase, electron transport Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
85	c2d3fD_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: D; PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
86	c1x1kD_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: D; PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
87	c1x1kC_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: C; PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
88	c2d3fE_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: E; PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
89	c1x1kA_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: A; PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
90	c1x1kB_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: B; PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
91	c2d3fF_	Alignment	not modelled	8.4	79	PDB header: structural protein Chain: F; PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
92	c3admC_	Alignment	not modelled	8.3	71	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
93	c4tniL_	Alignment	not modelled	8.3	15	PDB header: electron transport,photosynthesis Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
94	c4ub8L_	Alignment	not modelled	8.3	15	PDB header: electron transport, photosynthesis Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
95	c3a0hL_	Alignment	not modelled	8.3	15	PDB header: electron transport Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
96	c4rvyL_	Alignment	not modelled	8.3	15	PDB header: oxidoreductase Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
97	c3kziL_	Alignment	not modelled	8.3	15	PDB header: electron transport Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
98	c3prrL_	Alignment	not modelled	8.3	15	PDB header: photosynthesis Chain: L; PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
						PDB header: electron transport, photosynthesis

99	c4ub6l_	Alignment	not modelled	8.3	15	Chain: L; PDB Molecule: photosystem ii reaction center protein l; PDBTitle: native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
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