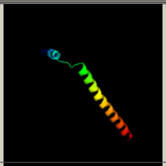
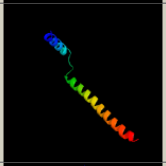
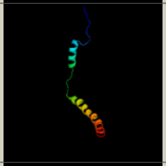
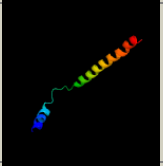
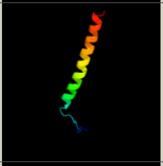
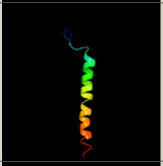
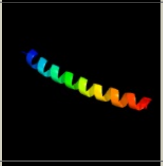
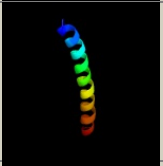
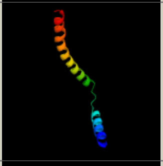
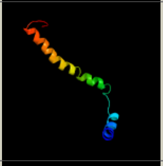
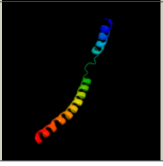
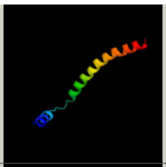
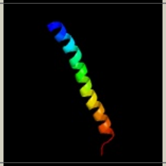
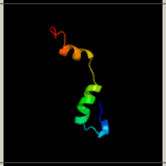
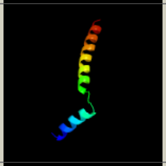
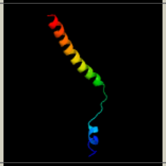
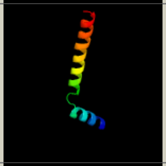
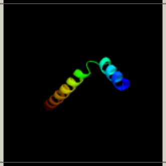
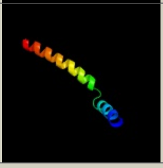
Email	mdejesus@rockefeller.edu
Description	RVBD0638_(secE)_733740_734225
Date	Fri Jul 26 01:50:20 BST 2019
Unique Job ID	f79453f90e8f182f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ch4E_	Alignment		99.8	26	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**protein translocase subunit sece; **PDBTitle:** peptide-bound state of thermus thermophilus secyeg
2	c5eulE_	Alignment		99.8	49	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** structure of the seca-secy complex with a translocating polypeptide2 substrate
3	c2akhZ_	Alignment		99.8	32	**PDB header:**protein transport **Chain:** Z: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a non-translocating2 secyeg protein-conducting channel into the cryo-em map of a secyeg-3 nascent chain-70s ribosome complex from e. coli
4	c3dinD_	Alignment		99.7	35	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
5	c2zjsE_	Alignment		99.0	28	**PDB header:**protein transport/immune system **Chain:** E: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** crystal structure of secye translocon from thermus thermophilus with a2 fab fragment
6	c2zqpE_	Alignment		98.9	27	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
7	c3dl8D_	Alignment		97.9	21	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
8	c3dl8C_	Alignment		97.9	21	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
9	d1rhzb_	Alignment		94.9	9	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
10	c2wwbB_	Alignment		93.7	14	**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
11	c2ww9B_	Alignment		92.1	9	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome

12	d1rh5b_	Alignment		80.1	8	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
13	c4cdiC_	Alignment		75.8	17	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**predicted protein; **PDBTitle:** crystal structure of acrb-acrz complex
14	d1wh8a_	Alignment		62.8	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
15	c1zrtD_	Alignment		60.8	12	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
16	c3mp7B_	Alignment		57.9	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
17	c2fynH_	Alignment		57.6	14	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
18	c1p84D_	Alignment		52.9	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
19	c3cwbQ_	Alignment		47.7	19	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
20	c2yiuE_	Alignment		45.7	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
21	c1qcrD_	Alignment	not modelled	39.4	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ubiquinol cytochrome c oxidoreductase; **PDBTitle:** crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
22	c2kogA_	Alignment	not modelled	32.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** lipid-bound synaptobrevin solution nmr structure
23	c2eqzA_	Alignment	not modelled	24.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group protein b3; **PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3
24	c3qf4B_	Alignment	not modelled	22.3	15	**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
25	d2e74b1	Alignment	not modelled	21.4	19	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
26	c4h1wB_	Alignment	not modelled	20.9	24	**PDB header:**hydrolase/hydrolase regulator **Chain:** B: **PDB Molecule:**sarcolipin; **PDBTitle:** e1 structure of the (sr) ca2+-atpase in complex with sarcolipin
27	c3w5aC_	Alignment	not modelled	20.9	24	**PDB header:**metal transport/membrane protein **Chain:** C: **PDB Molecule:**sarcolipin; **PDBTitle:** crystal structure of the calcium pump and sarcolipin from rabbit fast2 twitch skeletal muscle in the e1.mg2+ state
						PDB header:antimicrobial protein

28	c6fs4A_	Alignment	not modelled	20.0	31	**Chain:** A: **PDB Molecule:**alpha-s2-casein; **PDBTitle:** nmr structure of casocidin-ii antimicrobial peptide in 60% tfe
29	d2h8pc1	Alignment	not modelled	19.6	15	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
30	c3hd7A_	Alignment	not modelled	19.5	8	**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
31	d1v54d_	Alignment	not modelled	19.0	19	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
32	c1jdmA_	Alignment	not modelled	17.4	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sarcolipin; **PDBTitle:** nmr structure of sarcolipin
33	c4gn0D_	Alignment	not modelled	17.3	13	**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
34	d2axth1	Alignment	not modelled	16.7	20	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II 10 kDa phosphoprotein PsbH **Family:**PsbH-like
35	c2axtH_	Alignment	not modelled	16.7	20	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosystem ii reaction center h protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
36	c5gasN_	Alignment	not modelled	16.3	18	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**archaeal/vacuolar-type h+-atpase subunit i; **PDBTitle:** thermus thermophilus v/a-atpase, conformation 2
37	c2wg7B_	Alignment	not modelled	16.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phospholipase a2; **PDBTitle:** structure of oryza sativa (rice) pla2
38	c2wwbC_	Alignment	not modelled	16.0	25	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**protein transport protein sec61 subunit beta; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
39	c2ehbD_	Alignment	not modelled	15.9	18	**PDB header:**signalling protein/transferase **Chain:** D: **PDB Molecule:**cbl-interacting serine/threonine-protein kinase 24; **PDBTitle:** the structure of the c-terminal domain of the protein kinase atsos22 bound to the calcium sensor atsos3
40	d1j3xa_	Alignment	not modelled	15.8	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
41	c1j3xA_	Alignment	not modelled	15.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**high mobility group protein 2; **PDBTitle:** solution structure of the n-terminal domain of the hmgb2
42	c2co9A_	Alignment	not modelled	15.5	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
43	c6gy4B_	Alignment	not modelled	15.4	18	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein bicaudal c homolog 1; **PDBTitle:** crystal structure of the n-terminal kh domain of human bicc1
44	c3fwbB_	Alignment	not modelled	15.3	17	**PDB header:**cell cycle, transcription **Chain:** B: **PDB Molecule:**nuclear mrna export protein sac3; **PDBTitle:** sac3:sus1:cdc31 complex
45	c4il3B_	Alignment	not modelled	14.9	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ste24p; **PDBTitle:** crystal structure of s. mikatae ste24p
46	c2e6oA_	Alignment	not modelled	14.8	13	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1
47	d1wh6a_	Alignment	not modelled	14.2	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
48	c2y69Q_	Alignment	not modelled	13.6	19	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular oxygen
49	c6o7ua_	Alignment	not modelled	13.6	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:** **PDBTitle:** saccharomyces cerevisiae v-atpase stv1-vo
50	c4hd1A_	Alignment	not modelled	13.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**squalene synthase hpnc; **PDBTitle:** crystal structure of squalene synthase hpnc from alicyclobacillus2 acidocaldarius
51	c2ndjA_	Alignment	not modelled	13.0	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e member 3; **PDBTitle:** structural basis for kcne3 and estrogen modulation of the kcnq12 channel
52	c2m0qA_	Alignment	not modelled	11.7	16	**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
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**succinate dehydrogenase cytochrome b,

53	c1yq3C_	Alignment	not modelled	11.5	15	large subunit; **PDBTitle:** avian respiratory complex ii with oxaloacetate and ubiquinone
54	c2m3aA_	Alignment	not modelled	9.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein knl-2; **PDBTitle:** nmr solution structure of a myb-like dna binding domain of knl-2 from2 c. elegans
55	d2ezwa1	Alignment	not modelled	9.5	32	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
56	c2n28A_	Alignment	not modelled	9.0	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein vpu; **PDBTitle:** solid-state nmr structure of vpu
57	c2gofA_	Alignment	not modelled	8.7	18	**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
58	c2gohA_	Alignment	not modelled	8.7	18	**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
59	c1pi8A_	Alignment	not modelled	8.7	18	**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
60	c1pjeA_	Alignment	not modelled	8.7	18	**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
61	c1pi7A_	Alignment	not modelled	8.7	18	**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
62	d1q90d_	Alignment	not modelled	8.6	26	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
63	c2wmhA_	Alignment	not modelled	8.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fucolectin-related protein; **PDBTitle:** crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae tigr4 in3 complex with the h-disaccharide blood group antigen.
64	c2m59B_	Alignment	not modelled	8.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**vascular endothelial growth factor receptor 2; **PDBTitle:** spatial structure of dimeric vegfr2 membrane domain in dpc micelles
65	c2m59A_	Alignment	not modelled	8.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vascular endothelial growth factor receptor 2; **PDBTitle:** spatial structure of dimeric vegfr2 membrane domain in dpc micelles
66	c6m97A_	Alignment	not modelled	8.3	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chimera protein of high affinity copper uptake protein 1 **PDBTitle:** crystal structure of the high-affinity copper transporter ctr1
67	d2axti1	Alignment	not modelled	7.9	24	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
68	c3a0hi_	Alignment	not modelled	7.9	24	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**photosystem ii reaction center protein i; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
69	c4f9kA_	Alignment	not modelled	7.8	14	**PDB header:**transferase regulator **Chain:** A: **PDB Molecule:**camp-dependent protein kinase type i-beta regulatory **PDBTitle:** crystal structure of human camp-dependent protein kinase type i-beta2 regulatory subunit (fragment 11-73), northeast structural genomics3 consortium (nesg) target hr8613a
70	c3ipdB_	Alignment	not modelled	7.7	9	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
71	c2ly4A_	Alignment	not modelled	7.5	19	**PDB header:**nuclear protein/antitumour protein **Chain:** A: **PDB Molecule:**high mobility group protein b1; **PDBTitle:** hmgb1-facilitated p53 dna binding occurs via hmg-box/p532 transactivation domain interaction and is regulated by the acidic3 tail
72	c2wmkB_	Alignment	not modelled	7.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fucolectin-related protein; **PDBTitle:** crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae sp3-bs713 (sp3gh98) in complex with the a-lewisy pentasaccharide4 blood group antigen.
73	c4mrnB_	Alignment	not modelled	7.4	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter related protein; **PDBTitle:** structure of a bacterial atm1-family abc transporter
74	c6fs5A_	Alignment	not modelled	7.2	21	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**alpha-s2-casein; **PDBTitle:** nmr structure of casocidin-i antimicrobial peptide in 60% tfe
75	c2k21A_	Alignment	not modelled	7.1	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0

						and2 40 degree c
76	c3jcul_	Alignment	not modelled	6.8	18	**PDB header:**membrane protein **Chain:** I: **PDB Molecule:**protein photosystem ii reaction center protein i; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
77	c4y21A_	Alignment	not modelled	6.7	16	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**protein unc-13 homolog a; **PDBTitle:** crystal structure of munc13-1 mun domain
78	c6nd1D_	Alignment	not modelled	6.6	21	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**protein transport protein sbh1; **PDBTitle:** cryoem structure of the sec complex from yeast
79	d1x2la1	Alignment	not modelled	6.5	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
80	c2mfrA_	Alignment	not modelled	6.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**insulin receptor; **PDBTitle:** solution structure of the transmembrane domain of the insulin receptor2 in micelles
81	c5mx2T_	Alignment	not modelled	6.4	13	**PDB header:**oxidoreductase **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
82	c4aw6B_	Alignment	not modelled	6.4	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caax prenyl protease 1 homolog; **PDBTitle:** crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
83	c5b66T_	Alignment	not modelled	5.9	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure analysis of photosystem ii complex
84	c5b5et_	Alignment	not modelled	5.9	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure analysis of photosystem ii complex
85	c4il6T_	Alignment	not modelled	5.9	13	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** structure of sr-substituted photosystem ii
86	c5b5eT_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure analysis of photosystem ii complex
87	c3wu2t_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure analysis of photosystem ii complex
88	c4ub6t_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
89	c5kaft_	Alignment	not modelled	5.8	13	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** rt xfel structure of photosystem ii in the dark state at 3.0 a2 resolution
90	c4ub6T_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
91	c4ub8t_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
92	c3wu2T_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure analysis of photosystem ii complex
93	c5kaiT_	Alignment	not modelled	5.8	13	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
94	c5gtht_	Alignment	not modelled	5.8	13	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** native xfel structure of photosystem ii (dark dataset)
95	c5v2cT_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** re-refinement of crystal structure of photosystem ii complex
96	c5zznT_	Alignment	not modelled	5.8	13	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of photosystem ii from an sqdg-deficient mutant of2 thermosynechococcus elongatus
97	c4ub8T_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
98	c5b66t_	Alignment	not modelled	5.8	13	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure analysis of photosystem ii complex
99	c5zznt_	Alignment	not modelled	5.8	13	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of photosystem ii from an sqdg-deficient mutant of2 thermosynechococcus elongatus