

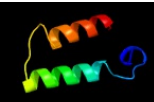


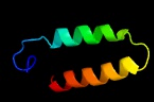





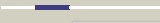

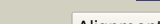









































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4uisB_	 Alignment		71.1	12	PDB header: hydrolase Chain: B: PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex PDB Entry: PDBe RCSB PDBj
2	d1dnpa1	 Alignment		36.0	15	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
3	d1rrza_	 Alignment		34.8	55	Fold: Spectrin repeat-like Superfamily: Glycogen synthesis protein GlgS Family: Glycogen synthesis protein GlgS PDB entry: PDBe RCSB PDBj
4	c1rrza_	 Alignment		34.8	55	PDB header: structural genomics,biosynthetic protein Chain: A: PDB Molecule: glycogen synthesis protein glgs; PDBTitle: solution structure of glgs protein from e. coli PDB Entry: PDBe RCSB PDBj
5	c7k82A_	 Alignment		30.4	35	PDB header: gene regulation Chain: A: PDB Molecule: swi/snf and rsc complexes subunit ssr4; PDBTitle: the x-ray crystal structure of ssr4, an s. pombe chromatin remodelling2 protein: sulfur sad PDB Entry: PDBe RCSB PDBj
6	c5zm0A_	 Alignment		25.4	17	PDB header: flavoprotein Chain: A: PDB Molecule: cryptochrome photoreceptor; PDBTitle: x-ray structure of animal-like cryptochrome from chlamydomonas2 reinhardtii PDB Entry: PDBe RCSB PDBj
7	c1tezB_	 Alignment		24.6	26	PDB header: lyase/dna Chain: B: PDB Molecule: deoxyribodipyrimidine photolyase; PDBTitle: complex between dna and the dna photolyase from anacystis nidulans PDB Entry: PDBe RCSB PDBj
8	c3cvyA_	 Alignment		23.3	21	PDB header: lyase/dna Chain: A: PDB Molecule: re11660p; PDBTitle: drosophila melanogaster (6-4) photolyase bound to repaired ds dna PDB Entry: PDBe RCSB PDBj
9	c6ptzA_	 Alignment		22.3	12	PDB header: circadian clock protein Chain: A: PDB Molecule: cryptochrome-1; PDBTitle: crystal structure of pigeon cryptochrome 4 mutant y319d in complex2 with flavin adenine dinucleotide PDB Entry: PDBe RCSB PDBj
10	c3fy4C_	 Alignment		20.0	13	PDB header: lyase Chain: C: PDB Molecule: 6-4 photolyase; PDBTitle: (6-4) photolyase crystal structure PDB Entry: PDBe RCSB PDBj
11	c6zz6D_	 Alignment		19.6	19	PDB header: cell cycle Chain: D: PDB Molecule: sister chromatid cohesion protein 2; PDBTitle: cryo-em structure of s.cerevisiae cohesin-scc2-dna complex PDB Entry: PDBe RCSB PDBj

12	c1np7A	Alignment		18.7	17	PDB header: lyase Chain: A: PDB Molecule: dna photolyase; PDBTitle: crystal structure analysis of synechocystis sp. pcc6803 cryptochrome PDB Entry: PDBe RCSB PDBj
13	d1owa1	Alignment		18.6	21	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
14	d1np7a1	Alignment		18.0	17	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
15	d1u3da1	Alignment		16.2	17	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
16	c4i6gA	Alignment		16.0	17	PDB header: transcription Chain: A: PDB Molecule: cryptochrome-2; PDBTitle: a vertebrate cryptochrome with fad PDB Entry: PDBe RCSB PDBj
17	c4ln0C	Alignment		16.0	38	PDB header: transcription Chain: C: PDB Molecule: transcription cofactor vestigial-like protein 4; PDBTitle: crystal structure of the vgl4-tead4 complex PDB Entry: PDBe RCSB PDBj
18	c6kiiA	Alignment		16.0	20	PDB header: dna binding protein, lyase Chain: A: PDB Molecule: deoxyribopyrimidine photolyase; PDBTitle: photolyase from arthrosira platensis PDB Entry: PDBe RCSB PDBj
19	d1ni5a4	Alignment		13.6	15	Fold: Mesj substrate recognition domain-like Superfamily: Mesj substrate recognition domain-like Family: Mesj substrate recognition domain-like PDB entry: PDBe RCSB PDBj
20	c4didB	Alignment		13.5	38	PDB header: hydrolase/hydrolase Chain: B: PDB Molecule: inositol phosphatase sopb; PDBTitle: crystal structure of salmonella effector n-terminal domain sopb in2 complex with cdc42 PDB Entry: PDBe RCSB PDBj
21	c6cfwl	Alignment	not modelled	13.4	46	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase PDB Entry: PDBe RCSB PDBj
22	c6hyeF	Alignment	not modelled	13.2	73	PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a) PDB Entry: PDBe RCSB PDBj
23	c3imoC	Alignment	not modelled	13.0	24	PDB header: unknown function Chain: C: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of vibrio cholerae. integron2 cassette protein vch_cass14 PDB Entry: PDBe RCSB PDBj
24	c3femB	Alignment	not modelled	12.8	73	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae PDB Entry: PDBe RCSB PDBj
25	c6hxeE	Alignment	not modelled	12.7	64	PDB header: plant protein Chain: E: PDB Molecule: pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate) PDB Entry: PDBe RCSB PDBj
26	c2zbtB	Alignment	not modelled	12.6	82	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 PDB Entry: PDBe RCSB PDBj
27	c2ejeA	Alignment	not modelled	12.6	33	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna

						PDB Entry: PDBe RCSB PDBj Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like PDB entry: PDBe RCSB PDBj
28	d3bbda1	Alignment	not modelled	12.3	17	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase nep1; PDBTitle: emg1 n1-specific pseudouridine methyltransferase PDB Entry: PDBe RCSB PDBj
29	c5faiA	Alignment	not modelled	12.2	29	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept-hcys-h-e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBj
30	c5f2yA	Alignment	not modelled	12.1	33	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj
31	c5ezeA	Alignment	not modelled	12.1	33	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-hcys-h-e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBj
32	c5f2yG	Alignment	not modelled	12.1	33	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj
33	c5ezeF	Alignment	not modelled	12.1	33	PDB header: ribosomal protein Chain: A: PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase PDB Entry: PDBe RCSB PDBj
34	c2v3jA	Alignment	not modelled	11.8	29	PDB header: transferase Chain: A: PDB Molecule: malate synthase a; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design PDB Entry: PDBe RCSB PDBj
35	c3cuza	Alignment	not modelled	11.7	22	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus PDB Entry: PDBe RCSB PDBj
36	c4firB	Alignment	not modelled	11.2	73	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj
37	c5ezeG	Alignment	not modelled	10.9	33	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s2; PDBTitle: cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae PDB Entry: PDBe RCSB PDBj
38	c6emlr	Alignment	not modelled	10.4	22	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like PDB entry: PDBe RCSB PDBj
39	d2v3ka1	Alignment	not modelled	10.3	29	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis PDB Entry: PDBe RCSB PDBj
40	c2nv2U	Alignment	not modelled	9.7	64	PDB header: signaling protein Chain: A: PDB Molecule: cryptochrome-1; PDBTitle: structure of full-length drosophila cryptochrome PDB Entry: PDBe RCSB PDBj
41	c3tvsA	Alignment	not modelled	9.6	15	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide core biosynthesis protein rfag; PDBTitle: structure of an n-terminal membrane-anchoring region of the2 glycosyltransferase waag PDB Entry: PDBe RCSB PDBj
42	c2n58A	Alignment	not modelled	9.5	60	PDB header: cell cycle Chain: D: PDB Molecule: protein caf40; PDBTitle: yeast not1 cn9bd-caf40 complex PDB Entry: PDBe RCSB PDBj
43	c4cv5D	Alignment	not modelled	9.2	21	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj
44	c5ezeC	Alignment	not modelled	9.1	37	PDB header: de novo protein Chain: E: PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj
45	c5ezeE	Alignment	not modelled	9.1	37	PDB header: de novo protein Chain: E: PDB Molecule: cc-hept-hcys-h-e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBj
46	c5f2yE	Alignment	not modelled	9.1	37	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj
47	c2d99A	Alignment	not modelled	9.1	20	PDB header: lyase (carbon-carbon) Chain: A: PDB Molecule: dna photolyase; PDBTitle: structure of deoxyribodipyrimidine photolyase
48	c1dnpA	Alignment	not modelled	9.0	15	

						PDB Entry: PDBe RCSB PDBj PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj
49	c2dn5A_	 Alignment	not modelled	9.0	25	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form PDB Entry: PDBe RCSB PDBj
50	c3ih9A_	 Alignment	not modelled	8.9	27	PDB header: signaling protein Chain: A: PDB Molecule: cryptochrome 1 apoprotein; PDBTitle: crystal structure of the phr domain of cryptochrome 1 from2 arabidopsis thaliana PDB Entry: PDBe RCSB PDBj
51	c1u3cA_	 Alignment	not modelled	8.6	14	PDB header: dna binding protein Chain: A: PDB Molecule: cryptochrome dash; PDBTitle: cryptochrome 3 from arabidopsis thaliana PDB Entry: PDBe RCSB PDBj
52	c2j4dA_	 Alignment	not modelled	8.6	20	PDB header: transcription Chain: A: PDB Molecule: rcd1 required for cell differentiation1 homolog; PDBTitle: crystal structure analysis of human rcd-1 conserved region PDB Entry: PDBe RCSB PDBj
53	c2fv2A_	 Alignment	not modelled	8.6	18	PDB header: transferase/transferase Chain: F: PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex PDB Entry: PDBe RCSB PDBj
54	c4adsF_	 Alignment	not modelled	8.2	64	PDB header: hydrolase Chain: F: PDB Molecule: mazg-like nucleoside triphosphate pyrophosphohydrolase; PDBTitle: crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese PDB Entry: PDBe RCSB PDBj
55	c2yf3F_	 Alignment	not modelled	7.9	35	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj
56	c2dn4A_	 Alignment	not modelled	7.9	20	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: cryo-em structure of psii at 1.95 angstrom resolution PDB Entry: PDBe RCSB PDBj
57	c7d1tY_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: cryo-em structure of psii at 2.08 angstrom resolution PDB Entry: PDBe RCSB PDBj
58	c7d1uY_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: cryo-em structure of psii at 1.95 angstrom resolution PDB Entry: PDBe RCSB PDBj
59	c7d1ty_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: cryo-em structure of psii at 2.08 angstrom resolution PDB Entry: PDBe RCSB PDBj
60	c3wu2Y_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex PDB Entry: PDBe RCSB PDBj
61	c7d1uy_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: structure of monomeric photosystem ii PDB Entry: PDBe RCSB PDBj
62	c5tisY_	 Alignment	not modelled	7.7	40	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution PDB Entry: PDBe RCSB PDBj
63	c7edaY_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: structure of monomeric photosystem ii PDB Entry: PDBe RCSB PDBj
64	c5kaiY_	 Alignment	not modelled	7.7	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: cryo-em structure of psii at 2.08 angstrom resolution PDB Entry: PDBe RCSB PDBj
65	d1q60a_	 Alignment	not modelled	7.5	20	Fold: GTF2I-like repeat Superfamily: GTF2I-like repeat Family: GTF2I-like repeat PDB entry: PDBe RCSB PDBj
66	c5ipxA_	 Alignment	not modelled	7.3	18	PDB header: viral protein Chain: A: PDB Molecule: orf49 protein; PDBTitle: structure of orf49 from kshv PDB Entry: PDBe RCSB PDBj
67	c5mx2y_	 Alignment	not modelled	7.2	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution PDB Entry: PDBe RCSB PDBj
68	c3a0by_	 Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of br-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBj

69	c3a0bY_		Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y; PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of br-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBj
70	c4tnky_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution PDB Entry: PDBe RCSB PDBj
71	c7nhoy_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: PDBTitle: structure of psii-m PDB Entry: PDBe RCSB PDBj
72	c4tnhy_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution PDB Entry: PDBe RCSB PDBj
73	c4tnkg_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: G; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution PDB Entry: PDBe RCSB PDBj
74	c4tnjy_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution PDB Entry: PDBe RCSB PDBj
75	c3prry_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein z; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer PDB Entry: PDBe RCSB PDBj
76	c4fbvy_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: fs x-ray diffraction of photosystem ii PDB Entry: PDBe RCSB PDBj
77	c4tniy_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution PDB Entry: PDBe RCSB PDBj
78	c7nhqy_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: PDBTitle: structure of psii-i prime (psii with psb28, and psb34) PDB Entry: PDBe RCSB PDBj
79	c4fbym_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: M; PDB Molecule: photosystem ii reaction center protein m; PDBTitle: fs x-ray diffraction of photosystem ii PDB Entry: PDBe RCSB PDBj
80	c3bz1y_		Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y; PDB Molecule: photosystem ii protein y; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer PDB Entry: PDBe RCSB PDBj
81	c4ixqg_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: G; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state PDB Entry: PDBe RCSB PDBj
82	c7nhpy_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: PDBTitle: structure of psii-i (psii with psb27, psb28, and psb34) PDB Entry: PDBe RCSB PDBj
83	c4ixrg_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: G; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state PDB Entry: PDBe RCSB PDBj
84	c4ixry_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state PDB Entry: PDBe RCSB PDBj
85	c4ixqy_		Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state PDB Entry: PDBe RCSB PDBj
86	c3a0hy_		Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y; PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of i-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBj
87	c3a0hY_		Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y; PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of i-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBj
88	c4tnhg_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: G; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution PDB Entry: PDBe RCSB PDBj
89	c4tnjg_		Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: G; PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution PDB Entry: PDBe RCSB PDBj
90	c3wu2y_		Alignment	not modelled	6.9	40	PDB header: electron transport, photosynthesis Chain: Y; PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure analysis of photosystem ii complex

						PDB Entry: PDBe RCSB PDBj
91	c3bz2y_	Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii protein y; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer PDB Entry: PDBe RCSB PDBj
92	c3kziy_	Alignment	not modelled	6.9	40	PDB header: electron transport Chain: Y: PDB Molecule: PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii PDB Entry: PDBe RCSB PDBj
93	c4tnig_	Alignment	not modelled	6.9	40	PDB header: electron transport,photosynthesis Chain: G: PDB Molecule: photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution PDB Entry: PDBe RCSB PDBj
94	c3prqy_	Alignment	not modelled	6.9	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii psbx protein; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer PDB Entry: PDBe RCSB PDBj
95	c3rgbG_	Alignment	not modelled	6.6	30	PDB header: oxidoreductase Chain: G: PDB Molecule: methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath) PDB Entry: PDBe RCSB PDBj
96	c6jloY_	Alignment	not modelled	6.6	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: xfel structure of cyanobacterial photosystem ii (2f state, dataset2) PDB Entry: PDBe RCSB PDBj
97	c7cjjY_	Alignment	not modelled	6.6	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: photosystem ii structure in the s2 state PDB Entry: PDBe RCSB PDBj
98	c7cjjy_	Alignment	not modelled	6.6	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: photosystem ii structure in the s2 state PDB Entry: PDBe RCSB PDBj
99	c6jlnY_	Alignment	not modelled	6.6	40	PDB header: photosynthesis Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: xfel structure of cyanobacterial photosystem ii (1f state, dataset2) PDB Entry: PDBe RCSB PDBj