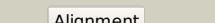
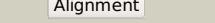
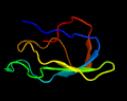
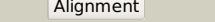
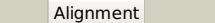
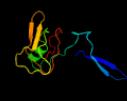
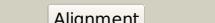
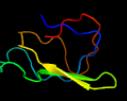
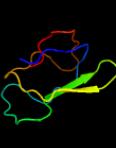
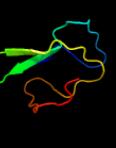
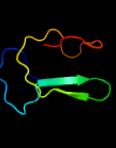
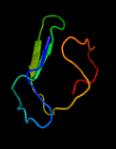


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD0437c_(psd)_525390_526085
Date	Tue Jul 23 14:50:51 BST 2019
Unique Job ID	9249badb6d232785

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1glaf_</a>			98.4	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
2	<a href="#">d2gpra_</a>			98.4	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
3	<a href="#">d2f3ga_</a>			98.3	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
4	<a href="#">d1gpra_</a>			98.2	13	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
5	<a href="#">c2ejgD_</a>			96.4	34	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> 149aa long hypothetical methylmalonyl-coa decarboxylase <b>PDBTitle:</b> crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
6	<a href="#">c2aukA_</a>			96.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> structure of e. coli rna polymerase beta' g/g' insert
7	<a href="#">c4hnvB_</a>			95.2	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of r54e mutant of s. aureus pyruvate carboxylase
8	<a href="#">c3n6rk_</a>			95.1	18	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
9	<a href="#">c2b8gA_</a>			95.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> biotin/lipoyl attachment protein; <b>PDBTitle:</b> solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
10	<a href="#">c3hb1A_</a>			94.9	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate carboxylase t908a mutant
11	<a href="#">c3bg5B_</a>			94.8	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate carboxylase

12	<a href="#">c5vz0D_</a>	Alignment		94.7	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
13	<a href="#">d1dcza_</a>	Alignment		94.5	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
14	<a href="#">d1bdoa_</a>	Alignment		94.4	22	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
15	<a href="#">c4qskB_</a>	Alignment		94.3	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
16	<a href="#">c3va7A_</a>	Alignment		94.3	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> klla0e08119p; <b>PDBTitle:</b> crystal structure of the kluyveromyces lactis urea carboxylase
17	<a href="#">c5ks8D_</a>	Alignment		94.2	23	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
18	<a href="#">c2ejmA_</a>	Alignment		93.7	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase subunit alpha; <b>PDBTitle:</b> solution structure of ruh-072, an apo-biotin domain form2 human acetyl coenzyme a carboxylase
19	<a href="#">d1ghja_</a>	Alignment		93.2	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
20	<a href="#">d1iyua_</a>	Alignment		92.9	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
21	<a href="#">c3bg3A_</a>	Alignment	not modelled	92.8	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
22	<a href="#">d1laba_</a>	Alignment	not modelled	92.5	22	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
23	<a href="#">c2l5tA_</a>	Alignment	not modelled	92.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase; <b>PDBTitle:</b> solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
24	<a href="#">c5ks8F_</a>	Alignment	not modelled	92.3	21	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
25	<a href="#">d1k8ma_</a>	Alignment	not modelled	92.1	14	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
26	<a href="#">c2dn8A_</a>	Alignment	not modelled	92.1	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> solution structure of rsg1 ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
27	<a href="#">c3u9sA_</a>	Alignment	not modelled	91.6	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, alpha-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
28	<a href="#">d1o78a_</a>	Alignment	not modelled	91.5	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains

29	<a href="#">c3tufB</a>	Alignment	not modelled	91.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation protein q; <b>PDBTitle:</b> structure of the spoiiq-spoiiah pore forming complex.
30	<a href="#">c2hsIB</a>	Alignment	not modelled	91.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative peptidase m23; <b>PDBTitle:</b> crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
31	<a href="#">d1gjoa</a>	Alignment	not modelled	90.4	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
32	<a href="#">c4rcnA</a>	Alignment	not modelled	90.3	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain acyl-coa carboxylase; <b>PDBTitle:</b> structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
33	<a href="#">d1gjxa</a>	Alignment	not modelled	89.3	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
34	<a href="#">c2q8iB</a>	Alignment	not modelled	89.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase component of <b>PDBTitle:</b> pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
35	<a href="#">c2kccA</a>	Alignment	not modelled	89.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> solution structure of biotinyl domain from human acetyl-2 coa carboxylase 2
36	<a href="#">d1y8ob1</a>	Alignment	not modelled	88.8	26	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
37	<a href="#">c3uz0D</a>	Alignment	not modelled	88.7	25	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> stage ii sporulation protein q; <b>PDBTitle:</b> crystal structure of spoiiah and spoiiq complex
38	<a href="#">c4bh5B</a>	Alignment	not modelled	86.4	21	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> murein hydrolase activator envc; <b>PDBTitle:</b> lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
39	<a href="#">c2dncA</a>	Alignment	not modelled	86.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> solution structure of rsg1 ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
40	<a href="#">d1ci3m2</a>	Alignment	not modelled	86.2	36	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
41	<a href="#">c5kvP</a>	Alignment	not modelled	86.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zoocin a endopeptidase; <b>PDBTitle:</b> solution structure of the catalytic domain of zoocin a
42	<a href="#">c5csIA</a>	Alignment	not modelled	85.2	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
43	<a href="#">c5j1IA</a>	Alignment	not modelled	84.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> toxr-activated gene (tage); <b>PDBTitle:</b> crystal structure of csd1-csd2 dimer i
44	<a href="#">d1e2wa2</a>	Alignment	not modelled	83.8	32	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
45	<a href="#">d1pmra</a>	Alignment	not modelled	83.7	15	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
46	<a href="#">c5j1mD</a>	Alignment	not modelled	83.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> toxr-activated gene (tage); <b>PDBTitle:</b> crystal structure of csd1-csd2 dimer ii
47	<a href="#">c2aujD</a>	Alignment	not modelled	82.7	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> structure of thermus aquaticus rna polymerase beta'-subunit2 insert
48	<a href="#">c4iqzD</a>	Alignment	not modelled	82.3	21	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> the crystal structure of a large insert in rna polymerase (rpoc)2 subunit from e. coli
49	<a href="#">c5b0hB</a>	Alignment	not modelled	81.7	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> leukocyte cell-derived chemotaxin-2; <b>PDBTitle:</b> crystal structure of human leukocyte cell-derived chemotaxin 2
50	<a href="#">c1e2vB</a>	Alignment	not modelled	81.0	32	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> n153q mutant of cytochrome f from chlamydomonas reinhardtii
51	<a href="#">c5kqbA</a>	Alignment	not modelled	80.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase m23; <b>PDBTitle:</b> identification and structural characterization of lytu
52	<a href="#">c1g90A</a>	Alignment	not modelled	79.6	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
53	<a href="#">c3sluB</a>	Alignment	not modelled	79.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> m23 peptidase domain protein; <b>PDBTitle:</b> crystal structure of nmb0315
54	<a href="#">c2gu1A</a>	Alignment	not modelled	79.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc peptidase; <b>PDBTitle:</b> crystal structure of a zinc containing peptidase from2

					vibrio cholerae
55	<a href="#">c2dneA</a>	Alignment	not modelled	78.3	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> solution structure of rsgj ruh-058, a lipoyl domain of human 2-oxacid dehydrogenase
56	<a href="#">c2b44A</a>	Alignment	not modelled	77.4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-glycine endopeptidase lytm; <b>PDBTitle:</b> truncated s. aureus lytm, p 32 2 1 crystal form
57	<a href="#">c2jxmB</a>	Alignment	not modelled	76.8	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
58	<a href="#">c4il6T</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> structure of sr-substituted photosystem ii
59	<a href="#">c5b5et</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
60	<a href="#">c5b66t</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
61	<a href="#">c5zznT</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of photosystem ii from an sqdg-deficient mutant of2 thermosynechococcus elongatus
62	<a href="#">c5v2ct</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> re-refinement of crystal structure of photosystem ii complex
63	<a href="#">c5h2ft</a>	Alignment	not modelled	76.6	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of the psbm-deletion mutant of photosystem ii
64	<a href="#">c5zznt</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of photosystem ii from an sqdg-deficient mutant of2 thermosynechococcus elongatus
65	<a href="#">c5kait</a>	Alignment	not modelled	76.6	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
66	<a href="#">c5kaiT</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
67	<a href="#">c4ub6T</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
68	<a href="#">c5v2cT</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> re-refinement of crystal structure of photosystem ii complex
69	<a href="#">c5ws6T</a>	Alignment	not modelled	76.5	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (preflash two-flash dataset)
70	<a href="#">c4ub8T</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
71	<a href="#">c5tisT</a>	Alignment	not modelled	76.5	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
72	<a href="#">c5ws6t</a>	Alignment	not modelled	76.5	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (preflash two-flash dataset)
73	<a href="#">c4il6t</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> structure of sr-substituted photosystem ii
74	<a href="#">c5tist</a>	Alignment	not modelled	76.5	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
75	<a href="#">c3wu2T</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
76	<a href="#">c5kaft</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 3.0 a2 resolution
77	<a href="#">c5gtit</a>	Alignment	not modelled	76.5	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (two flash dataset)
78	<a href="#">c3wu2t</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
79	<a href="#">c4ub8t</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
80	<a href="#">c4ub6t</a>	Alignment	not modelled	76.5	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native structure of photosystem ii (dataset-1) by a

					femtosecond x-ray2 laser
81	<a href="#">c5gtiT</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (two flash dataset)
82	<a href="#">c5gthT</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (dark dataset)
83	<a href="#">c5ws5t</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (preflash dark dataset)
84	<a href="#">c5b5eT</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure analysis of photosystem ii complex
85	<a href="#">c5gtht</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (dark dataset)
86	<a href="#">c5h2fT</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of the psbm-deletion mutant of photosystem ii
87	<a href="#">c5ws5T</a>	Alignment	not modelled	76.5	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> native xfel structure of photosystem ii (preflash dark dataset)
88	<a href="#">d2axtt1</a>	Alignment	not modelled	76.4	30 <b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein T, PsbT <b>Family:</b> PsbT-like
89	<a href="#">c4rvyT</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
90	<a href="#">c5e79T</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> macromolecular diffractive imaging using imperfect crystals
91	<a href="#">c2axtt</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center t protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
92	<a href="#">c5e7ct</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> macromolecular diffractive imaging using imperfect crystals - bragg2 data
93	<a href="#">c5e79t</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> macromolecular diffractive imaging using imperfect crystals
94	<a href="#">c3arcT</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
95	<a href="#">c4rvyt</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
96	<a href="#">c2axtT</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center t protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
97	<a href="#">c5e7cT</a>	Alignment	not modelled	76.4	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> macromolecular diffractive imaging using imperfect crystals - bragg2 data
98	<a href="#">c4fbgy</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> photosystem q(b) protein 1; <b>PDBTitle:</b> fs x-ray diffraction of photosystem ii
99	<a href="#">c4ixrt</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, first illuminated state
100	<a href="#">c4fbT</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> fs x-ray diffraction of photosystem ii
101	<a href="#">c3prqT</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with2 terbutrynl (part 1 of 2). this file contains first monomer of psii3 dimer
102	<a href="#">c4ixqt</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, dark state
103	<a href="#">c4tnjt</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
104	<a href="#">c3prrT</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with2 terbutrynl (part 2 of 2). this file contains second monomer of psii3 dimer
105	<a href="#">c3bz2T</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer
106	<a href="#">c4tnit</a>	Alignment	not modelled	76.3	30 <b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t;

100	<a href="#">c4tntT</a>	Alignment	not modelled	76.3	30	<b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution <b>PDB header:</b> electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
107	<a href="#">c3bz1T</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
108	<a href="#">c4tnht</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
109	<a href="#">c4ixqT</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, dark state
110	<a href="#">c4tniT</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
111	<a href="#">c4tnkT</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
112	<a href="#">c4tnjT</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
113	<a href="#">c4tnhT</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
114	<a href="#">c4ixrT</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt fs x-ray diffraction of photosystem ii, first illuminated state
115	<a href="#">c4tnkt</a>	Alignment	not modelled	76.3	30	<b>PDB header:</b> electron transport,photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
116	<a href="#">c5kaft</a>	Alignment	not modelled	76.2	30	<b>PDB header:</b> electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> rt xfel structure of photosystem ii in the dark state at 3.0 a2 resolution
117	<a href="#">c1s5lT</a>	Alignment	not modelled	76.2	30	<b>PDB header:</b> photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii psbt protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
118	<a href="#">c1s5lt</a>	Alignment	not modelled	76.2	30	<b>PDB header:</b> photosynthesis <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii psbt protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
119	<a href="#">c3a0bt</a>	Alignment	not modelled	76.1	30	<b>PDB header:</b> electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
120	<a href="#">c3kz1T</a>	Alignment	not modelled	76.1	30	<b>PDB header:</b> electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of monomeric form of cyanobacterial photosystem ii