
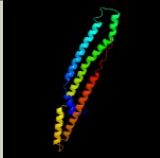

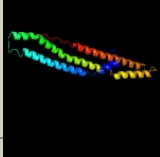

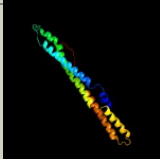

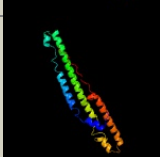

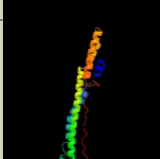

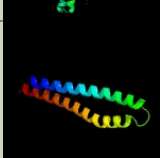

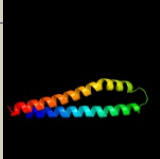

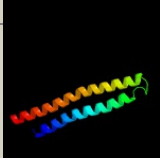

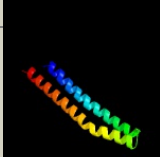

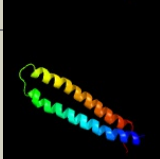

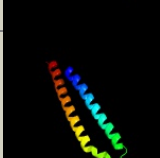


Phyre2

Email mdejesus@rockefeller.edu
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 Date Fri Aug 9 18:20:09 BST 2019
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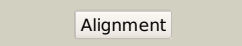
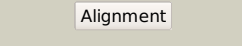
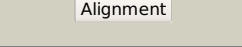
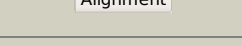
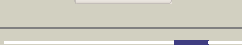

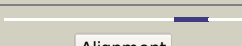




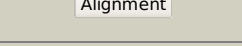
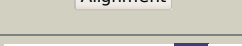
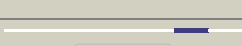
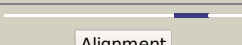



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38B_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/pe protein complex from mycobacterium tuberculosis
2	d2g38b1	 Alignment		100.0	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c5xfsB_	 Alignment		100.0	34	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with espG5 from m.2 tuberculosis
4	c4xy3A_	 Alignment		100.0	16	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		99.3	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.4	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		98.3	18	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		98.3	15	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		98.2	18	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.7	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		97.6	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		97.5	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		97.3	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		96.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	Alignment		96.1	10	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	Alignment		89.1	14	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	c3q4hB_	Alignment		43.5	9	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxhg complex2 (msmeg_0620-msmeg_0621)
18	c1xyr6_	Alignment		18.7	31	PDB header: virus Chain: 6: PDB Molecule: genome polypeptide, coat protein vp3; PDB Fragment: residues 620-630 PDBTitle: poliovirus 135s cell entry intermediate
19	d2ix0a4	Alignment		15.8	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNB domain-like
20	c2iu1A_	Alignment		14.6	14	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
21	c3p5tE_	Alignment	not modelled	13.9	40	PDB header: rna binding protein Chain: E: PDB Molecule: cleavage and polyadenylation specificity factor subunit 5; PDBTitle: cfim25-cfim68 complex
22	d2gtsa1	Alignment	not modelled	13.2	13	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
23	d2r7da2	Alignment	not modelled	13.2	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNB domain-like
24	d2vnud4	Alignment	not modelled	13.0	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNB domain-like
25	c1bkvA_	Alignment	not modelled	12.7	19	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
26	c1bkvC_	Alignment	not modelled	11.9	19	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
27	c1bkvB_	Alignment	not modelled	11.9	19	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
28	c2r7fA_	Alignment	not modelled	10.6	18	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease ii family protein; PDBTitle: crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63 PDB header: translation

29	c2fulE_	Alignment	not modelled	10.2	19	Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
30	c3h6pD_	Alignment	not modelled	9.1	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
31	d1pj3a2	Alignment	not modelled	9.0	9	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
32	c2j8qB_	Alignment	not modelled	8.6	40	PDB header: nuclear protein Chain: B: PDB Molecule: cleavage and polyadenylation specificity factor 5; PDBTitle: crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.
33	d1gq2a2	Alignment	not modelled	8.2	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
34	c5b5et_	Alignment	not modelled	8.2	56	PDB header: electron transport, photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure analysis of photosystem ii complex
35	c4il6T_	Alignment	not modelled	8.2	56	PDB header: electron transport Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: structure of sr-substituted photosystem ii
36	c1s5IT_	Alignment	not modelled	8.1	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii psbt protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
37	c1s5lt_	Alignment	not modelled	8.1	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii psbt protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
38	d1o0sa2	Alignment	not modelled	7.9	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
39	c4ixqt_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state
40	c4tniT_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
41	c4ixrt_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
42	c3prrT_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
43	c3bz1T_	Alignment	not modelled	7.7	56	PDB header: electron transport Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
44	c4tnjT_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
45	c4tnkT_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
46	c4tnjt_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
47	c4tnht_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
48	c4fbyT_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: fs x-ray diffraction of photosystem ii
49	c4tnhT_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
50	c4ixrT_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
51	c4ixqT_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state
52	c4fbyg_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: G: PDB Molecule: photosystem q(b) protein 1; PDBTitle: fs x-ray diffraction of photosystem ii
53	c3prqT_	Alignment	not modelled	7.7	56	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
54	c3bz2T_	Alignment	not modelled	7.7	56	PDB header: electron transport Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer

55	c4tnkt_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third illumination at 5.2 a resolution
56	c4tnit_	Alignment	not modelled	7.7	56	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third illumination at 4.6 a resolution
57	c3wzhA_	Alignment	not modelled	6.6	10	PDB header: transcription Chain: A; PDB Molecule: uncharacterized protein af_1864; PDBTitle: crystal structure of afcsx3
58	d1paqa_	Alignment	not modelled	6.5	18	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
59	c1paqA_	Alignment	not modelled	6.5	18	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
60	c2y5tG_	Alignment	not modelled	6.2	50	PDB header: immune system Chain: G; PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
61	c2f6aj_	Alignment	not modelled	6.2	43	PDB header: cell adhesion/structural protein Chain: J; PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
62	c2vnuD_	Alignment	not modelled	6.1	11	PDB header: hydrolase/rna Chain: D; PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: crystal structure of sc rrp44
63	c2y5tE_	Alignment	not modelled	5.9	50	PDB header: immune system Chain: E; PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
64	c6c7nD_	Alignment	not modelled	5.9	18	PDB header: oxidoreductase Chain: D; PDB Molecule: malic enzyme; PDBTitle: monoclinic form of malic enzyme from sorghum at 2 angstroms resolution
65	c2f6aG_	Alignment	not modelled	5.8	43	PDB header: cell adhesion/structural protein Chain: G; PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
66	c2f6aF_	Alignment	not modelled	5.8	43	PDB header: cell adhesion/structural protein Chain: F; PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
67	c2f6aH_	Alignment	not modelled	5.8	43	PDB header: cell adhesion/structural protein Chain: H; PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
68	c2f6aE_	Alignment	not modelled	5.8	43	PDB header: cell adhesion/structural protein Chain: E; PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
69	c2f6aI_	Alignment	not modelled	5.8	43	PDB header: cell adhesion/structural protein Chain: I; PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
70	c1vw45_	Alignment	not modelled	5.7	10	PDB header: ribosome Chain: 5; PDB Molecule: 54s ribosomal protein I3, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
71	c5xguB_	Alignment	not modelled	5.7	22	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease r; PDBTitle: escherichia coli. rnase r
72	c2aw5A_	Alignment	not modelled	5.7	27	PDB header: oxidoreductase Chain: A; PDB Molecule: nadp-dependent malic enzyme; PDBTitle: crystal structure of a human malic enzyme
73	c3juiA_	Alignment	not modelled	5.6	27	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
74	d2vk9a1	Alignment	not modelled	5.6	31	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
75	c3wjaA_	Alignment	not modelled	5.4	27	PDB header: oxidoreductase Chain: A; PDB Molecule: nadp-dependent malic enzyme; PDBTitle: the crystal structure of human cytosolic nadp(+)-dependent malic2 enzyme in apo form
76	c1gz3B_	Alignment	not modelled	5.2	9	PDB header: oxidoreductase Chain: B; PDB Molecule: nad-dependent malic enzyme, mitochondrial; PDBTitle: molecular mechanism for the regulation of human mitochondrial nad(p)+2 dependent malic enzyme by atp and fumarate
77	c1qr6A_	Alignment	not modelled	5.2	9	PDB header: oxidoreductase Chain: A; PDB Molecule: malic enzyme 2; PDBTitle: human mitochondrial nad(p)-dependent malic enzyme
78	c5tisT_	Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
79	c5zznt_	Alignment	not modelled	5.1	63	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
80	c3wu2T_	Alignment	not modelled	5.1	63	PDB header: electron transport, photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure analysis of photosystem ii complex

81	c5kaiT_	 Alignment	not modelled	5.1	63	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
82	c5kafT_	 Alignment	not modelled	5.1	63	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
83	c5tist_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
84	c5kaft_	 Alignment	not modelled	5.1	63	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
85	c5kaiT_	 Alignment	not modelled	5.1	63	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
86	c5ws6T_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: native xfel structure of photosystem ii (preflash two-flash dataset)
87	c4ub6T_	 Alignment	not modelled	5.1	63	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
88	c5gthT_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: native xfel structure of photosystem ii (dark dataset)
89	c4ub8T_	 Alignment	not modelled	5.1	63	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
90	c5zznT_	 Alignment	not modelled	5.1	63	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
91	c4ub8T_	 Alignment	not modelled	5.1	63	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	c4ub6T_	 Alignment	not modelled	5.1	63	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
93	c5v2cT_	 Alignment	not modelled	5.1	63	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
94	c5ws6T_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: native xfel structure of photosystem ii (preflash two-flash dataset)
95	c5h2ft_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of the psbm-deletion mutant of photosystem ii
96	c4il6T_	 Alignment	not modelled	5.1	63	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: structure of sr-substituted photosystem ii
97	c5gtiT_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: native xfel structure of photosystem ii (two flash dataset)
98	c5gtit_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: native xfel structure of photosystem ii (two flash dataset)
99	c5ws5T_	 Alignment	not modelled	5.1	63	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: native xfel structure of photosystem ii (preflash dark dataset)