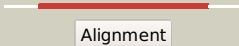



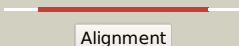

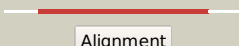
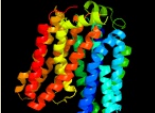
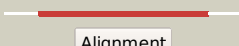

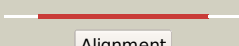

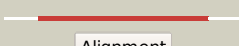











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2333c_(-)_2606718_2608331
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	dd014bf23ec246a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pw4a_</a>	 Alignment		100.0	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
2	<a href="#">c4zp0A_</a>	 Alignment		100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
3	<a href="#">c3wdoA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
4	<a href="#">c6e9oA_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactonate transport; <b>PDBTitle:</b> e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
5	<a href="#">c4ldsB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcab; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
6	<a href="#">c4cl5B_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate transporter 1.1; <b>PDBTitle:</b> crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
7	<a href="#">c6h7dA_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transport protein 10; <b>PDBTitle:</b> crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
8	<a href="#">c6gs7A_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide and tripeptide permease a; <b>PDBTitle:</b> crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
9	<a href="#">c4ikyA_</a>	 Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide abc transporter (permease); <b>PDBTitle:</b> crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
10	<a href="#">c5c65A_</a>	 Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> structure of the human glucose transporter glut3 / slc2a3
11	<a href="#">c4apsB_</a>	 Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> di- or tripeptide h+ symporter; <b>PDBTitle:</b> crystal structure of a pot family peptide transporter in an inward2 open conformation.

12	<a href="#">c2gfpA_</a>	Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
13	<a href="#">c4gbzA_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-proton symporter; <b>PDBTitle:</b> the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
14	<a href="#">c6g9xB_</a>	Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> major facilitator superfamily mfs_1; <b>PDBTitle:</b> crystal structure of a mfs transporter at 2.54 angstrom resolution
15	<a href="#">c6exsA_</a>	Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter permease; <b>PDBTitle:</b> crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
16	<a href="#">c6ei3A_</a>	Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
17	<a href="#">c4j05A_</a>	Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
18	<a href="#">c4ybaB_</a>	Alignment		100.0	12	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> rat glut5 with fv in the outward-open form
19	<a href="#">c3o7pA_</a>	Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
20	<a href="#">c4w6vA_</a>	Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-/tripeptide transporter; <b>PDBTitle:</b> crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
21	<a href="#">c2xutC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
22	<a href="#">d1pv7a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
23	<a href="#">c1pv7B_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lactose permease; <b>PDBTitle:</b> crystal structure of lactose permease with tdg
24	<a href="#">c4pypA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> crystal structure of the human glucose transporter glut1
25	<a href="#">c4lepB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton:oligopeptide symporter pot family; <b>PDBTitle:</b> structural insights into substrate recognition in proton dependent2 oligopeptide transporters
26	<a href="#">c4q65A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide permease d; <b>PDBTitle:</b> structure of the e. coli peptide transporter ybgh
27	<a href="#">c4iu8A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
28	<a href="#">c4iu9A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter
						<b>PDB header:</b> transport protein

29	<a href="#">c5aynA_</a>	Alignment	not modelled	100.0	18	<b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
30	<a href="#">c5aymA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
31	<a href="#">c4m64D_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> melibiose carrier protein; <b>PDBTitle:</b> 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
32	<a href="#">c6ob7A_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> equilibrative nucleoside transporter 1; <b>PDBTitle:</b> human equilibrative nucleoside transporter-1, dilazep bound
33	<a href="#">c6nbxG_</a>	Alignment	not modelled	65.3	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
34	<a href="#">c4r0cB_</a>	Alignment	not modelled	62.4	9	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> abgt putative transporter family; <b>PDBTitle:</b> crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology
35	<a href="#">c3b9yA_</a>	Alignment	not modelled	56.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter family rh-like protein; <b>PDBTitle:</b> crystal structure of the nitrosomonas europaea rh protein
36	<a href="#">c6cfwl_</a>	Alignment	not modelled	34.0	6	<b>PDB header:</b> membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
37	<a href="#">c3qngD_</a>	Alignment	not modelled	28.9	5	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
38	<a href="#">c4djiA_</a>	Alignment	not modelled	21.1	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
39	<a href="#">c5iwsA_</a>	Alignment	not modelled	21.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-n(pi)-phosphohistidine-sugar phosphotransferase <b>PDBTitle:</b> crystal structure of the transporter malt, the eic domain from the2 maltose-specific phosphotransferase system
40	<a href="#">d2aw2a1</a>	Alignment	not modelled	17.2	63	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
41	<a href="#">c2h31A_</a>	Alignment	not modelled	17.2	67	<b>PDB header:</b> ligase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> multifunctional protein ade2; <b>PDBTitle:</b> crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
42	<a href="#">d1xaua_</a>	Alignment	not modelled	16.4	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
43	<a href="#">c2g9pA_</a>	Alignment	not modelled	16.1	21	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide latarcin 2a; <b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
44	<a href="#">c3a0bT_</a>	Alignment	not modelled	12.6	25	<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
45	<a href="#">c3arct_</a>	Alignment	not modelled	12.6	25	<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
46	<a href="#">c4ja0A_</a>	Alignment	not modelled	12.2	67	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution
47	<a href="#">c3prrT_</a>	Alignment	not modelled	11.2	22	<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 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
48	<a href="#">c3prqT_</a>	Alignment	not modelled	11.2	22	<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 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
49	<a href="#">c4fbyg_</a>	Alignment	not modelled	11.2	22	<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
50	<a href="#">c4tnkT_</a>	Alignment	not modelled	11.2	22	<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
51	<a href="#">c4tnjT_</a>	Alignment	not modelled	11.2	22	<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
52	<a href="#">c4tnhT_</a>	Alignment	not modelled	11.2	22	<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
						<b>PDB header:</b> photosynthesis

53	<a href="#">c4fbyT_</a>	Alignment	not modelled	11.2	22	<b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> fs x-ray diffraction of photosystem ii
54	<a href="#">c4tnkt_</a>	Alignment	not modelled	11.2	22	<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
55	<a href="#">c4tniT_</a>	Alignment	not modelled	11.2	22	<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
56	<a href="#">c4ixrT_</a>	Alignment	not modelled	11.2	22	<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
57	<a href="#">c4tnit_</a>	Alignment	not modelled	11.2	22	<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
58	<a href="#">c4ixrt_</a>	Alignment	not modelled	11.2	22	<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
59	<a href="#">c3bz2T_</a>	Alignment	not modelled	11.2	22	<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
60	<a href="#">c4ixqt_</a>	Alignment	not modelled	11.2	22	<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
61	<a href="#">c3bz1T_</a>	Alignment	not modelled	11.2	22	<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
62	<a href="#">c4ixqT_</a>	Alignment	not modelled	11.2	22	<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
63	<a href="#">c4tnjt_</a>	Alignment	not modelled	11.2	22	<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
64	<a href="#">c4tnht_</a>	Alignment	not modelled	11.2	22	<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
65	<a href="#">c5xpdA_</a>	Alignment	not modelled	10.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> sugar transporter; <b>PDBTitle:</b> sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
66	<a href="#">c6r5kA_</a>	Alignment	not modelled	9.8	16	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> pan2-pan3 deadenylation complex catalytic subunit pan2; <b>PDBTitle:</b> cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
67	<a href="#">d1dtdb_</a>	Alignment	not modelled	9.7	32	<b>Fold:</b> Carboxypeptidase inhibitor <b>Superfamily:</b> Carboxypeptidase inhibitor <b>Family:</b> Carboxypeptidase inhibitor
68	<a href="#">c5mx2T_</a>	Alignment	not modelled	9.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
69	<a href="#">c2jlnA_</a>	Alignment	not modelled	9.4	7	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
70	<a href="#">c4r1iB_</a>	Alignment	not modelled	9.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> aminobenzoyl-glutamate transporter; <b>PDBTitle:</b> structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
71	<a href="#">c4pj0T_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
72	<a href="#">c4pj0T_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
73	<a href="#">c5mx2t_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T; <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
74	<a href="#">c4rvyT_</a>	Alignment	not modelled	9.0	25	<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)
75	<a href="#">c5e7ct_</a>	Alignment	not modelled	9.0	25	<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
76	<a href="#">c3a0hT_</a>	Alignment	not modelled	9.0	25	<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 i-substituted photosystem ii complex
77	<a href="#">c5e79t_</a>	Alignment	not modelled	9.0	25	<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
78	<a href="#">c3arcT_</a>	Alignment	not modelled	9.0	25	<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

79	<a href="#">c3a0ht_</a>	Alignment	not modelled	9.0	25	<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 i-substituted photosystem ii complex
80	<a href="#">c3kzIT_</a>	Alignment	not modelled	9.0	25	<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
81	<a href="#">c4rvyt_</a>	Alignment	not modelled	9.0	25	<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)
82	<a href="#">d2axtt1</a>	Alignment	not modelled	9.0	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein T, PsbT <b>Family:</b> PsbT-like
83	<a href="#">c5e7cT_</a>	Alignment	not modelled	9.0	25	<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
84	<a href="#">c2axtT_</a>	Alignment	not modelled	9.0	25	<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
85	<a href="#">c2axtt_</a>	Alignment	not modelled	9.0	25	<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
86	<a href="#">c5e79T_</a>	Alignment	not modelled	9.0	25	<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
87	<a href="#">c1s5It_</a>	Alignment	not modelled	9.0	25	<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
88	<a href="#">c1s5IT_</a>	Alignment	not modelled	9.0	25	<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
89	<a href="#">d1lghb_</a>	Alignment	not modelled	9.0	17	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
90	<a href="#">c4px7A_</a>	Alignment	not modelled	8.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylglycerophosphatase; <b>PDBTitle:</b> crystal structure of lipid phosphatase e. coli pgpb
91	<a href="#">c6et5u_</a>	Alignment	not modelled	8.2	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> U; <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
92	<a href="#">c3v5uA_</a>	Alignment	not modelled	7.5	15	<b>PDB header:</b> metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized membrane protein mj0091; <b>PDBTitle:</b> structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
93	<a href="#">c4kppA_</a>	Alignment	not modelled	7.2	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
94	<a href="#">c5i6cB_</a>	Alignment	not modelled	7.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> uric acid-xanthine permease; <b>PDBTitle:</b> the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
95	<a href="#">c2knpA_</a>	Alignment	not modelled	6.8	67	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> mcocc-1; <b>PDBTitle:</b> isolation and characterization of peptides from momordica2 cochinchinensis seeds.
96	<a href="#">c2kncA_</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
97	<a href="#">d2nr9a1</a>	Alignment	not modelled	6.7	13	<b>Fold:</b> Rhomboid-like <b>Superfamily:</b> Rhomboid-like <b>Family:</b> Rhomboid-like
98	<a href="#">c5b66T_</a>	Alignment	not modelled	6.4	26	<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
99	<a href="#">c4i16t_</a>	Alignment	not modelled	6.3	26	<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