Phyre^2

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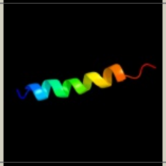
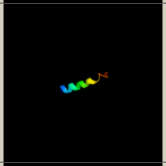
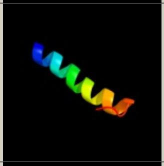
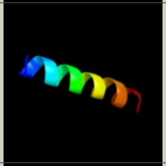
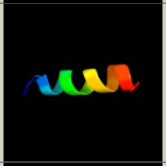
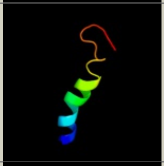
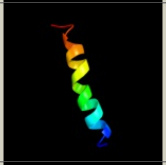
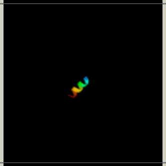
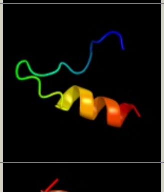
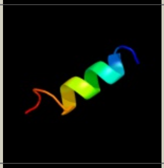
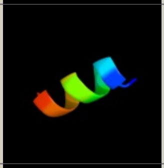
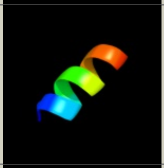
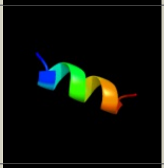
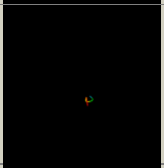
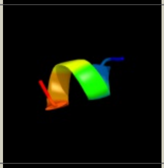
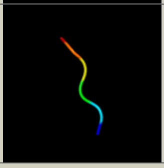
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lw52_	Alignment		56.2	21	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from photosystem i; **PDB Fragment:**residues 81-246; **PDBTitle:** improved model of plant photosystem i
2	c2wsf2_	Alignment		54.2	21	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from **PDBTitle:** improved model of plant photosystem i
3	c2wse4_	Alignment		50.6	29	**PDB header:**photosynthesis **Chain:** 4: **PDB Molecule:**chlorophyll a-b binding protein p4, **PDBTitle:** improved model of plant photosystem i
4	c3pl9A_	Alignment		48.6	25	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**chlorophyll a-b binding protein; **PDBTitle:** crystal structure of spinach minor light-harvesting complex cp29 at2 2.80 angstrom resolution
5	d1rwta_	Alignment		48.3	40	**Fold:**Chlorophyll a-b binding protein **Superfamily:**Chlorophyll a-b binding protein **Family:**Chlorophyll a-b binding protein
6	c2wse3_	Alignment		36.3	40	**PDB header:**photosynthesis **Chain:** 3: **PDB Molecule:**lhca3; **PDBTitle:** improved model of plant photosystem i
7	c2o011_	Alignment		35.0	44	**PDB header:**photosynthesis **Chain:** 1: **PDB Molecule:**at3g54890; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
8	c2o014_	Alignment		34.4	29	**PDB header:**photosynthesis **Chain:** 4: **PDB Molecule:**psi light-harvesting antenna chlorophyll a/b- **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
9	c2o012_	Alignment		31.9	21	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
10	c3brvB_	Alignment		31.3	38	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo/ikkb association domain structure
11	c1afoB_	Alignment		31.2	40	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures

12	c2o013_	Alignment		24.1	44	**PDB header:**photosynthesis **Chain:** 3: **PDB Molecule:**psi type iii chlorophyll a/b-binding protein; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
13	c2wsc1_	Alignment		19.9	44	**PDB header:**photosynthesis **Chain:** 1: **PDB Molecule:**at3g54890; **PDBTitle:** improved model of plant photosystem i
14	c2q7cC_	Alignment		12.7	64	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**fusion protein between yeast variant gcn4 and **PDBTitle:** crystal structure of iqn17
15	c2h3oA_	Alignment		8.4	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
16	c1wazA_	Alignment		8.1	42	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
17	c2vxoB_	Alignment		7.5	83	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
18	c3cyoA_	Alignment		6.6	75	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane protein; **PDBTitle:** structure of a longer thermalstable core domain of hiv-12 gp41 containing the enfuvirtide resistance mutation n43d3 and complementary mutation e137k
19	c3o3zA_	Alignment		5.7	75	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** complex of a chimeric alpha/beta-peptide based on the gp41 chr domain2 bound to a gp41 nhr domain peptide
20	c3uowB_	Alignment		5.7	83	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
21	d1h41a2	Alignment	not modelled	5.3	56	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**alpha-D-glucuronidase, N-terminal domain