








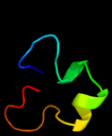



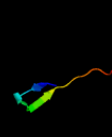





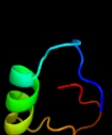

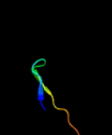
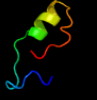










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0257_(-)_309699_310073
Date	Tue Jul 23 14:50:32 BST 2019
Unique Job ID	a7564b79ad7f34f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jcuS_	 Alignment		50.9	43	PDB header: membrane protein Chain: S; PDB Molecule: chlorophyll a-b binding protein 26 kd (cp26); PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
2	c4rku4_	 Alignment		27.0	57	PDB header: photosynthesis Chain: 4; PDB Molecule: chlorophyll a-b binding protein p4, chloroplastic; PDBTitle: crystal structure of plant photosystem i at 3 angstrom resolution
3	c4q51A_	 Alignment		26.2	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative molybdenum cofactor biosynthesis2 protein f from burkholderia cenocepacia j2315
4	c6ijo6_	 Alignment		18.6	54	PDB header: photosynthesis Chain: 6; PDB Molecule: lhca6; PDBTitle: photosystem i of chlamydomonas reinhardtii
5	c6igz6_	 Alignment		18.4	48	PDB header: plant protein Chain: 6; PDB Molecule: lhca-g; PDBTitle: structure of psi-lhci
6	c4xk88_	 Alignment		16.9	43	PDB header: photosynthesis Chain: 8; PDB Molecule: chlorophyll a-b binding protein 3, chloroplastic; PDB Fragment: unp residues 2-81; PDBTitle: crystal structure of plant photosystem i-lhci super-complex at 2.82 angstrom resolution
7	c5q4yA_	 Alignment		13.8	44	PDB header: signaling protein Chain: A; PDB Molecule: chemotaxis protein; PDBTitle: structural basis for carboxylic acid recognition by a cache2 chemosensory domain.
8	d1rwta_	 Alignment		13.7	50	Fold: Chlorophyll a-b binding protein Superfamily: Chlorophyll a-b binding protein Family: Chlorophyll a-b binding protein
9	c3jcuR_	 Alignment		13.3	50	PDB header: membrane protein Chain: R; PDB Molecule: chlorophyll a-b binding protein 29 kd (cp29); PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
10	c6igz7_	 Alignment		13.2	52	PDB header: plant protein Chain: 7; PDB Molecule: lhca-h; PDBTitle: structure of psi-lhci
11	c3ub9B_	 Alignment		12.9	0	PDB header: membrane protein Chain: B; PDB Molecule: chemoreceptor tlpb; PDBTitle: periplasmic portion of the helicobacter pylori chemoreceptor tlpb with2 hydroxyurea bound

12	c6igz0_	Alignment		12.5	43	PDB header: plant protein Chain: 0; PDB Molecule: lhca-j; PDBTitle: structure of psi-lhci
13	c6igz3_	Alignment		12.2	40	PDB header: plant protein Chain: 3; PDB Molecule: lhca-j; PDBTitle: structure of psi-lhci
14	c5mdx4_	Alignment		12.1	38	PDB header: photosynthesis Chain: 4; PDB Molecule: chlorophyll a-b binding protein, chloroplastic; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
15	c6igz9_	Alignment		11.8	45	PDB header: plant protein Chain: 9; PDB Molecule: lhca-i; PDBTitle: structure of psi-lhci
16	c6ijo4_	Alignment		11.6	57	PDB header: photosynthesis Chain: 4; PDB Molecule: lhca4; PDBTitle: photosystem i of chlamydomonas reinhardtii
17	c2o012_	Alignment		11.6	80	PDB header: photosynthesis Chain: 2; PDB Molecule: type ii chlorophyll a/b binding protein from photosystem i; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
18	c6ijj8_	Alignment		11.5	30	PDB header: membrane protein Chain: 8; PDB Molecule: lhca8; PDBTitle: photosystem i of chlamydomonas reinhardtii
19	d1e50b_	Alignment		10.3	28	Fold: Core binding factor beta, CBF Superfamily: Core binding factor beta, CBF Family: Core binding factor beta, CBF
20	c6ijj7_	Alignment		10.2	52	PDB header: membrane protein Chain: 7; PDB Molecule: lhca7; PDBTitle: photosystem i of chlamydomonas reinhardtii
21	d1n26a1	Alignment	not modelled	10.2	57	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
22	c6jo52_	Alignment	not modelled	8.9	67	PDB header: photosynthesis Chain: 2; PDB Molecule: chlorophyll a-b binding protein, chloroplastic; PDBTitle: structure of the green algal photosystem i supercomplex with light-2 harvesting complex i
23	c2jm2A_	Alignment	not modelled	8.7	47	PDB header: hormone/growth factor Chain: A; PDB Molecule: insulin-like growth factor-binding protein 6; PDBTitle: structure of the n-terminal subdomain of insulin-like2 growth factor (igf) binding protein-6 and its interactions3 with igfs
24	d1fp5a1	Alignment	not modelled	8.6	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
25	c6ijo2_	Alignment	not modelled	8.5	48	PDB header: photosynthesis Chain: 2; PDB Molecule: lhca2; PDBTitle: photosystem i of chlamydomonas reinhardtii
26	c6nk6B_	Alignment	not modelled	8.3	26	PDB header: virus like particle/signaling protein Chain: B; PDB Molecule: e1 glycoprotein; PDBTitle: electron cryo-microscopy of chikungunya vlp in complex with mouse2 mxra8 receptor
27	c2l5bA_	Alignment	not modelled	6.8	50	PDB header: apoptosis Chain: A; PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
28	c3j0cG_	Alignment	not modelled	6.8	33	PDB header: virus Chain: G; PDB Molecule: e1 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic

						resolution cryo-em map
29	c3bvcA_	Alignment	not modelled	6.7	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ism_01780; PDBTitle: crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
30	c2dytA_	Alignment	not modelled	6.6	67	PDB header: ligase Chain: A: PDB Molecule: autophagy-related protein 3; PDBTitle: the crystal structure of saccharomyces cerevisiae atg3
31	d1t0fa2	Alignment	not modelled	6.5	64	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: TnsA endonuclease, N-terminal domain
32	c2yewB_	Alignment	not modelled	6.5	21	PDB header: virus Chain: B: PDB Molecule: e1 envelope glycoprotein; PDBTitle: modeling barmah forest virus structural proteins
33	c4k08A_	Alignment	not modelled	6.2	33	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis sensory transducer; PDBTitle: periplasmic sensor domain of chemotaxis protein, adeh_3718
34	c3j0fG_	Alignment	not modelled	5.8	54	PDB header: virus Chain: G: PDB Molecule: e1 envelope glycoprotein; PDBTitle: sindbis virion
35	c1ywke_	Alignment	not modelled	5.8	50	PDB header: isomerase Chain: E: PDB Molecule: 4-deoxy-l-threo-5-hexosulose-uronate ketol- PDBTitle: crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
36	c3oa2B_	Alignment	not modelled	5.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: wbpb; PDBTitle: crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
37	c1v5aA_	Alignment	not modelled	5.7	60	PDB header: toxin Chain: A: PDB Molecule: covalitoxin-i; PDBTitle: solution structure of covalitoxin i
38	c3vx8C_	Alignment	not modelled	5.7	56	PDB header: ligase Chain: C: PDB Molecule: autophagy-related protein 3; PDBTitle: crystal structure of arabidopsis thaliana atg7ntd-atg3 complex
39	c5zgh2_	Alignment	not modelled	5.7	57	PDB header: photosynthesis Chain: 2: PDB Molecule: lhcr2; PDBTitle: cryo-em structure of the red algal psi-lhcr
40	c6igz2_	Alignment	not modelled	5.4	52	PDB header: plant protein Chain: 2: PDB Molecule: lhca-c; PDBTitle: structure of psi-lhci
41	d1ywka1	Alignment	not modelled	5.4	50	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Kdul-like
42	c2o011_	Alignment	not modelled	5.2	70	PDB header: photosynthesis Chain: 1: PDB Molecule: at3g54890; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution