
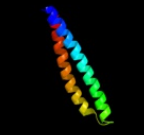

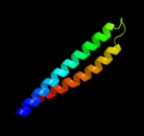

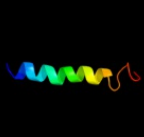







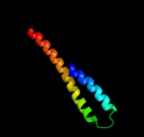







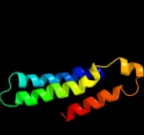

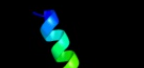


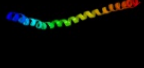
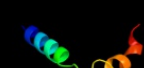





Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nfoA_	 Alignment		90.9	12	PDB header: lipid transport Chain: A; PDB Molecule: apolipoprotein e2; PDBTitle: apolipoprotein e2 (apoe2, d154a mutation)
2	d1gs9a_	 Alignment		86.5	11	Fold: Four-helical up-and-down bundle Superfamily: Apolipoprotein Family: Apolipoprotein
3	c3kdpH_	 Alignment		73.7	27	PDB header: hydrolase Chain: H; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
4	c3kdpG_	 Alignment		73.7	27	PDB header: hydrolase Chain: G; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
5	c2x43S_	 Alignment		65.8	10	PDB header: membrane protein Chain: S; PDB Molecule: sherp; PDBTitle: structural basis of molecular recognition by sherp at membrane2 surfaces
6	c3r2pA_	 Alignment		52.3	8	PDB header: lipid transport Chain: A; PDB Molecule: apolipoprotein a-i; PDBTitle: 2.2 angstrom crystal structure of c terminal truncated human2 apolipoprotein a-i reveals the assembly of hdl by dimerization.
7	c2vs0B_	 Alignment		42.6	11	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	d1wa8b1	 Alignment		40.8	10	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	c2a01B_	 Alignment		39.6	18	PDB header: lipid transport Chain: B; PDB Molecule: apolipoprotein a-i; PDBTitle: crystal structure of lipid-free human apolipoprotein a-i
10	c3gvmA_	 Alignment		39.2	6	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
11	d1eq1a_	 Alignment		29.7	14	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III

12	dlwa8a1	Alignment		25.2	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c2jwaA_	Alignment		21.9	36	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
14	c3onjA_	Alignment		21.8	11	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti 1; PDBTitle: crystal structure of yeast vti1p_habc domain
15	clav1B_	Alignment		21.8	7	PDB header: lipid transport Chain: B: PDB Molecule: apolipoprotein a-i; PDBTitle: crystal structure of human apolipoprotein a-i
16	c1p58F_	Alignment		21.4	18	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
17	dlf16a_	Alignment		21.3	21	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
18	c3lw5K_	Alignment		20.0	44	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x psak; PDBTitle: improved model of plant photosystem i
19	c3e0sA_	Alignment		18.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 chlorobium tepidum
20	c215bA_	Alignment		16.5	33	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
21	dlnekd_	Alignment	not modelled	16.2	15	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
22	dl12pa_	Alignment	not modelled	15.5	16	Fold: Single transmembrane helix Superfamily: F1F0 ATP synthase subunit B, membrane domain Family: F1F0 ATP synthase subunit B, membrane domain
23	dlvcsa1	Alignment	not modelled	13.9	7	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
24	dl1i6la_	Alignment	not modelled	13.8	4	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
25	c2v8sV_	Alignment	not modelled	12.3	10	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
26	c2kncB_	Alignment	not modelled	12.3	15	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfa1iib-beta3 transmembrane-cytoplasmic2 heterocomplex
27	c2p2uA_	Alignment	not modelled	12.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: host-nuclease inhibitor protein gam, putative; PDBTitle: crystal structure of putative host-nuclease inhibitor2 protein gam from desulfovibrio vulgaris
28	c3m91B_	Alignment	not modelled	10.7	17	PDB header: hydrolase regulator Chain: B: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the

					mycobacterium3 tuberculosis proteasomal atpase mpa
29	d1fioa_	Alignment	not modelled	10.2	14 Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
30	d1ryka_	Alignment	not modelled	10.1	9 Fold: SAM domain-like Superfamily: Hypothetical protein Yjbj Family: Hypothetical protein Yjbj
31	c2ww9B_	Alignment	not modelled	8.9	14 PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
32	d1s35a1	Alignment	not modelled	8.8	9 Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
33	c2j5dA_	Alignment	not modelled	8.4	16 PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: nmr structure of bnip3 transmembrane domain in lipid2 bicelles
34	d1eiya1	Alignment	not modelled	8.3	21 Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Phenylalanyl-tRNA synthetase (PheRS)
35	d1c99a_	Alignment	not modelled	7.4	28 Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C
36	d1q2ha_	Alignment	not modelled	7.1	10 Fold: Dimerisation interlock Superfamily: Phenylalanine zipper Family: Adapter protein APS, dimerisation domain
37	c2kp6A_	Alignment	not modelled	6.9	8 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
38	c1n54A_	Alignment	not modelled	6.7	9 PDB header: rna binding protein Chain: A: PDB Molecule: 80 kda nuclear cap binding protein; PDBTitle: cap binding complex m7gpppg free
39	c3a0hX_	Alignment	not modelled	6.7	44 PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
40	c3a0bX_	Alignment	not modelled	6.7	44 PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
41	c3a0hx_	Alignment	not modelled	6.7	44 PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
42	c3a0bx_	Alignment	not modelled	6.7	44 PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
43	c3ipdB_	Alignment	not modelled	6.5	11 PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
44	c3prhB_	Alignment	not modelled	6.5	9 PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase val144pro mutant from b. subtilis
45	c2kbvA_	Alignment	not modelled	6.4	20 PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger
46	d1lvfa_	Alignment	not modelled	6.3	8 Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
47	c3sz3A_	Alignment	not modelled	6.1	12 PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
48	c2ka1B_	Alignment	not modelled	6.1	16 PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
49	c2ka2A_	Alignment	not modelled	6.1	16 PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
50	c1s5lx_	Alignment	not modelled	6.0	44 PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii psbx protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
51	d1dqna_	Alignment	not modelled	5.8	16 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
52	c2ka1A_	Alignment	not modelled	5.7	13 PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
53	c2ka2B_	Alignment	not modelled	5.7	13 PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide

					dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
54	d1rhzb_	Alignment	not modelled	5.7	21 Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
55	c1q90L_	Alignment	not modelled	5.6	33 PDB header: photosynthesis Chain: L: PDB Molecule: cytochrome b6f complex subunit pet1; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
56	d1q90I_	Alignment	not modelled	5.6	33 Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
57	c3hd7A_	Alignment	not modelled	5.4	15 PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
58	d1t72a_	Alignment	not modelled	5.4	13 Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
59	c3py7A_	Alignment	not modelled	5.4	18 PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,paxillin Id1,protein e6 PDBTitle: crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with Id1 motif of paxillin at 2.3a resolution