














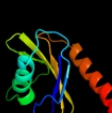


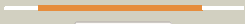


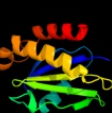


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2j3wa1</a>	 Alignment		100.0	100	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Sedlin (SEDL)
2	<a href="#">c2j3tC_</a>	 Alignment		100.0	11	<b>PDB header:</b> transport <b>Chain:</b> C: <b>PDB Molecule:</b> trafficking protein particle complex subunit 1; <b>PDBTitle:</b> the crystal structure of the bet3-trs33-bet5-trs23 complex.
3	<a href="#">c3cueM_</a>	 Alignment		100.0	18	<b>PDB header:</b> protein transport <b>Chain:</b> M: <b>PDB Molecule:</b> transport protein particle 23 kda subunit; <b>PDBTitle:</b> crystal structure of a trapp subassembly activating the rab ypt1p
4	<a href="#">c3pr6A_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trapp-associated protein tca17; <b>PDBTitle:</b> crystal structure analysis of yeast trapp associate protein tca17
5	<a href="#">c2zmvB_</a>	 Alignment		100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trafficking protein particle complex subunit 4; <b>PDBTitle:</b> crystal structure of synbindin
6	<a href="#">c3cueO_</a>	 Alignment		100.0	19	<b>PDB header:</b> protein transport <b>Chain:</b> O: <b>PDB Molecule:</b> transport protein particle 18 kda subunit; <b>PDBTitle:</b> crystal structure of a trapp subassembly activating the rab ypt1p
7	<a href="#">c3kyqA_</a>	 Alignment		94.3	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> synaptobrevin homolog ykt6; <b>PDBTitle:</b> lipid-induced conformational switch controls fusion activity of longin2 domain snare ykt6
8	<a href="#">d1gw5m2</a>	 Alignment		91.2	13	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Clathrin coat assembly domain
9	<a href="#">d1ioua_</a>	 Alignment		86.6	7	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Synatpobrevin N-terminal domain
10	<a href="#">c2hf6A_</a>	 Alignment		84.3	6	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> coatomer subunit zeta-1; <b>PDBTitle:</b> solution structure of human zeta-cop
11	<a href="#">c2dmwA_</a>	 Alignment		63.7	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptobrevin-like 1 variant; <b>PDBTitle:</b> solution structure of the longin domain of synaptobrevin-2 like protein 1

12	<a href="#">c2jkrM_</a>	Alignment		63.4	13	<b>PDB header:</b> endocytosis <b>Chain:</b> M: <b>PDB Molecule:</b> ap-2 complex subunit mu-1; <b>PDBTitle:</b> ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse
13	<a href="#">c3egdC_</a>	Alignment		61.7	9	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vesicle-trafficking protein sec22b; <b>PDBTitle:</b> crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22 and bound3 to the transport signal sequence of vesicular stomatitis4 virus glycoprotein
14	<a href="#">c2nupC_</a>	Alignment		61.7	9	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> vesicle-trafficking protein sec22b; <b>PDBTitle:</b> crystal structure of the human sec23a/24a heterodimer,2 complexed with the snare protein sec22b
15	<a href="#">c1w63P_</a>	Alignment		47.0	3	<b>PDB header:</b> endocytosis <b>Chain:</b> P: <b>PDB Molecule:</b> adaptor-related protein complex 1, mu 1 subunit; <b>PDBTitle:</b> ap1 clathrin adaptor core
16	<a href="#">c4b93A_</a>	Alignment		42.7	13	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 7; <b>PDBTitle:</b> complex of vamp7 cytoplasmic domain with 2nd ankyrin repeat2 domain of varp
17	<a href="#">d1lfqa_</a>	Alignment		40.3	10	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Synatpobrevin N-terminal domain
18	<a href="#">c1mp9B_</a>	Alignment		21.0	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> tata-binding protein; <b>PDBTitle:</b> ttp from a mesothermophilic archaeon, sulfobolus2 acidocaldarius
19	<a href="#">d1gw5s_</a>	Alignment		20.4	11	<b>Fold:</b> Profilin-like <b>Superfamily:</b> SNARE-like <b>Family:</b> Clathrin coat assembly domain
20	<a href="#">c4b0aA_</a>	Alignment		18.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 1, linker, <b>PDBTitle:</b> the high-resolution structure of ytpb-ytaf1 identifies2 conserved and competing interaction surfaces in3 transcriptional activation
21	<a href="#">c1d3uA_</a>	Alignment	not modelled	17.7	8	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> tata-binding protein; <b>PDBTitle:</b> tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
22	<a href="#">c4eiya_</a>	Alignment	not modelled	17.5	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine receptor a2a/soluble cytochrome b562 chimera; <b>PDBTitle:</b> crystal structure of the chimeric protein of a2aar-bril in complex2 with zm241385 at 1.8a resolution
23	<a href="#">c1yd6A_</a>	Alignment	not modelled	17.4	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uvrc; <b>PDBTitle:</b> crystal structure of the gij-yig n-terminal endonuclease2 domain of uvrc from bacillus caldodenax
24	<a href="#">c1rm1A_</a>	Alignment	not modelled	17.1	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> tata-box binding protein; <b>PDBTitle:</b> structure of a yeast tfiia/tpb/tata-box dna complex
25	<a href="#">c1ngmM_</a>	Alignment	not modelled	17.1	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor tfiid; <b>PDBTitle:</b> crystal structure of a yeast brf1-tpb-dna ternary complex
26	<a href="#">c1w63T_</a>	Alignment	not modelled	15.2	6	<b>PDB header:</b> endocytosis <b>Chain:</b> T: <b>PDB Molecule:</b> adapter-related protein complex 1 sigma 1a <b>PDBTitle:</b> ap1 clathrin adaptor core
27	<a href="#">c2z8uQ_</a>	Alignment	not modelled	13.6	10	<b>PDB header:</b> transcription <b>Chain:</b> Q: <b>PDB Molecule:</b> tata-box-binding protein; <b>PDBTitle:</b> methanococcus jannaschii ttp
28	<a href="#">d1e0na_</a>	Alignment	not modelled	13.6	17	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain

29	<a href="#">c3eikB_</a>	Alignment	not modelled	12.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tata-box-binding protein; <b>PDBTitle:</b> double stranded dna binding protein
30	<a href="#">c3trjC_</a>	Alignment	not modelled	11.5	10	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
31	<a href="#">c3bcyA_</a>	Alignment	not modelled	10.9	39	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein yer067w; <b>PDBTitle:</b> crystal structure of yer067w
32	<a href="#">c3emIA_</a>	Alignment	not modelled	10.6	24	<b>PDB header:</b> membrane protein, receptor <b>Chain:</b> A: <b>PDB Molecule:</b> human adenosine a2a receptor/t4 lysozyme chimera; <b>PDBTitle:</b> the 2.6 a crystal structure of a human a2a adenosine receptor bound to 2 zm241385.
33	<a href="#">c4ax2A_</a>	Alignment	not modelled	9.5	27	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> rap1b; <b>PDBTitle:</b> new type vi-secreted toxins and self-resistance proteins in 2 serratia marcescens
34	<a href="#">d1qnaa2</a>	Alignment	not modelled	9.2	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
35	<a href="#">d2cxha1</a>	Alignment	not modelled	9.0	22	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Brix domain
36	<a href="#">c2cxhA_</a>	Alignment	not modelled	9.0	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable brix-domain ribosomal biogenesis protein; <b>PDBTitle:</b> crystal structure of probable ribosomal biogenesis protein from 2 aeropyrum pernix k1
37	<a href="#">d1cdwa2</a>	Alignment	not modelled	7.4	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
38	<a href="#">d1es6a1</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> EV matrix protein <b>Superfamily:</b> EV matrix protein <b>Family:</b> EV matrix protein
39	<a href="#">c3tcqA_</a>	Alignment	not modelled	6.9	29	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein vp40; <b>PDBTitle:</b> crystal structure of matrix protein vp40 from ebola virus sudan
40	<a href="#">d1h2ca_</a>	Alignment	not modelled	6.9	29	<b>Fold:</b> EV matrix protein <b>Superfamily:</b> EV matrix protein <b>Family:</b> EV matrix protein
41	<a href="#">c3rzeA_</a>	Alignment	not modelled	6.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histamine h1 receptor, lysozyme chimera; <b>PDBTitle:</b> structure of the human histamine h1 receptor in complex with doxepin
42	<a href="#">c1h2dA_</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein vp40; <b>PDBTitle:</b> ebola virus matrix protein vp40 n-terminal domain in 2 complex with rna (low-resolution vp40[31-212] variant).
43	<a href="#">c2go51_</a>	Alignment	not modelled	6.5	10	<b>PDB header:</b> translation/rna <b>Chain:</b> 1: <b>PDB Molecule:</b> signal recognition particle receptor alpha <b>PDBTitle:</b> structure of signal recognition particle receptor (sr) in 2 complex with signal recognition particle (srp) and 3 ribosome nascent chain complex
44	<a href="#">d1d2zb_</a>	Alignment	not modelled	5.6	16	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH domain, DD
45	<a href="#">c1z5sD_</a>	Alignment	not modelled	5.1	23	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> ran-binding protein 2; <b>PDBTitle:</b> crystal structure of a complex between ubc9, sumo-1, 2 rangap1 and nup358/ranbp2