
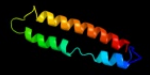
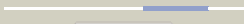
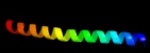
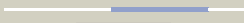


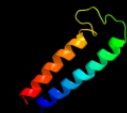



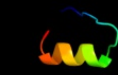












Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dnxA_	 Alignment		32.4	16	PDB header: transport protein Chain: A: PDB Molecule: syntaxin-12; PDBTitle: solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
2	c3t97B_	 Alignment		27.8	15	PDB header: protein transport Chain: B: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
3	d1s94a_	 Alignment		24.8	18	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
4	c1s94A_	 Alignment		24.8	18	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: s-syntaxin; PDBTitle: crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
5	d2daha1	 Alignment		24.2	23	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
6	d2dnaa1	 Alignment		23.6	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
7	d2bwba1	 Alignment		21.9	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
8	c2cwbA_	 Alignment		21.8	23	PDB header: protein binding Chain: A: PDB Molecule: chimera of immunoglobulin g binding protein g PDBTitle: solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
9	d1veja1	 Alignment		21.3	23	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
10	c1wr1B_	 Alignment		20.4	14	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like protein dsk2; PDBTitle: the complex sturcture of dsk2p uba with ubiquitin
11	c1m1jA_	 Alignment		18.5	14	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands

12	c1vp7D_	Alignment		18.5	10	PDB header: hydrolase Chain: D: PDB Molecule: exodeoxyribonuclease vii small subunit; PDBTitle: crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
13	c2dnaA_	Alignment		17.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
14	c2dahA_	Alignment		16.8	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-3; PDBTitle: solution structure of the c-terminal uba domain in the2 human ubiquilin 3
15	c2jy5A_	Alignment		16.0	18	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
16	c3a2aC_	Alignment		15.8	32	PDB header: transport protein Chain: C: PDB Molecule: voltage-gated hydrogen channel 1; PDBTitle: the structure of the carboxyl-terminal domain of the human voltage-2 gated proton channel hv1
17	c1deqO_	Alignment		14.3	10	PDB header: PDB COMPND:
18	c2eamA_	Alignment		11.7	31	PDB header: signaling protein Chain: A: PDB Molecule: putative 47 kda protein; PDBTitle: solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
19	c1ydiB_	Alignment		11.6	22	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: alpha-actinin 4; PDBTitle: human vinculin head domain (vh1, 1-258) in complex with2 human alpha-actinin's vinculin-binding site (residues 731-3 760)
20	d1o5ha_	Alignment		10.4	15	Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like
21	c1flIA_	Alignment	not modelled	10.3	13	PDB header: apoptosis Chain: A: PDB Molecule: tnf receptor associated factor 3; PDBTitle: molecular basis for cd40 signaling mediated by traf3
22	c4a1cD_	Alignment	not modelled	9.8	19	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l11; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
23	c2dl0A_	Alignment	not modelled	9.5	31	PDB header: signaling protein Chain: A: PDB Molecule: sam and sh3 domain-containing protein 1; PDBTitle: solution structure of the sam-domain of the sam and sh32 domain containing protein 1
24	c1n73C_	Alignment	not modelled	8.7	10	PDB header: blood clotting Chain: C: PDB Molecule: fibrin gamma chain; PDBTitle: fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
25	c2k4pA_	Alignment	not modelled	8.2	19	PDB header: signaling protein Chain: A: PDB Molecule: phosphatidylinositol-3,4,5-trisphosphate 5- PDBTitle: solution structure of ship2-sam
26	d1q08a_	Alignment	not modelled	8.1	21	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
27	d1tafa_	Alignment	not modelled	8.0	27	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
28	d2pa2a1	Alignment	not modelled	7.7	26	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L10e
						PDB header: endocytosis/exocytosis

29	c3c98B_	Alignment	not modelled	7.5	12	Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: revised structure of the munc18a-syntaxin1 complex
30	c2qkqA_	Alignment	not modelled	7.4	19	PDB header: transferase Chain: A: PDB Molecule: ephrin type-b receptor 4; PDBTitle: structure of the sam domain of human ephrin type-b receptor2 4
31	d1xn7a_	Alignment	not modelled	7.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein YhgG
32	c2d46A_	Alignment	not modelled	7.3	58	PDB header: metal transport Chain: A: PDB Molecule: calcium channel, voltage-dependent, beta 4 PDBTitle: solution structure of the human beta4a-a domain
33	d1b0xa_	Alignment	not modelled	7.2	31	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
34	c1b0xA_	Alignment	not modelled	7.2	31	PDB header: transferase Chain: A: PDB Molecule: protein (epha4 receptor tyrosine kinase); PDBTitle: the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
35	d1v38a_	Alignment	not modelled	6.8	38	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
36	d1ug7a_	Alignment	not modelled	6.8	46	Fold: Four-helical up-and-down bundle Superfamily: Domain from hypothetical 2610208m17rik protein Family: Domain from hypothetical 2610208m17rik protein
37	c2cp8A_	Alignment	not modelled	6.7	15	PDB header: protein binding Chain: A: PDB Molecule: next to brca1 gene 1 protein; PDBTitle: solution structure of the rsgi ruh-046, a uba domain from2 human next to brca1 gene 1 protein (kiaa0049 protein)3 r923h variant
38	c2ke7A_	Alignment	not modelled	6.6	31	PDB header: protein binding Chain: A: PDB Molecule: ankyrin repeat and sterile alpha motif domain- PDBTitle: nmr structure of the first sam domain from aida1
39	c1sfcD_	Alignment	not modelled	6.1	18	PDB header: transport protein Chain: D: PDB Molecule: protein (snap-25b); PDBTitle: neuronal synaptic fusion complex
40	d1ez3a_	Alignment	not modelled	6.0	17	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
41	c2fxpA_	Alignment	not modelled	5.8	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein; PDBTitle: solution structure of the sars-coronavirus hr2 domain
42	c3dpqE_	Alignment	not modelled	5.7	24	PDB header: chaperone, peptide binding protein Chain: E: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrolic acid-derived3 inhibitor peptide (form b)
43	c2e8nA_	Alignment	not modelled	5.6	31	PDB header: transferase, signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
44	c3pvpA_	Alignment	not modelled	5.6	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
45	c2npsD_	Alignment	not modelled	5.5	19	PDB header: transport protein Chain: D: PDB Molecule: syntaxin-6; PDBTitle: crystal structure of the early endosomal snare complex
46	c2zshB_	Alignment	not modelled	5.3	27	PDB header: hormone receptor Chain: B: PDB Molecule: della protein gai; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
47	d1sgga_	Alignment	not modelled	5.3	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
48	d1gm5a1	Alignment	not modelled	5.2	17	Fold: Four-helical up-and-down bundle Superfamily: RecG, N-terminal domain Family: RecG, N-terminal domain
49	c3zqsB_	Alignment	not modelled	5.2	19	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase fanc1; PDBTitle: human fanc1 central domain