

























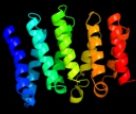



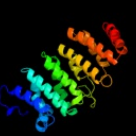




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pbva_	 Alignment		100.0	46	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
2	c2r09A_	 Alignment		100.0	45	PDB header: signaling protein Chain: A: PDB Molecule: cytohesin-3; PDBTitle: crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor
3	d1ku1a_	 Alignment		100.0	37	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
4	d1bc9a_	 Alignment		100.0	49	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
5	d2r09a1	 Alignment		100.0	48	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
6	d1re0b_	 Alignment		100.0	38	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
7	d1r8se_	 Alignment		100.0	49	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
8	d1xsza1	 Alignment		100.0	40	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
9	c1xsza_	 Alignment		100.0	38	PDB header: signaling protein Chain: A: PDB Molecule: guanine nucleotide exchange protein; PDBTitle: the structure of raf
10	c3l8nA_	 Alignment		100.0	92	PDB header: nucleotide-binding protein, metal-bindin Chain: A: PDB Molecule: brefeldin a-inhibited guanine nucleotide-exchange PDBTitle: crystal structure of a domain of brefeldin a-inhibited2 guanine nucleotide-exchange protein 2 (brefeldina-inhibited3 gep 2) from homo sapiens (human). northeast structural4 genomics consortium target id hr5562a
11	d1u6gc_	 Alignment		98.1	13	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat

12	c1m5n5_	Alignment		97.4	13	PDB header: protein transport Chain: S: PDB Molecule: importin beta-1 subunit; PDBTitle: crystal structure of heat repeats (1-11) of importin b2 bound to the non-classical nls(67-94) of pthrp
13	c4a0cB_	Alignment		97.1	12	PDB header: cell cycle Chain: B: PDB Molecule: cullin-associated nedd8-dissociated protein 1; PDBTitle: structure of the cand1-cul4b-rbx1 complex
14	d2bpta1	Alignment		96.9	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
15	c2qk1A_	Alignment		96.8	13	PDB header: protein binding Chain: A: PDB Molecule: protein stu2; PDBTitle: structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
16	c4k92B_	Alignment		96.5	7	PDB header: structural protein Chain: B: PDB Molecule: clip-associating protein 1; PDBTitle: a cryptic tog domain with a distinct architecture underlies clasp-2 dependent bipolar spindle formation
17	c4ffbC_	Alignment		96.4	11	PDB header: hydrolase Chain: C: PDB Molecule: protein stu2; PDBTitle: a tog:alpha/beta-tubulin complex structure reveals conformation-based2 mechanisms for a microtubule polymerase
18	c2qk2A_	Alignment		96.2	12	PDB header: protein binding Chain: A: PDB Molecule: lp04448p; PDBTitle: structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1
19	c3b2aA_	Alignment		96.1	9	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the archaeal heat-like repeats protein ton_19372 from thermococcus onnurineus na1
20	c4g3aA_	Alignment		95.9	13	PDB header: cell cycle Chain: A: PDB Molecule: clip-associating protein; PDBTitle: crystal structure of mast/orbit n-terminal domain
21	d1qbkb_	Alignment	not modelled	95.6	8	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
22	c2db0B_	Alignment	not modelled	94.6	9	PDB header: protein binding Chain: B: PDB Molecule: 253aa long hypothetical protein; PDBTitle: crystal structure of ph0542
23	c3w3zA_	Alignment		93.7	11	PDB header: protein transport/nuclear protein Chain: A: PDB Molecule: importin subunit beta-3; PDBTitle: crystal structure of kap121p bound to rangtp
24	d1libr_	Alignment	not modelled	93.1	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
25	c1w63A_	Alignment	not modelled	92.8	8	PDB header: endocytosis Chain: A: PDB Molecule: adapter-related protein complex 1 gamma 1 PDBTitle: ap1 clathrin adaptor core
26	d1wa5c_	Alignment	not modelled	92.4	9	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
27	c3c5wA_	Alignment	not modelled	92.4	11	PDB header: hydrolase Chain: A: PDB Molecule: pp2a a subunit; PDBTitle: complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
						PDB header: transport protein

28	c2ot8B_	Alignment	not modelled	90.1	10	Chain: B: PDB Molecule: transportin-1; PDBTitle: karyopherin beta2/transportin-hnrnp nls complex
29	d1ee4a_	Alignment	not modelled	89.7	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
30	c2jdqB_	Alignment	not modelled	89.3	13	PDB header: protein transport Chain: B: PDB Molecule: importin alpha-1 subunit; PDBTitle: c-terminal domain of influenza a virus polymerase pb22 subunit in complex with human importin alpha5
31	d1w9ca_	Alignment	not modelled	88.4	13	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Exportin HEAT-like repeat
32	c3nowA_	Alignment	not modelled	88.3	11	PDB header: protein binding Chain: A: PDB Molecule: unc-45 protein, sd10334p; PDBTitle: unc-45 from drosophila melanogaster
33	d1xm9a1	Alignment	not modelled	87.5	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Plakophilin 1 helical region
34	d1gw5b_	Alignment	not modelled	85.4	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin adaptor core protein
35	c2ynsA_	Alignment	not modelled	83.9	9	PDB header: transport protein Chain: A: PDB Molecule: importin subunit alpha-1a; PDBTitle: rimp_alpha_b54nls
36	c2c1tA_	Alignment	not modelled	76.8	12	PDB header: protein transport/membrane protein Chain: A: PDB Molecule: importin alpha subunit; PDBTitle: structure of the kap60p:nup2 complex
37	c2z6hA_	Alignment	not modelled	76.7	10	PDB header: cell adhesion Chain: A: PDB Molecule: catenin beta-1; PDBTitle: crystal structure of beta-catenin armadillo repeat region2 and its c-terminal domain
38	c4hxtA_	Alignment	not modelled	73.5	9	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein or329; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or329
39	c3nmwA_	Alignment	not modelled	72.3	10	PDB header: cell adhesion/cell cycle Chain: A: PDB Molecule: apc variant protein; PDBTitle: crytal structure of armadillo repeats domain of apc
40	c4db9A_	Alignment	not modelled	69.8	13	PDB header: de novo protein Chain: A: PDB Molecule: armadillo repeat protein, yiiim3aiii; PDBTitle: designed armadillo repeat protein (yiiim3aiii)
41	c3slaB_	Alignment	not modelled	67.6	8	PDB header: signaling protein Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
42	c3opbA_	Alignment	not modelled	67.1	16	PDB header: protein binding Chain: A: PDB Molecule: swi5-dependent ho expression protein 4; PDBTitle: crystal structure of she4p
43	c3sl9B_	Alignment	not modelled	66.6	8	PDB header: signaling protein, protein binding Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
44	c3sl9E_	Alignment	not modelled	66.6	8	PDB header: signaling protein, protein binding Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
45	d1jdha_	Alignment	not modelled	66.2	8	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
46	c4i2wA_	Alignment	not modelled	66.1	10	PDB header: chaperone/protein binding Chain: A: PDB Molecule: protein unc-45; PDBTitle: crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
47	c1vsv5_	Alignment	not modelled	65.5	12	PDB header: hydrolase Chain: 5: PDB Molecule: proteasome activator blm10; PDBTitle: proteasome activator complex
48	c2of3A_	Alignment	not modelled	65.4	9	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
49	c2x19B_	Alignment	not modelled	65.2	11	PDB header: nuclear transport Chain: B: PDB Molecule: importin-13; PDBTitle: crystal structure of importin13 - rangtp complex
50	c1dvpA_	Alignment	not modelled	62.8	14	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
51	c3gq2B_	Alignment	not modelled	62.5	14	PDB header: transport protein Chain: B: PDB Molecule: general vesicular transport factor p115; PDBTitle: crystal structure of the dimer of the p115 tether globular head domain
52	c3l6yE_	Alignment	not modelled	61.8	10	PDB header: cell adhesion Chain: E: PDB Molecule: catenin delta-1; PDBTitle: crystal structure of p120 catenin in complex with e-cadherin
53	d1q1sc_	Alignment	not modelled	61.4	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
54	c3slaA_	Alignment	not modelled	57.9	8	PDB header: signaling protein Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin

55	c2qnaA	Alignment		57.7	12	PDB header: transport protein Chain: A: PDB Molecule: importin subunit beta-1; PDBTitle: crystal structure of human importin-beta (127-876) in complex with the2 ibb-domain of snurportin1 (1-65)
56	c3s4wB	Alignment	not modelled	57.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: fanconi anemia group d2 protein homolog; PDBTitle: structure of the fanci-fancd2 complex
57	c2l1lB	Alignment	not modelled	53.3	14	PDB header: nuclear protein Chain: B: PDB Molecule: exportin-1; PDBTitle: nmr solution structure of the phi0 pki nes peptide in complex with2 crm1-rangtp
58	c3zyqA	Alignment	not modelled	51.3	21	PDB header: signaling Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
59	c2m9xA	Alignment	not modelled	49.9	19	PDB header: transferase Chain: A: PDB Molecule: microtubule-associated serine/threonine-protein kinase 1; PDBTitle: solution nmr structure of microtubule-associated serine/threonine-2 protein kinase 1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr9151a
60	c3sl9A	Alignment	not modelled	49.3	8	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
61	c3slaD	Alignment	not modelled	49.3	8	PDB header: signaling protein Chain: D: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
62	c3sl9G	Alignment	not modelled	48.0	8	PDB header: signaling protein, protein binding Chain: G: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
63	c4fgvA	Alignment	not modelled	47.3	13	PDB header: transport protein Chain: A: PDB Molecule: chromosome region maintenance 1 (crm1) or exportin 1 PDBTitle: crystal structure of free crm1 (crystal form 1)
64	c3trkA	Alignment	not modelled	46.3	14	PDB header: hydrolase Chain: A: PDB Molecule: nonstructural polyprotein; PDBTitle: structure of the chikungunya virus nsp2 protease
65	c1x5bA	Alignment	not modelled	44.4	16	PDB header: protein binding Chain: A: PDB Molecule: signal transducing adaptor molecule 2; PDBTitle: the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
66	c2w3cA	Alignment	not modelled	42.1	11	PDB header: transport protein Chain: A: PDB Molecule: general vesicular transport factor p115; PDBTitle: globular head region of the human general vesicular2 transport factor p115
67	c3slaC	Alignment	not modelled	40.8	13	PDB header: signaling protein Chain: C: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
68	c1wa5B	Alignment	not modelled	39.2	10	PDB header: nuclear transport Chain: B: PDB Molecule: importin alpha subunit; PDBTitle: crystal structure of the exportin cse1p complexed with its2 cargo (kap60p) and rangtp
69	d1wa5b	Alignment	not modelled	39.2	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
70	d2jdia1	Alignment	not modelled	38.4	16	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
71	d1v9va1	Alignment	not modelled	38.0	20	Fold: Bromodomain-like Superfamily: MAST3 pre-PK domain-like Family: MAST3 pre-PK domain-like
72	c2nnpE	Alignment	not modelled	36.9	12	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: serine/threonine-protein phosphatase 2a 56 kda regulatory PDBTitle: structure of the protein phosphatase 2a holoenzyme
73	d2nppb1	Alignment	not modelled	36.9	12	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: B56-like
74	c3u0rA	Alignment	not modelled	36.9	18	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: apoptosis inhibitor 5; PDBTitle: helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules
75	d1s1ma2	Alignment	not modelled	35.6	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	d2vo1a1	Alignment	not modelled	34.1	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c2z6gA	Alignment	not modelled	33.7	10	PDB header: cell adhesion Chain: A: PDB Molecule: b-catenin; PDBTitle: crystal structure of a full-length zebrafish beta-catenin
78	c3tjzB	Alignment	not modelled	32.7	13	PDB header: protein transport/protein binding Chain: B: PDB Molecule: coatomer subunit gamma; PDBTitle: crystal structure of arf1 bound to the gamma/zeta-cop core complex
						Fold: alpha-alpha superhelix

79	d1rz4a2	Alignment	not modelled	31.9	25	Superfamily: ARM repeat Family: Eukaryotic translation initiation factor 3 subunit 12, eIF3k, N-terminal domain
80	c2lkrL	Alignment	not modelled	30.4	11	PDB header: endocytosis Chain: L: PDB Molecule: ap-2 complex subunit alpha-2; PDBTitle: ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse
81	c2h7vD	Alignment	not modelled	30.0	22	PDB header: signaling protein Chain: D: PDB Molecule: protein kinase ypka; PDBTitle: co-crystal structure of ypka-rac1
82	c4db8B	Alignment	not modelled	28.9	16	PDB header: de novo protein Chain: B: PDB Molecule: armadillo-repeat protein; PDBTitle: designed armadillo-repeat protein
83	c1o1nA	Alignment	not modelled	28.4	12	PDB header: oxygen storage/transport Chain: A: PDB Molecule: hemoglobin alpha chain; PDBTitle: deoxy hemoglobin (a-glyglygly-c:v1m,l29w; b,d:v1m)
84	d1l8qa1	Alignment	not modelled	27.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
85	c1rz4A	Alignment	not modelled	26.6	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit 11; PDBTitle: crystal structure of human eif3k
86	c3nvaB	Alignment	not modelled	25.1	24	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
87	c1pjmB	Alignment	not modelled	24.6	11	PDB header: protein transport Chain: B: PDB Molecule: importin alpha-2 subunit; PDBTitle: mouse importin alpha-bipartite nls from human2 retinoblastoma protein complex
88	c2ad5B	Alignment	not modelled	24.5	26	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
89	d1o5ha	Alignment	not modelled	24.4	14	Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like
90	d1dvpA1	Alignment	not modelled	24.3	13	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
91	c2eqxA	Alignment	not modelled	23.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kelch repeat and btb domain-containing protein 4; PDBTitle: solution structure of the back domain of kelch repeat and2 btb domain-containing protein 4
92	c2fbqA	Alignment	not modelled	23.2	17	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of transcriptional regulator pa3006
93	c3npiB	Alignment	not modelled	22.9	21	PDB header: gene regulation Chain: B: PDB Molecule: tetr family regulatory protein; PDBTitle: crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
94	c1vcnA	Alignment	not modelled	22.9	19	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
95	c3oqsA	Alignment	not modelled	22.8	11	PDB header: protein transport Chain: A: PDB Molecule: importin subunit alpha-2; PDBTitle: crystal structure of importin-alpha bound to a clic4 nls peptide
96	c2po4A	Alignment	not modelled	22.3	18	PDB header: transferase Chain: A: PDB Molecule: virion rna polymerase; PDBTitle: x-ray crystal structure of polymerase domain of the2 bacteriophage n4 virion rna polymerase
97	d1j1va	Alignment	not modelled	22.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
98	c3ifqB	Alignment	not modelled	21.4	11	PDB header: cell adhesion Chain: B: PDB Molecule: plakoglobin; PDBTitle: interaction of plakoglobin and beta-catenin with desmosomal2 cadherins
99	c3v6aA	Alignment	not modelled	20.9	12	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: apoptosis inhibitor 5; PDBTitle: helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules
100	c3a6pA	Alignment	not modelled	20.4	10	PDB header: protein transport/nuclear protein/rna Chain: A: PDB Molecule: exportin-5; PDBTitle: crystal structure of exportin-5:rangtp:pre-mirna complex
101	c2lmdA	Alignment	not modelled	20.3	21	PDB header: transcription Chain: A: PDB Molecule: prospero homeobox protein 1; PDBTitle: minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b