




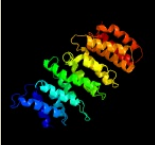


















Phyre2

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Description	Undefined
Date	Thu Mar 3 22:43:07 GMT 2016
Unique Job ID	edd35b2779667bf5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b3ua_	 Alignment		99.2	16	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat
2	d1u6gc_	 Alignment		98.9	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat
3	c4a0cB_	 Alignment		98.9	14	PDB header: cell cycle Chain: B; PDB Molecule: cullin-associated nedd8-dissociated protein 1; PDBTitle: structure of the cand1-cul4b-rbx1 complex
4	c3c5wA_	 Alignment		98.6	15	PDB header: hydrolase Chain: A; PDB Molecule: pp2a a subunit; PDBTitle: complex between pp2a-specific methyltransferase pme-1 and pp2a core2 enzyme
5	d1gw5b_	 Alignment		98.4	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin adaptor core protein
6	c4r10A_	 Alignment		98.1	13	PDB header: cell adhesion/protein binding Chain: A; PDB Molecule: protein humpback-2; PDBTitle: a conserved phosphorylation switch controls the interaction between2 cadherin and beta-catenin in vitro and in vivo
7	c1m5nS_	 Alignment		98.0	22	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
8	c1w63A_	 Alignment		97.7	15	PDB header: endocytosis Chain: A; PDB Molecule: adapter-related protein complex 1 gamma 1 PDBTitle: ap1 clathrin adaptor core
9	c4qmjA_	 Alignment		97.6	15	PDB header: protein binding Chain: A; PDB Molecule: cytoskeleton-associated protein 5; PDBTitle: the xmap215 family drives microtubule polymerization using a2 structurally diverse tog array
10	d1jdha_	 Alignment		97.6	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
11	c2qk2A_	 Alignment		97.6	21	PDB header: protein binding Chain: A; PDB Molecule: lp04448p; PDBTitle: structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1

12	c3w3zA_	Alignment		97.6	16	PDB header: protein transport/nuclear protein Chain: A; PDB Molecule: importin subunit beta-3; PDBTitle: crystal structure of kap121p bound to rangtp
13	c2jkrL_	Alignment		97.6	20	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
14	c4g3aA_	Alignment		97.6	14	PDB header: cell cycle Chain: A; PDB Molecule: clip-associating protein; PDBTitle: crystal structure of mast/orbit n-terminal domain
15	c2z6hA_	Alignment		97.6	14	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
16	c4db9A_	Alignment		97.5	15	PDB header: de novo protein Chain: A; PDB Molecule: armadillo repeat protein, yiiim3aiii; PDBTitle: designed armadillo repeat protein (yiiim3aiii)
17	c5dn7A_	Alignment		97.5	13	PDB header: structural protein Chain: A; PDB Molecule: protein fam179b; PDBTitle: crescerin uses a tog domain array to regulate microtubules in the2 primary cilium
18	d1qbkB_	Alignment		97.4	16	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
19	c2db0B_	Alignment		97.4	17	PDB header: protein binding Chain: B; PDB Molecule: 253aa long hypothetical protein; PDBTitle: crystal structure of ph0542
20	c3b2aA_	Alignment		97.4	16	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
21	c4d4eA_	Alignment	not modelled	97.3	15	PDB header: de novo protein Chain: A; PDB Molecule: armadillo repeat protein arm00016; PDBTitle: crystal structure of computationally designed armadillo2 repeat proteins for modular peptide recognition.
22	c4hxtA_	Alignment	not modelled	97.2	15	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
23	c2qk1A_	Alignment	not modelled	97.1	14	PDB header: protein binding Chain: A; PDB Molecule: protein stu2; PDBTitle: structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
24	c4y5jA_	Alignment	not modelled	97.0	16	PDB header: protein binding Chain: A; PDB Molecule: mini spindles tog3; PDBTitle: drosophila melanogaster mini spindles tog3
25	c2iw3B_	Alignment	not modelled	97.0	18	PDB header: translation Chain: B; PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
26	c1xqrA_	Alignment	not modelled	96.9	12	PDB header: chaperone Chain: A; PDB Molecule: hspbp1 protein; PDBTitle: crystal structure of the hspbp1 core domain
27	c4xrkA_	Alignment	not modelled	96.9	14	PDB header: transport protein Chain: A; PDB Molecule: importin beta; PDBTitle: crystal structure of importin beta in a polyethylene glycol condition
28	c4plrA_	Alignment	not modelled	96.9	16	PDB header: peptide binding protein Chain: A; PDB Molecule: arm00008; PDBTitle: crystal structures of designed armadillo repeat proteins: implications2 of construct design and crystallization conditions on overall3 structure.

29	c4qmhA	Alignment	not modelled	96.7	11	PDB header: protein binding Chain: A: PDB Molecule: lp04448p; PDBTitle: the xmap215 family drives microtubule polymerization using a2 structurally diverse tog array
30	d2bpta1	Alignment	not modelled	96.7	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
31	d1ee4a	Alignment	not modelled	96.6	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
32	c4db8B	Alignment	not modelled	96.4	15	PDB header: de novo protein Chain: B: PDB Molecule: armadillo-repeat protein; PDBTitle: designed armadillo-repeat protein
33	d1xqra1	Alignment	not modelled	96.4	12	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HspBP1 domain
34	c2of3A	Alignment	not modelled	96.3	14	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
35	c2c1tA	Alignment	not modelled	96.2	12	PDB header: protein transport/membrane protein Chain: A: PDB Molecule: importin alpha subunit; PDBTitle: structure of the kap60p:nup2 complex
36	d1ibrb	Alignment	not modelled	96.2	12	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
37	c3ltjA	Alignment	not modelled	96.0	19	PDB header: protein binding Chain: A: PDB Molecule: alpharep-4; PDBTitle: structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats
38	c3wozA	Alignment	not modelled	96.0	12	PDB header: structural protein Chain: A: PDB Molecule: clip-associating protein 2; PDBTitle: crystal structure of clasp2 tog domain (tog3)
39	c3ifqB	Alignment	not modelled	95.9	16	PDB header: cell adhesion Chain: B: PDB Molecule: plakoglobin; PDBTitle: interaction of plakoglobin and beta-catenin with desmosomal2 cadherins
40	c4k92B	Alignment	not modelled	95.9	12	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
41	c4gmnA	Alignment	not modelled	95.8	19	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural basis of rp15 recognition by syo1
42	c4d50A	Alignment	not modelled	95.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: deoxyhypusine hydroxylase; PDBTitle: structure of human deoxyhypusine hydroxylase
43	c3nowA	Alignment	not modelled	95.5	12	PDB header: protein binding Chain: A: PDB Molecule: unc-45 protein, sd10334p; PDBTitle: unc-45 from drosophila melanogaster
44	c4rv1F	Alignment	not modelled	95.5	14	PDB header: de novo protein Chain: F: PDB Molecule: engineered protein or497; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium (nesg) target or497.
45	c3sl9A	Alignment	not modelled	95.5	11	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
46	c3slaD	Alignment	not modelled	95.5	11	PDB header: signaling protein Chain: D: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
47	c3oqsA	Alignment	not modelled	95.4	15	PDB header: protein transport Chain: A: PDB Molecule: importin subunit alpha-2; PDBTitle: crystal structure of importin-alpha bound to a clic4 nls peptide
48	d1q1sc	Alignment	not modelled	95.4	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
49	c5a1vG	Alignment	not modelled	95.4	19	PDB header: transport protein Chain: G: PDB Molecule: coatomeer subunit beta'; PDBTitle: the structure of the copi coat linkage i
50	d1te4a	Alignment	not modelled	95.3	19	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat
51	c4xl5C	Alignment	not modelled	95.3	29	PDB header: protein binding Chain: C: PDB Molecule: bgfp-a; PDBTitle: x-ray structure of bgfp-a / egfp complex
52	c2ot8B	Alignment	not modelled	95.3	13	PDB header: transport protein Chain: B: PDB Molecule: transportin-1; PDBTitle: karyopherin beta2/transportin-hnrrpm nls complex
53	c2qnaA	Alignment	not modelled	95.1	14	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)
54	c4xriA	Alignment	not modelled	95.0	15	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of importin beta in an ammonium sulfate condition
55	c3sl9G	Alignment	not modelled	94.9	9	PDB header: signaling protein, protein binding Chain: G: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9

56	c3u0rA_	Alignment	not modelled	94.5	15	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
57	c1pjmB_	Alignment	not modelled	94.4	14	PDB header: protein transport Chain: B: PDB Molecule: importin alpha-2 subunit; PDBTitle: mouse importin alpha-bipartite nls from human2 retinoblastoma protein complex
58	c3gq2B_	Alignment	not modelled	94.4	10	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
59	c2w3cA_	Alignment	not modelled	94.4	10	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
60	d1qgra_	Alignment	not modelled	94.3	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
61	c3slaB_	Alignment	not modelled	93.8	12	PDB header: signaling protein Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
62	c5ewpA_	Alignment	not modelled	93.7	15	PDB header: protein binding Chain: A: PDB Molecule: aro (armadillo repeats only protein); PDBTitle: aro (armadillo repeats only protein) from plasmodium falciparum
63	c3gb8A_	Alignment	not modelled	93.6	14	PDB header: transport protein Chain: A: PDB Molecule: exportin-1; PDBTitle: crystal structure of crm1/snurportin-1 complex
64	c3gjxD_	Alignment	not modelled	93.4	11	PDB header: protein transport Chain: D: PDB Molecule: exportin-1; PDBTitle: crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
65	c1vsv5_	Alignment	not modelled	93.1	20	PDB header: hydrolase Chain: 5: PDB Molecule: proteasome activator blm10; PDBTitle: proteasome activator complex
66	c3l9tA_	Alignment	not modelled	92.7	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein smu.31; PDBTitle: the crystal structure of smu.31 from streptococcus mutans ua159
67	c3m1iC_	Alignment	not modelled	92.5	8	PDB header: protein transport Chain: C: PDB Molecule: exportin-1; PDBTitle: crystal structure of yeast crm1 (xpo1p) in complex with yeast ranbp12 (yrb1p) and yeast rangtp (gsp1pgtp)
68	d1wa5b_	Alignment	not modelled	91.7	13	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
69	c1wa5B_	Alignment	not modelled	91.7	13	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
70	c2z6gA_	Alignment	not modelled	91.5	15	PDB header: cell adhesion Chain: A: PDB Molecule: b-catenin; PDBTitle: crystal structure of a full-length zebrafish beta-catenin
71	c4ffbC_	Alignment	not modelled	91.4	12	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
72	c3nmwA_	Alignment	not modelled	88.8	16	PDB header: cell adhesion/cell cycle Chain: A: PDB Molecule: apc variant protein; PDBTitle: crytal structure of armadillo repeats domain of apc
73	c4rxhB_	Alignment	not modelled	88.6	11	PDB header: transport protein Chain: B: PDB Molecule: importin subunit alpha; PDBTitle: crystal structure of importin-alpha from neurospora crassa complexed2 with sv40nls
74	c2ynsA_	Alignment	not modelled	88.3	9	PDB header: transport protein Chain: A: PDB Molecule: importin subunit alpha-1a; PDBTitle: rimp_alpha_b54nls
75	c2jdB_	Alignment	not modelled	88.3	11	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
76	c4i2wA_	Alignment	not modelled	88.2	12	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
77	c4pjwA_	Alignment	not modelled	88.1	18	PDB header: cell cycle Chain: A: PDB Molecule: cohesin subunit sa-2; PDBTitle: crystal structure of human stromal antigen 2 (sa2) in complex with2 sister chromatid cohesion protein 1 (scc1), with bound mes
78	c4uaeA_	Alignment	not modelled	88.1	12	PDB header: protein transport Chain: A: PDB Molecule: importin subunit alpha-3; PDBTitle: importin alpha 3 delta ibb in complex with influenza pb2 nuclear2 localization domain
79	c3slaA_	Alignment	not modelled	87.6	10	PDB header: signaling protein Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
80	c4fgvA_	Alignment	not modelled	87.3	11	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)
81	c3nmzB_	Alignment	not modelled	85.6	18	PDB header: cell adhesion/cell cycle Chain: B: PDB Molecule: apc variant protein; PDBTitle: crytal structure of apc complexed with asef

82	d1lrva_	Alignment	not modelled	85.3	16	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Leucine-rich repeat variant
83	c3sl9E_	Alignment	not modelled	84.7	11	PDB header: signaling protein, protein binding Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
84	c3sl9B_	Alignment	not modelled	84.7	11	PDB header: signaling protein, protein binding Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
85	d1wa5c_	Alignment	not modelled	84.3	12	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
86	c4c0pD_	Alignment	not modelled	83.0	16	PDB header: transport protein Chain: D: PDB Molecule: transportin-3; PDBTitle: unliganded transportin 3
87	c3tt9A_	Alignment	not modelled	82.5	12	PDB header: cell adhesion Chain: A: PDB Molecule: plakophilin-2; PDBTitle: crystal structure of the stable degradation fragment of human2 plakophilin 2 isoform a (pkp2a) c752r variant
88	c3v6aA_	Alignment	not modelled	82.4	16	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
89	c3slaE_	Alignment	not modelled	82.3	12	PDB header: signaling protein Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
90	d1v18a1	Alignment	not modelled	80.1	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
91	c3bctA_	Alignment	not modelled	77.4	10	PDB header: armadillo repeat Chain: A: PDB Molecule: beta-catenin; PDBTitle: the armadillo repeat region from murine beta-catenin
92	d1xm9a1	Alignment	not modelled	76.6	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Plakophilin 1 helical region
93	c5a1yM_	Alignment	not modelled	75.4	11	PDB header: transport protein Chain: M: PDB Molecule: coatamer subunit gamma-1; PDBTitle: the structure of the copi coat linkage iv
94	c3zjyE_	Alignment	not modelled	75.2	13	PDB header: translation Chain: E: PDB Molecule: importin-13; PDBTitle: crystal structure of importin 13 - rangtp - eif1a complex
95	c3slaC_	Alignment	not modelled	70.9	11	PDB header: signaling protein Chain: C: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
96	c3l6yA_	Alignment	not modelled	69.8	13	PDB header: cell adhesion Chain: A: PDB Molecule: catenin delta-1; PDBTitle: crystal structure of p120 catenin in complex with e-cadherin
97	c2x19B_	Alignment	not modelled	68.2	11	PDB header: nuclear transport Chain: B: PDB Molecule: importin-13; PDBTitle: crystal structure of importin13 - rangtp complex
98	c3t7uA_	Alignment	not modelled	57.2	15	PDB header: cell adhesion Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: a new crytal structure of apc-arm
99	d1ho8a_	Alignment	not modelled	57.1	23	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Regulatory subunit H of the V-type ATPase
100	d1ohea1	Alignment	not modelled	55.8	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
101	c3ibvB_	Alignment	not modelled	45.5	14	PDB header: rna binding protein Chain: B: PDB Molecule: exportin-t; PDBTitle: karyopherin cytosolic state
102	d1hf8a2	Alignment	not modelled	43.7	19	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: Phosphoinositide-binding clathrin adaptor, N-terminal domain
103	c3tjzB_	Alignment	not modelled	42.4	14	PDB header: protein transport/protein binding Chain: B: PDB Molecule: coatamer subunit gamma; PDBTitle: crystal structure of arf1 bound to the gamma/zeta-cop core complex
104	d1s0yb_	Alignment	not modelled	34.6	15	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
105	c3ej9D_	Alignment	not modelled	34.3	15	PDB header: hydrolase Chain: D: PDB Molecule: beta-subunit of trans-3-chloroacrylic acid dehalogenase; PDBTitle: structural and mechanistic analysis of trans-3-chloroacrylic acid2 dehalogenase activity
106	c1ls4A_	Alignment	not modelled	32.3	26	PDB header: lipid transport Chain: A: PDB Molecule: apolipophorin-iii; PDBTitle: nmr structure of apolipophorin-iii from locusta migratoria
107	d1lsha1	Alignment	not modelled	32.0	12	Fold: alpha-alpha superhelix Superfamily: Lipovitellin-phosvitin complex, superhelical domain Family: Lipovitellin-phosvitin complex, superhelical domain
108	d1aepa_	Alignment	not modelled	30.2	26	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III

109	c3evrA_	Alignment	not modelled	29.9	17	PDB header: signaling protein Chain: A: PDB Molecule: myosin light chain kinase, green fluorescent PDBTitle: crystal structure of calcium bound monomeric gcamp2
110	c1vsv7_	Alignment	not modelled	29.4	11	PDB header: hydrolase Chain: 7: PDB Molecule: proteasome activator blm10; PDBTitle: proteasome activator complex
111	d1h2vc1	Alignment	not modelled	28.8	18	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
112	d1oyza_	Alignment	not modelled	27.6	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat
113	c3eyiB_	Alignment	not modelled	24.2	35	PDB header: dna binding protein/dna Chain: B: PDB Molecule: z-dna-binding protein 1; PDBTitle: the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
114	c2l4mA_	Alignment	not modelled	23.9	35	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the zbeta domain of human dai and its binding2 modes to b- and z-dna
115	c2l1lB_	Alignment	not modelled	23.6	13	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
116	c2vxgB_	Alignment	not modelled	22.0	23	PDB header: gene regulation Chain: B: PDB Molecule: cg6181-pa, isoform a; PDBTitle: crystal structure of the conserved c-terminal region of ge-2 1
117	d2i9ca1	Alignment	not modelled	21.9	28	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: RPA1889-like
118	c1lshA_	Alignment	not modelled	21.8	14	PDB header: lipid binding protein Chain: A: PDB Molecule: lipovitellin (lv-1n, lv-1c); PDBTitle: lipid-protein interactions in lipovitellin
119	d1hx8a2	Alignment	not modelled	21.5	17	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: Phosphoinositide-binding clathrin adaptor, N-terminal domain
120	d1skva_	Alignment	not modelled	20.6	38	Fold: ROP-like Superfamily: Hypothetical protein D-63 Family: Hypothetical protein D-63