


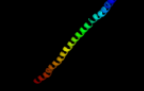




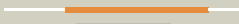
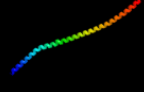



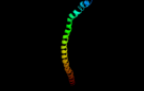
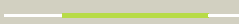
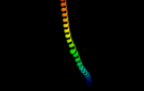

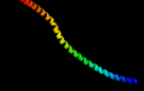

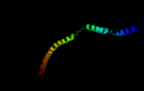


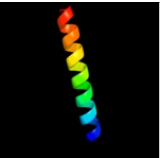
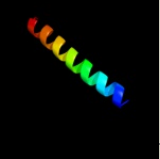
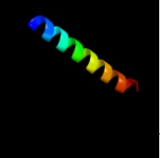
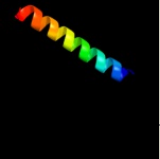
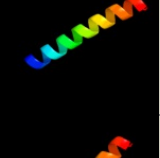
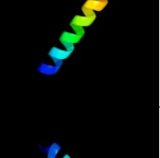
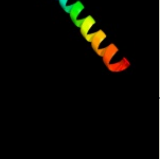
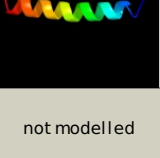


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2eqbC_</a>	 Alignment		99.8	31	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> C: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor sec2; <b>PDBTitle:</b> crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
2	<a href="#">c2e7sM_</a>	 Alignment		99.2	29	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> M: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor sec2; <b>PDBTitle:</b> crystal structure of the yeast sec2p gef domain
3	<a href="#">c3ol1A_</a>	 Alignment		87.8	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
4	<a href="#">c3kltB_</a>	 Alignment		82.0	15	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of a vimentin fragment
5	<a href="#">c2fxmB_</a>	 Alignment		81.8	23	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin heavy chain, cardiac muscle beta isoform; <b>PDBTitle:</b> structure of the human beta-myosin s2 fragment
6	<a href="#">c1y4cA_</a>	 Alignment		74.9	12	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed <b>PDBTitle:</b> designed helical protein fusion mbp
7	<a href="#">c1deqD_</a>	 Alignment		74.7	20	<b>PDB header:</b> <b>PDB COMPND:</b>
8	<a href="#">c3q8tB_</a>	 Alignment		65.8	16	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> beclin-1; <b>PDBTitle:</b> crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
9	<a href="#">c1ei3C_</a>	 Alignment		65.4	12	<b>PDB header:</b> <b>PDB COMPND:</b>
10	<a href="#">c1deqF_</a>	 Alignment		64.9	9	<b>PDB header:</b> <b>PDB COMPND:</b>
11	<a href="#">c1ztaA_</a>	 Alignment		61.3	15	<b>PDB header:</b> dna-binding motif <b>Chain:</b> A: <b>PDB Molecule:</b> leucine zipper monomer; <b>PDBTitle:</b> the solution structure of a leucine-zipper motif peptide

12	<a href="#">c1rb6C_</a>	Alignment		61.1	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
13	<a href="#">c1ij2C_</a>	Alignment		59.2	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
14	<a href="#">c1ij3C_</a>	Alignment		58.4	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
15	<a href="#">c1ij3B_</a>	Alignment		58.4	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
16	<a href="#">c3k7zA_</a>	Alignment		58.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
17	<a href="#">c3k7zB_</a>	Alignment		58.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
18	<a href="#">c1rb1B_</a>	Alignment		58.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
19	<a href="#">c1rb1A_</a>	Alignment		58.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
20	<a href="#">c1swiA_</a>	Alignment		58.3	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with2 benzene
21	<a href="#">c3ojaB_</a>	Alignment	not modelled	57.4	9	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
22	<a href="#">c3dtpA_</a>	Alignment	not modelled	57.3	23	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and <b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
23	<a href="#">c1ij2B_</a>	Alignment	not modelled	56.7	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
24	<a href="#">c2o7hF_</a>	Alignment	not modelled	56.1	15	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> crystal structure of trimeric coiled coil gcn4 leucine zipper
25	<a href="#">c3u59C_</a>	Alignment	not modelled	53.8	11	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> tropomyosin beta chain; <b>PDBTitle:</b> n-terminal 98-aa fragment of smooth muscle tropomyosin beta
26	<a href="#">c1ce0B_</a>	Alignment	not modelled	49.8	8	<b>PDB header:</b> hiv-1 envelope protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (leucine zipper model h38-p1); <b>PDBTitle:</b> trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
27	<a href="#">c1wt6B_</a>	Alignment	not modelled	48.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> myotonic-protein kinase; <b>PDBTitle:</b> coiled-coil domain of dmpk
28	<a href="#">c1bf5A_</a>	Alignment	not modelled	43.8	8	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex

29	<a href="#">c3t97A_</a>	Alignment	not modelled	42.8	26	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear pore glycoprotein p62; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup62/nup54
30	<a href="#">c1cosB_</a>	Alignment	not modelled	42.8	27	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> B: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
31	<a href="#">c1cosC_</a>	Alignment	not modelled	42.8	27	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> C: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
32	<a href="#">c1cosA_</a>	Alignment	not modelled	42.8	27	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coiled serine; <b>PDBTitle:</b> crystal structure of a synthetic triple-stranded alpha-2 helical bundle
33	<a href="#">c2o98P_</a>	Alignment	not modelled	42.3	23	<b>PDB header:</b> protein binding <b>Chain:</b> P: <b>PDB Molecule:</b> plasma membrane h+ atpase; <b>PDBTitle:</b> structure of the 14-3-3 / h+-atpase plant complex
34	<a href="#">c2pnvA_</a>	Alignment	not modelled	40.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
35	<a href="#">c2xztA_</a>	Alignment	not modelled	37.9	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
36	<a href="#">c1coiA_</a>	Alignment	not modelled	37.6	19	<b>PDB header:</b> alpha-helical bundle <b>Chain:</b> A: <b>PDB Molecule:</b> coil-vald; <b>PDBTitle:</b> designed trimeric coiled coil-vald
37	<a href="#">c1bg1A_</a>	Alignment	not modelled	36.3	9	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
38	<a href="#">c2d3eD_</a>	Alignment	not modelled	34.0	19	<b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 <b>PDBTitle:</b> crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
39	<a href="#">d1cxzb_</a>	Alignment	not modelled	33.8	14	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> HR1 repeat <b>Family:</b> HR1 repeat
40	<a href="#">c3ipkA_</a>	Alignment	not modelled	29.3	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> agi/ii; <b>PDBTitle:</b> crystal structure of a3vp1 of agi/ii of streptococcus mutans
41	<a href="#">c3vkhD_</a>	Alignment	not modelled	29.1	6	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> crystal structure of an motor protein
42	<a href="#">c3m48A_</a>	Alignment	not modelled	28.1	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4 leucine zipper peptide mutant
43	<a href="#">c3batB_</a>	Alignment	not modelled	27.8	20	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin heavy chain, striated muscle/general <b>PDBTitle:</b> crystal structure of the n-terminal region of the scallop2 myosin rod, monoclinic (p21) form
44	<a href="#">c1zilB_</a>	Alignment	not modelled	27.3	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
45	<a href="#">c1zilA_</a>	Alignment	not modelled	27.3	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the dimeric2 state
46	<a href="#">c1zimC_</a>	Alignment	not modelled	25.8	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the trimeric2 state
47	<a href="#">c1zimA_</a>	Alignment	not modelled	25.8	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the trimeric2 state
48	<a href="#">c1zimB_</a>	Alignment	not modelled	25.8	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn16gln in the trimeric2 state
49	<a href="#">c3ghgK_</a>	Alignment	not modelled	25.3	15	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
50	<a href="#">c3ghgD_</a>	Alignment	not modelled	24.1	15	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> fibrinogen alpha chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
51	<a href="#">c3hnbW_</a>	Alignment	not modelled	22.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
52	<a href="#">c2ztaB_</a>	Alignment	not modelled	22.9	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4 leucine zipper; <b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
53	<a href="#">c2ztaA_</a>	Alignment	not modelled	22.9	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4 leucine zipper; <b>PDBTitle:</b> x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
						<b>PDB header:</b> metal binding protein

54	<a href="#">c3ilgA_</a>	Alignment	not modelled	22.1	15	<b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> crystal structure of a gcn4 leucine zipper mutant at 1.6 a2 resolution
55	<a href="#">c1ce9C_</a>	Alignment	not modelled	21.0	15	<b>PDB header:</b> helix capping <b>Chain:</b> C: <b>PDB Molecule:</b> protein (gcn4-pmse); <b>PDBTitle:</b> helix capping in the gcn4 leucine zipper
56	<a href="#">c1ce9A_</a>	Alignment	not modelled	21.0	15	<b>PDB header:</b> helix capping <b>Chain:</b> A: <b>PDB Molecule:</b> protein (gcn4-pmse); <b>PDBTitle:</b> helix capping in the gcn4 leucine zipper
57	<a href="#">c1ce9D_</a>	Alignment	not modelled	21.0	15	<b>PDB header:</b> helix capping <b>Chain:</b> D: <b>PDB Molecule:</b> protein (gcn4-pmse); <b>PDBTitle:</b> helix capping in the gcn4 leucine zipper
58	<a href="#">c1ce9B_</a>	Alignment	not modelled	21.0	15	<b>PDB header:</b> helix capping <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gcn4-pmse); <b>PDBTitle:</b> helix capping in the gcn4 leucine zipper
59	<a href="#">c1yv0I_</a>	Alignment	not modelled	20.9	30	<b>PDB header:</b> contractile protein <b>Chain:</b> I: <b>PDB Molecule:</b> tropomyosin i, fast skeletal muscle; <b>PDBTitle:</b> crystal structure of skeletal muscle tropomyosin in the ca2+-2 free state
60	<a href="#">c2b9cA_</a>	Alignment	not modelled	20.6	13	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> striated-muscle alpha tropomyosin; <b>PDBTitle:</b> structure of tropomyosin's mid-region: bending and binding2 sites for actin
61	<a href="#">c3p8mD_</a>	Alignment	not modelled	20.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> human dynein light chain (dynl12) in complex with an in vitro evolved2 peptide dimerized by leucine zipper
62	<a href="#">c1ij2A_</a>	Alignment	not modelled	19.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
63	<a href="#">c1zikB_</a>	Alignment	not modelled	19.2	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn161lys in the dimeric2 state
64	<a href="#">c1zikA_</a>	Alignment	not modelled	19.2	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant asn161lys in the dimeric2 state
65	<a href="#">c2x6pA_</a>	Alignment	not modelled	18.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
66	<a href="#">c2x6pC_</a>	Alignment	not modelled	18.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
67	<a href="#">c2x6pB_</a>	Alignment	not modelled	18.8	27	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> coil ser l19c; <b>PDBTitle:</b> crystal structure of coil ser l19c
68	<a href="#">c3qsvD_</a>	Alignment	not modelled	18.6	31	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> mothers against decapentaplegic homolog 4; <b>PDBTitle:</b> structural basis for dna recognition by constitutive smad4 mh1 dimers
69	<a href="#">c1griA_</a>	Alignment	not modelled	18.6	19	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> grea protein; <b>PDBTitle:</b> grea transcript cleavage factor from escherichia coli
70	<a href="#">c3kmpA_</a>	Alignment	not modelled	18.5	18	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> smad1-mh1; <b>PDBTitle:</b> crystal structure of smad1-mh1/dna complex
71	<a href="#">c3k7zC_</a>	Alignment	not modelled	18.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
72	<a href="#">c1rb1C_</a>	Alignment	not modelled	18.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
73	<a href="#">c1rb6B_</a>	Alignment	not modelled	17.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
74	<a href="#">c1rb4B_</a>	Alignment	not modelled	17.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
75	<a href="#">c1rb4A_</a>	Alignment	not modelled	17.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
76	<a href="#">c1swiB_</a>	Alignment	not modelled	17.2	15	<b>PDB header:</b> leucine zipper <b>Chain:</b> B: <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with2 benzene
77	<a href="#">c2no2A_</a>	Alignment	not modelled	16.9	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> huntingtin-interacting protein 1; <b>PDBTitle:</b> crystal structure of the dl1rkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
78	<a href="#">c1i84V_</a>	Alignment	not modelled	16.1	19	<b>PDB header:</b> contractile protein <b>Chain:</b> V: <b>PDB Molecule:</b> smooth muscle myosin heavy chain; <b>PDBTitle:</b> cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment
79	<a href="#">c1rb5C_</a>	Alignment	not modelled	16.1	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant

					as2 n16a trigonal form <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
80	<a href="#">c1ij3A_</a>	Alignment	not modelled	15.8	15
81	<a href="#">c1degO_</a>	Alignment	not modelled	15.7	12
82	<a href="#">c1rb5B_</a>	Alignment	not modelled	15.4	15
83	<a href="#">c1rb6A_</a>	Alignment	not modelled	15.4	15
84	<a href="#">c1rb5A_</a>	Alignment	not modelled	15.4	15
85	<a href="#">c2p4vA_</a>	Alignment	not modelled	15.3	19
86	<a href="#">c3m9bK_</a>	Alignment	not modelled	15.0	8
87	<a href="#">c2efrB_</a>	Alignment	not modelled	15.0	19
88	<a href="#">c2wpzA_</a>	Alignment	not modelled	14.6	12
89	<a href="#">c2v66C_</a>	Alignment	not modelled	14.2	23
90	<a href="#">c2jgoA_</a>	Alignment	not modelled	13.7	23
91	<a href="#">c2jgoB_</a>	Alignment	not modelled	13.7	23
92	<a href="#">c3ljmC_</a>	Alignment	not modelled	13.7	23
93	<a href="#">c3ljmB_</a>	Alignment	not modelled	13.7	23
94	<a href="#">c2jgoC_</a>	Alignment	not modelled	13.7	23
95	<a href="#">c3ljmA_</a>	Alignment	not modelled	13.7	23
96	<a href="#">c2wpzB_</a>	Alignment	not modelled	13.5	12
97	<a href="#">c1aq5C_</a>	Alignment	not modelled	13.4	7
98	<a href="#">c2cceB_</a>	Alignment	not modelled	13.2	15
99	<a href="#">c2wpzC_</a>	Alignment	not modelled	12.9	12