Phyre^2

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Description	P77658
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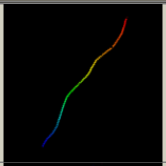
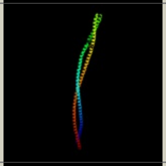
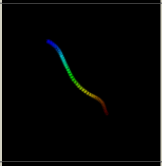
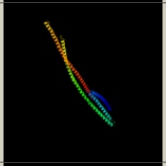
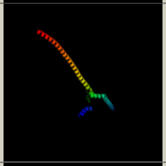
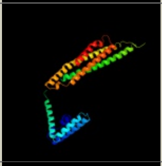
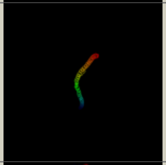
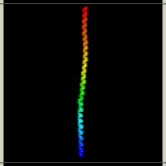
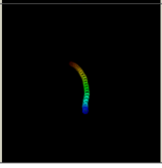
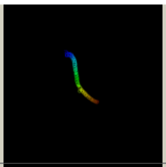
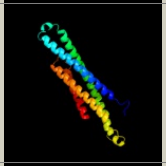
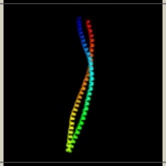
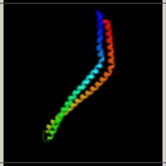
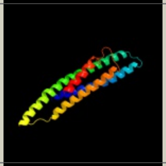
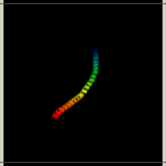
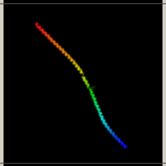
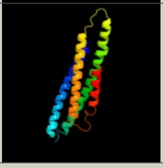
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c1gA_	Alignment		99.0	6	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
2	c2ch7A_	Alignment		98.4	10	**PDB header:**chemotaxis **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
3	c2oevA_	Alignment		97.6	7	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
4	c2efrB_	Alignment		97.3	12	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
5	c2oexB_	Alignment		97.1	8	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** structure of alix/aip1 v domain
6	c1ciiA_	Alignment		96.9	12	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
7	c3ojaB_	Alignment		96.3	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
8	c1yvlB_	Alignment		95.3	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
9	c2d3eD_	Alignment		95.3	13	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
10	c3u59C_	Alignment		94.9	6	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
11	c2fxmB_	Alignment		94.6	8	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment

12	c2b9cA_	Alignment		94.5	9	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**striated-muscle alpha tropomyosin; **PDBTitle:** structure of tropomyosin's mid-region: bending and binding2 sites for actin
13	c1bg1A_	Alignment		94.5	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
14	c3l9oA_	Alignment		94.2	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
15	c3g67A_	Alignment		94.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
16	c3na7A_	Alignment		93.7	10	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
17	c1bf5A_	Alignment		93.7	8	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
18	c3ol1A_	Alignment		93.7	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
19	c3o0zD_	Alignment		93.7	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human rock i
20	c3cwgA_	Alignment		93.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
21	c3ghgK_	Alignment	not modelled	93.4	10	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
22	c4a55B_	Alignment	not modelled	93.0	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
23	c2gl2B_	Alignment	not modelled	92.7	13	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
24	c1deqO_	Alignment	not modelled	92.2	12	**PDB header:** **PDB COMPND:**
25	c1qu7A_	Alignment	not modelled	90.9	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
26	c2y3aB_	Alignment	not modelled	89.5	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
27	c1y4cA_	Alignment	not modelled	89.1	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
28	c1ei3E_	Alignment	not modelled	88.6	6	**PDB header:** **PDB COMPND:**

29	c2v66C_	Alignment	not modelled	87.9	9	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** crystal structure of the coiled-coil domain of ndel1 (a.a.2 58 to 169)c
30	c2wpqA_	Alignment	not modelled	86.8	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment; **PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
31	c1deqF_	Alignment	not modelled	85.9	11	**PDB header:** **PDB COMPND:**
32	c2dq3A_	Alignment	not modelled	83.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
33	c1deqD_	Alignment	not modelled	83.1	8	**PDB header:** **PDB COMPND:**
34	c2v1yB_	Alignment	not modelled	80.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
35	c2v71A_	Alignment	not modelled	80.2	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
36	c1hciB_	Alignment	not modelled	80.0	8	**PDB header:**triple-helix coiled coil **Chain:** B: **PDB Molecule:**alpha-actinin 2; **PDBTitle:** crystal structure of the rod domain of alpha-actinin
37	c1ei3C_	Alignment	not modelled	79.0	8	**PDB header:** **PDB COMPND:**
38	c3dtpA_	Alignment	not modelled	78.9	10	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
39	c3u1aC_	Alignment	not modelled	77.0	6	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
40	c2e7sM_	Alignment	not modelled	75.8	14	**PDB header:**endocytosis/exocytosis **Chain:** M: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the yeast sec2p gef domain
41	c3ojaA_	Alignment	not modelled	73.8	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
42	c1jchC_	Alignment	not modelled	73.6	9	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
43	c3hnwB_	Alignment	not modelled	72.6	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
44	c2i1jA_	Alignment	not modelled	69.9	9	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
45	c1l8dB_	Alignment	not modelled	69.4	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
46	c3a7pB_	Alignment	not modelled	69.4	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
47	c2qihA_	Alignment	not modelled	66.3	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein uspa1; **PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
48	c3hizB_	Alignment	not modelled	64.6	8	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
49	c3iv1F_	Alignment	not modelled	56.7	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**tumor susceptibility gene 101 protein; **PDBTitle:** coiled-coil domain of tumor susceptibility gene 101
50	c3r6nA_	Alignment	not modelled	56.2	7	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**desmoplakin; **PDBTitle:** crystal structure of a rigid four spectrin repeat fragment of the2 human desmoplakin plakin domain
51	c2rd0B_	Alignment	not modelled	53.3	9	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a human p110alpha/p85alpha complex
52	c3qh9A_	Alignment	not modelled	49.8	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
53	c2eqbC_	Alignment	not modelled	43.9	12	**PDB header:**endocytosis/exocytosis **Chain:** C: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex

54	c3layF_	Alignment	not modelled	42.0	14	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
55	c2jeeA_	Alignment	not modelled	38.6	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
56	c1ic2B_	Alignment	not modelled	34.7	9	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**tropomyosin alpha chain, skeletal muscle; **PDBTitle:** deciphering the design of the tropomyosin molecule
57	c2v4hA_	Alignment	not modelled	32.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
58	c2xdjF_	Alignment	not modelled	32.8	10	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
59	c3ipkA_	Alignment	not modelled	30.1	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
60	c1sjjB_	Alignment	not modelled	29.7	10	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**actinin; **PDBTitle:** cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
61	c2no2A_	Alignment	not modelled	29.4	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of the dllrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
62	d1seta1	Alignment	not modelled	28.2	11	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
63	c3m9bK_	Alignment	not modelled	24.8	5	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
64	c3n4xB_	Alignment	not modelled	22.4	8	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
65	c1ci6A_	Alignment	not modelled	22.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
66	c3qo8A_	Alignment	not modelled	21.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
67	c1gd2G_	Alignment	not modelled	21.3	10	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
68	c1gk4A_	Alignment	not modelled	20.4	8	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
69	c3q0xA_	Alignment	not modelled	18.8	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centriole protein; **PDBTitle:** n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
70	d2ap3a1	Alignment	not modelled	17.9	7	**Fold:**Four-helical up-and-down bundle **Superfamily:**MW0975(SA0943)-like **Family:**MW0975(SA0943)-like
71	c1x8yA_	Alignment	not modelled	17.6	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
72	c2wt7B_	Alignment	not modelled	16.7	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
73	c1wt6B_	Alignment	not modelled	16.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**myotonin-protein kinase; **PDBTitle:** coiled-coil domain of dmpk
74	c2zvnF_	Alignment	not modelled	15.8	17	**PDB header:**signaling protein/transcription **Chain:** F: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cozi domain incomplex with diubiquitin in p2121212 space group
75	c2x7aB_	Alignment	not modelled	15.5	5	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
76	c2bsgA_	Alignment	not modelled	15.5	9	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** the modeled structure of fibritin (gpwac) of bacteriophage2 t4 based on cryo-em reconstruction of the extended tail of3 bacteriophage t4
77	c2pmsD_	Alignment	not modelled	15.5	11	**PDB header:**metal transport, hydrolase **Chain:** D: **PDB Molecule:**pneumococcal surface protein a (pspa); **PDBTitle:** crystal structure of the complex of human lactoferrin n-lobe and2 lactoferrin-binding domain of pneumococcal surface protein a
78	c1fosF_	Alignment	not modelled	15.4	10	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
79	c2ke4A_	Alignment	not modelled	15.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4;

79	c2ke4A_	Alignment	not modelled	13.4	12	**PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
80	c3batB_	Alignment	not modelled	15.2	14	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, striated muscle/general **PDBTitle:** crystal structure of the n-terminal region of the scallop2 myosin rod, monoclinic (p21) form
81	c3cvfA_	Alignment	not modelled	14.8	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
82	c1n73C_	Alignment	not modelled	14.6	6	**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
83	c2hpcF_	Alignment	not modelled	13.3	9	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
84	c1t2kD_	Alignment	not modelled	11.4	10	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**cyclic-amp-dependent transcription factor atf-2; **PDBTitle:** structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
85	c2p22C_	Alignment	not modelled	11.2	15	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein srn2; **PDBTitle:** structure of the yeast escrt-i heterotetramer core
86	c1g8xB_	Alignment	not modelled	10.9	8	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**myosin ii heavy chain fused to alpha-actinin 3; **PDBTitle:** structure of a genetically engineered molecular motor
87	c3cveC_	Alignment	not modelled	10.7	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**homer protein homolog 1; **PDBTitle:** crystal structure of the carboxy terminus of homer1
88	c1yv0I_	Alignment	not modelled	10.4	8	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i, fast skeletal muscle; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 free state
89	c1junB_	Alignment	not modelled	10.4	11	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
90	c3mkxC_	Alignment	not modelled	9.9	13	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
91	c3m06F_	Alignment	not modelled	9.6	10	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of traf2
92	c1fosE_	Alignment	not modelled	9.2	13	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**p55-c-fos proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
93	c1u4qB_	Alignment	not modelled	9.1	12	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** crystal structure of repeats 15, 16 and 17 of chicken brain2 alpha spectrin
94	c1ru7B_	Alignment	not modelled	9.0	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** 1934 human h1 hemagglutinin
95	c2xgjA_	Alignment	not modelled	8.8	18	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
96	c2e43A_	Alignment	not modelled	8.7	11	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**ccaat/enhancer-binding protein beta; **PDBTitle:** crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
97	c3lssA_	Alignment	not modelled	8.6	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
98	c1ik9B_	Alignment	not modelled	8.0	8	**PDB header:**gene regulation/ligase **Chain:** B: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
99	c2w6aB_	Alignment	not modelled	7.9	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain