Phyre^2

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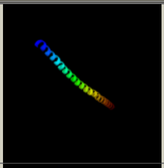
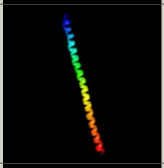
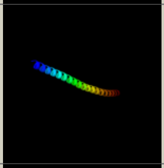
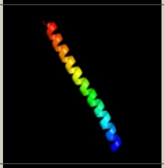
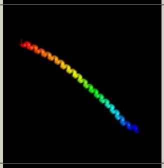
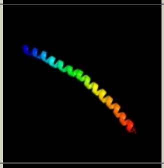
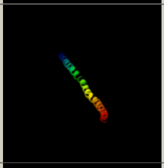
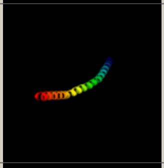
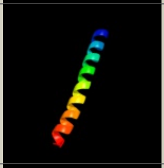
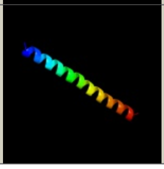
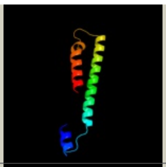
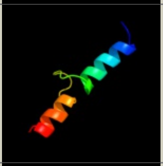
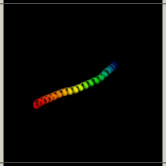
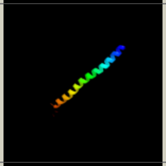
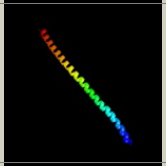
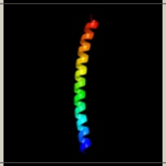
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jeeA_	Alignment		100.0	100	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
2	c3u59C_	Alignment		91.8	18	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
3	c3ghgK_	Alignment		89.3	12	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
4	c3ojaB_	Alignment		89.1	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
5	c2w6aB_	Alignment		86.4	38	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
6	c2fxmB_	Alignment		81.4	14	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
7	c1cz7C_	Alignment		79.5	13	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**microtubule motor protein ncd; **PDBTitle:** the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
8	c1deqO_	Alignment		78.9	11	**PDB header:** **PDB COMPND:**
9	c3ol1A_	Alignment		78.8	12	**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
10	c2yy0D_	Alignment		78.5	41	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
11	c1gd2G_	Alignment		78.4	27	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna

12	c1yvlB_	Alignment		77.5	10	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
13	c1dipA_	Alignment		75.7	50	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
14	c1ei3E_	Alignment		75.6	7	**PDB header:** **PDB COMPND:**
15	c1j1dF_	Alignment		71.8	16	**PDB header:**contractile protein **Chain:** F: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
16	c2b9cA_	Alignment		71.1	10	**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
17	c2wt7B_	Alignment		69.7	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
18	c2v66C_	Alignment		69.4	14	**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
19	c3o0zD_	Alignment		68.9	15	**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	d1an2a_	Alignment		66.7	13	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
21	c2d3eD_	Alignment	not modelled	66.4	16	**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
22	c2oqqB_	Alignment	not modelled	65.1	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
23	c3mudA_	Alignment	not modelled	65.1	24	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**dna repair protein xrcc4, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
24	c1c1gA_	Alignment	not modelled	65.0	20	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
25	c1bg1A_	Alignment	not modelled	64.8	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
26	c2w6bA_	Alignment	not modelled	64.5	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** crystal structure of the trimeric beta-pix coiled-coil2 domain
27	d1x4ta1	Alignment	not modelled	63.9	32	**Fold:**Long alpha-hairpin **Superfamily:**ISY1 domain-like **Family:**ISY1 N-terminal domain-like
						PDB header:transcription/dna

28	c1fosE_	Alignment	not modelled	63.5	25	**Chain:** E: **PDB Molecule:**p55-c-fos proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
29	d2p90a1	Alignment	not modelled	63.3	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Cgl1923-like **Family:**Cgl1923-like
30	c3hizB_	Alignment	not modelled	62.9	9	**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
31	c1ci6A_	Alignment	not modelled	62.8	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
32	c3a7pB_	Alignment	not modelled	62.1	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
33	c2efrB_	Alignment	not modelled	60.1	11	**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
34	c1fosF_	Alignment	not modelled	59.3	26	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
35	c2gd7B_	Alignment	not modelled	59.3	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hexim1 protein; **PDBTitle:** the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
36	d1uklc_	Alignment	not modelled	57.3	33	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
37	c2e43A_	Alignment	not modelled	56.2	31	**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
38	c1bf5A_	Alignment	not modelled	56.0	18	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
39	c3hnwB_	Alignment	not modelled	54.7	23	**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
40	c3qo8A_	Alignment	not modelled	53.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
41	c2v71A_	Alignment	not modelled	52.6	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
42	d1am9a_	Alignment	not modelled	51.9	35	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
43	d1r05a_	Alignment	not modelled	50.7	15	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
44	c2j5uB_	Alignment	not modelled	49.8	41	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
45	c2w83C_	Alignment	not modelled	49.6	22	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**c-jun-amino-terminal kinase-interacting protein **PDBTitle:** crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4
46	d1nkpb_	Alignment	not modelled	49.6	13	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
47	c3q4fG_	Alignment	not modelled	47.6	30	**PDB header:**dna binding protein/protein binding **Chain:** G: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of xrcc4/xlf-cernunnos complex
48	c1ei3C_	Alignment	not modelled	45.9	16	**PDB header:** **PDB COMPND:**
49	c1rb1B_	Alignment	not modelled	45.4	38	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
50	c1rb1A_	Alignment	not modelled	45.4	38	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
51	c3k7zA_	Alignment	not modelled	45.4	38	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
52	c3k7zB_	Alignment	not modelled	45.4	38	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
53	d1nkpa_	Alignment	not modelled	45.1	23	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain

54	d1nlwa_	Alignment	not modelled	45.1	18	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
55	c2gl2B_	Alignment	not modelled	45.1	14	**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
56	c1ij2C_	Alignment	not modelled	45.0	38	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
57	c1ij3C_	Alignment	not modelled	44.9	38	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
58	c3dtpA_	Alignment	not modelled	43.5	16	**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
59	c3a5tB_	Alignment	not modelled	43.5	22	**PDB header:**transcription regulator/dna **Chain:** B: **PDB Molecule:**transcription factor mafg; **PDBTitle:** crystal structure of mafg-dna complex
60	c1ytzI_	Alignment	not modelled	43.4	18	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 activated state
61	c1ij2B_	Alignment	not modelled	43.4	38	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
62	c1ci6B_	Alignment	not modelled	41.3	32	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
63	c1ciiA_	Alignment	not modelled	37.9	16	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
64	c1junB_	Alignment	not modelled	37.9	23	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
65	c1deqF_	Alignment	not modelled	37.6	10	**PDB header:** **PDB COMPND:**
66	c3na7A_	Alignment	not modelled	36.8	8	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
67	c1t2kD_	Alignment	not modelled	35.0	24	**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
68	c1ik9B_	Alignment	not modelled	32.6	24	**PDB header:**gene regulation/ligase **Chain:** B: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
69	c3l9oA_	Alignment	not modelled	32.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
70	c3cwgA_	Alignment	not modelled	29.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
71	c2zxxA_	Alignment	not modelled	29.9	22	**PDB header:**cell cycle/replication **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of cdt1/geminin complex
72	c2ve7A_	Alignment	not modelled	27.7	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**kinetochore protein hec1, kinetochore protein spc25; **PDBTitle:** crystal structure of a bonsai version of the human ndc802 complex
73	c1dh3A_	Alignment	not modelled	27.2	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcription factor creb; **PDBTitle:** crystal structure of a creb bzip-cre complex reveals the2 basis for creb faimly selective dimerization and dna3 binding
74	d1hloa_	Alignment	not modelled	25.7	11	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
75	c2v4hA_	Alignment	not modelled	25.6	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
76	c3m9bK_	Alignment	not modelled	24.0	17	**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
77	c2v1yB_	Alignment	not modelled	23.2	16	**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
78	d1nlwe_	Alignment	not modelled	22.8	26	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain

79	d2ncda_	Alignment	not modelled	22.4	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
80	c4a55B_	Alignment	not modelled	19.8	17	**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
81	c2xgjA_	Alignment	not modelled	19.7	13	**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
82	c1fmhA_	Alignment	not modelled	19.4	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
83	c1debA_	Alignment	not modelled	19.2	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
84	c1yv0I_	Alignment	not modelled	19.0	18	**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
85	c2y3aB_	Alignment	not modelled	19.0	12	**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
86	c1h3oA_	Alignment	not modelled	18.9	38	**PDB header:**transcription/tbp-associated factors **Chain:** A: **PDB Molecule:**transcription initiation factor tfiid 135 kda **PDBTitle:** crystal structure of the human taf4-taf122 (tafii135-tafii20) complex
87	d1h3oa_	Alignment	not modelled	18.9	38	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
88	c2zvnF_	Alignment	not modelled	17.3	23	**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
89	c2xdjF_	Alignment	not modelled	17.2	19	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
90	d1uk5a_	Alignment	not modelled	16.5	12	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
91	d1u2ma_	Alignment	not modelled	15.9	28	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
92	c2x7aB_	Alignment	not modelled	15.1	36	**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
93	c2wukD_	Alignment	not modelled	15.0	20	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
94	c3lssA_	Alignment	not modelled	14.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
95	c1ztaA_	Alignment	not modelled	14.2	33	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
96	c2wvrB_	Alignment	not modelled	14.1	24	**PDB header:**replication **Chain:** B: **PDB Molecule:**geminin; **PDBTitle:** human cdt1:geminin complex
97	c1jocA_	Alignment	not modelled	14.0	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
98	c3mtuD_	Alignment	not modelled	13.8	8	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**tropomyosin alpha-1 chain, microtubule-associated protein **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
99	d1seta1	Alignment	not modelled	13.4	18	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)