Phyre2

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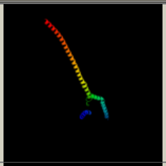
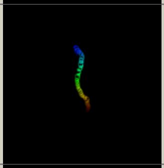
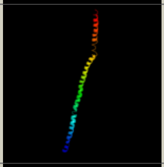
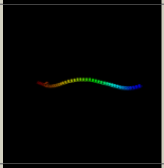
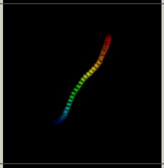
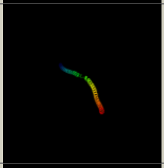
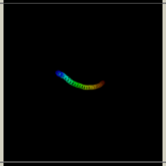
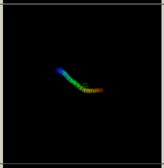
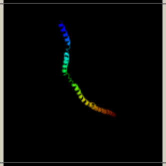
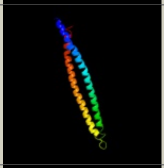
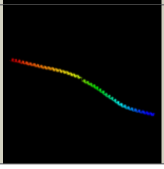
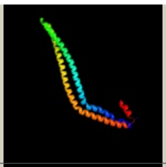
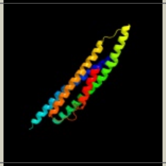
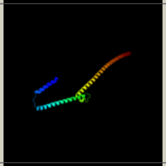
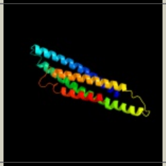
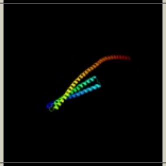
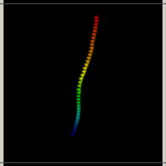
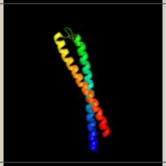
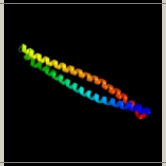
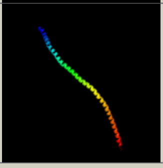
Description	P0AFM6
Date	Thu Jan 5 11:26:46 GMT 2012
Unique Job ID	30ef9878c4e902c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ojaB_	Alignment		96.4	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
2	c3ghgK_	Alignment		96.3	7	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
3	c1deqO_	Alignment		93.6	9	**PDB header:** **PDB COMPND:**
4	c2efrB_	Alignment		93.2	13	**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	c1ei3E_	Alignment		92.9	10	**PDB header:** **PDB COMPND:**
6	c2d3eD_	Alignment		92.8	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
7	c2fxmB_	Alignment		92.4	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
8	c2b9cA_	Alignment		91.1	14	**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
9	c1deqF_	Alignment		90.6	13	**PDB header:** **PDB COMPND:**
10	c2rd0B_	Alignment		89.9	12	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a human p110alpha/p85alpha complex
11	c3o0zD_	Alignment		88.5	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human rock i

12	c3na7A_	Alignment		87.9	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
13	c1bf5A_	Alignment		85.4	8	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
14	c3ojaA_	Alignment		85.4	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
15	c3cwgA_	Alignment		83.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
16	c1ciiA_	Alignment		80.5	10	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
17	c2v71A_	Alignment		80.0	10	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
18	c1l8dB_	Alignment		79.9	10	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
19	c4a55B_	Alignment		79.2	13	**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
20	c3dtpA_	Alignment		70.7	13	**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
21	c3ipkA_	Alignment	not modelled	69.5	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
22	c1y4cA_	Alignment	not modelled	67.9	7	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
23	c3hizB_	Alignment	not modelled	66.7	15	**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
24	d1vmaa1	Alignment	not modelled	66.1	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
25	c3ol1A_	Alignment	not modelled	64.0	11	**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
26	c3u59C_	Alignment	not modelled	63.5	12	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
27	c1c1gA_	Alignment	not modelled	59.8	14	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
28	c3iv1F_	Alignment	not modelled	57.8	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**tumor susceptibility gene 101 protein;

						PDBTitle: coiled-coil domain of tumor susceptibility gene 101
29	c2jeeA_	Alignment	not modelled	53.2	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
30	c1ei3C_	Alignment	not modelled	52.4	15	**PDB header:** **PDB COMPND:**
31	c2v66C_	Alignment	not modelled	52.2	7	**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
32	c1bg1A_	Alignment	not modelled	51.7	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
33	c3hnwB_	Alignment	not modelled	43.5	12	**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
34	c1deqD_	Alignment	not modelled	42.5	5	**PDB header:** **PDB COMPND:**
35	c2gl2B_	Alignment	not modelled	42.2	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
36	c2y3aB_	Alignment	not modelled	42.2	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
37	c2v1yB_	Alignment	not modelled	37.9	13	**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
38	c3movB_	Alignment	not modelled	35.7	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
39	c3kltB_	Alignment	not modelled	33.8	7	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of a vimentin fragment
40	c3u1aC_	Alignment	not modelled	31.6	9	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
41	c1yvlB_	Alignment	not modelled	29.1	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
42	c1gk4A_	Alignment	not modelled	28.3	11	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
43	d1fxka_	Alignment	not modelled	27.9	13	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
44	d2gqba1	Alignment	not modelled	25.3	27	**Fold:**RPA2825-like **Superfamily:**RPA2825-like **Family:**RPA2825-like
45	c3a7pB_	Alignment	not modelled	21.9	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
46	c1vmaA_	Alignment	not modelled	21.7	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
47	c1x8yA_	Alignment	not modelled	18.7	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
48	d1r05a_	Alignment	not modelled	17.4	16	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
49	d2daha1	Alignment	not modelled	16.9	36	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
50	d2bwba1	Alignment	not modelled	15.6	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
51	c1jchC_	Alignment	not modelled	15.4	7	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
52	c2xdjF_	Alignment	not modelled	14.3	9	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
53	c1junB_	Alignment	not modelled	13.6	17	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
54	c2zvfG_	Alignment	not modelled	13.4	13	**PDB header:**ligase **Chain:** G: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2

						synthetase c-terminal dimerization domain
55	c3n4xB_	Alignment	not modelled	13.4	10	**PDB header:**replication **Chain:** B: **PDB Molecule:**monopolin complex subunit csm1; **PDBTitle:** structure of csm1 full-length
56	c1m1jA_	Alignment	not modelled	13.4	13	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
57	c2dnaA_	Alignment	not modelled	12.7	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
58	c2qa7B_	Alignment	not modelled	11.7	13	**PDB header:**actin binding **Chain:** B: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
59	c1gk7A_	Alignment	not modelled	11.6	20	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 1a fragment (1a)
60	d2cp8a1	Alignment	not modelled	11.2	50	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
61	c3qh9A_	Alignment	not modelled	11.2	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
62	c3he4A_	Alignment	not modelled	10.9	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip6; **PDBTitle:** heterospecific coiled-coil pair synzip5:synzip6
63	c3m9bK_	Alignment	not modelled	10.4	10	**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	c1ic2B_	Alignment	not modelled	9.8	19	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**tropomyosin alpha chain, skeletal muscle; **PDBTitle:** deciphering the design of the tropomyosin molecule
65	d1z0kb1	Alignment	not modelled	9.7	9	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
66	c1ci6A_	Alignment	not modelled	9.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
67	c2jy5A_	Alignment	not modelled	9.7	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
68	c1fosF_	Alignment	not modelled	9.6	10	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
69	c2hpcF_	Alignment	not modelled	9.3	12	**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.
70	c1sjjB_	Alignment	not modelled	9.2	6	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**actinin; **PDBTitle:** cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
71	c2wukD_	Alignment	not modelled	9.2	18	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
72	c3layF_	Alignment	not modelled	9.0	11	**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
73	d1lvfa_	Alignment	not modelled	8.9	18	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
74	c3p8cD_	Alignment	not modelled	8.8	10	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**wiskott-aldrich syndrome protein family member 1; **PDBTitle:** structure and control of the actin regulatory wave complex
75	c2kxoA_	Alignment	not modelled	8.8	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
76	c1jccC_	Alignment	not modelled	8.7	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**major outer membrane lipoprotein; **PDBTitle:** crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
77	c1gd2G_	Alignment	not modelled	8.6	15	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
78	d2dnaa1	Alignment	not modelled	8.6	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
79	d1fxkc_	Alignment	not modelled	8.5	19	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
						PDB header:ribosome

80	c3og02_	Alignment	not modelled	8.4	33	**Chain:** 2: **PDB Molecule:**50s ribosomal protein l34; **PDBTitle:** crystal structure of the e. coli ribosome bound to clindamycin. this2 file contains the 50s subunit of the second 70s ribosome.
81	c1t2kD_	Alignment	not modelled	8.4	15	**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
82	c1novE_	Alignment	not modelled	8.3	21	**PDB header:**virus **Chain:** E: **PDB Molecule:**nodamura virus coat proteins; **PDBTitle:** nodamura virus
83	d1k8ib2	Alignment	not modelled	8.1	38	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
84	c1htmB_	Alignment	not modelled	8.1	13	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain; **PDBTitle:** structure of influenza haemagglutinin at the ph of membrane2 fusion
85	c3qw3B_	Alignment	not modelled	8.1	17	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**orotidine-5-phosphate decarboxylase/orotate **PDBTitle:** structure of leishmania donovani omp decarboxylase
86	c2dahA_	Alignment	not modelled	8.1	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-3; **PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3
87	d1yzma1	Alignment	not modelled	8.1	8	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
88	c2zdiC_	Alignment	not modelled	8.0	13	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**prefoldin subunit alpha; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
89	c2no2A_	Alignment	not modelled	7.9	14	**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
90	c3cvfA_	Alignment	not modelled	7.7	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
91	c3orb2_	Alignment	not modelled	7.7	33	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**50s ribosomal protein l34; **PDBTitle:** crystal structure of the e. coli ribosome bound to cem-101. this file2 contains the 50s subunit of the first 70s ribosome bound to cem-101.
92	c3onjA_	Alignment	not modelled	7.6	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t-snare vti1; **PDBTitle:** crystal structure of yeast vti1p_habc domain
93	c3g67A_	Alignment	not modelled	7.6	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
94	c2cwbA_	Alignment	not modelled	7.5	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
95	d1khia2	Alignment	not modelled	7.5	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
96	c1kddC_	Alignment	not modelled	7.4	19	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
97	d1vcsa1	Alignment	not modelled	7.4	7	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
98	c1wr1B_	Alignment	not modelled	7.3	30	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
99	d1veja1	Alignment	not modelled	7.3	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain