Phyre^2

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Description	P0AAA9
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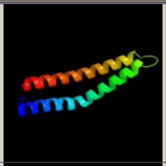
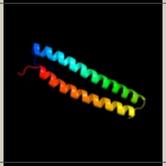
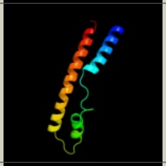
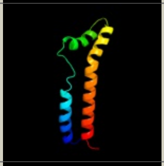
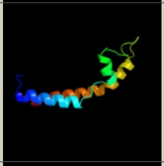
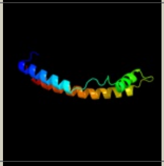
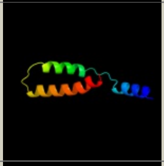
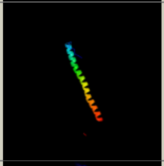
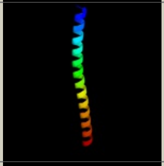
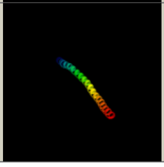
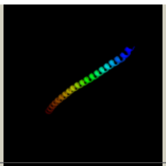
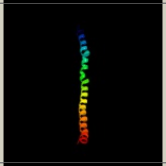
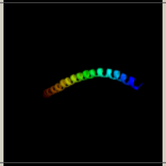
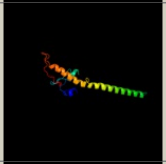
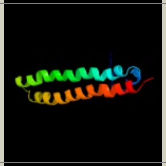
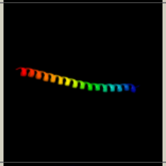
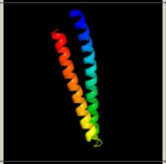
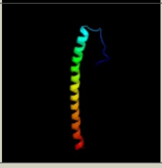
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3layF_	Alignment		99.8	71	**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
2	c3epvB_	Alignment		99.3	16	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
3	c3qzcA_	Alignment		99.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic protein cpxp; **PDBTitle:** structure of the periplasmic stress response protein cpxp
4	c3oeoD_	Alignment		98.9	17	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**spheroplast protein y; **PDBTitle:** the crystal structure e. coli spy
5	c3o39A_	Alignment		98.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**periplasmic protein related to spheroblast formation; **PDBTitle:** crystal structure of spy
6	c3itfA_	Alignment		98.9	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein
7	d1gqea_	Alignment		83.6	22	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
8	c1j1eC_	Alignment		78.7	17	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
9	c2w6aB_	Alignment		77.0	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
10	c2gl2B_	Alignment		75.4	15	**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
11	c1ei3E_	Alignment		73.7	5	**PDB header:** **PDB COMPND:**

12	c3ojaB_	Alignment		72.3	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
13	c3ghgK_	Alignment		70.9	8	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
14	c1deqF_	Alignment		68.7	12	**PDB header:** **PDB COMPND:**
15	c3bt6B_	Alignment		68.0	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin
16	c2ke4A_	Alignment		67.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
17	c1deqO_	Alignment		67.7	8	**PDB header:** **PDB COMPND:**
18	c3hnwB_	Alignment		67.3	13	**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
19	d1cuna2	Alignment		67.1	16	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
20	c1yv0I_	Alignment		66.8	21	**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
21	c2gd7B_	Alignment	not modelled	63.5	12	**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
22	d1s35a2	Alignment	not modelled	63.4	16	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
23	c3kltB_	Alignment	not modelled	59.4	13	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of a vimentin fragment
24	c2w9yA_	Alignment	not modelled	53.6	12	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**fatty acid/retinol binding protein protein 7, **PDBTitle:** the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
25	c2iakA_	Alignment	not modelled	53.3	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**bullous pemphigoid antigen 1, isoform 5; **PDBTitle:** crystal structure of a protease resistant fragment of the plakin2 domain of bullous pemphigoid antigen1 (bpag1)
26	d2spca_	Alignment	not modelled	51.1	19	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
27	c2v7sA_	Alignment	not modelled	50.2	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable conserved lipoprotein lppa; **PDBTitle:** crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
28	d2oeza1	Alignment	not modelled	49.1	23	**Fold:**YacF-like **Superfamily:**YacF-like **Family:**YacF-like

29	c2jo8B_	Alignment	not modelled	49.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
30	c3m9bK_	Alignment	not modelled	48.1	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
31	d1vqov1	Alignment	not modelled	48.0	17	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
32	c2a3dA_	Alignment	not modelled	46.5	23	**PDB header:**three-helix bundle **Chain:** A: **PDB Molecule:**protein (de novo three-helix bundle); **PDBTitle:** solution structure of a de novo designed single chain three-2 helix bundle (a3d)
33	c3d5cX_	Alignment	not modelled	46.5	17	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
34	c3ls1A_	Alignment	not modelled	45.4	18	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
35	d1quua1	Alignment	not modelled	44.3	16	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
36	c1wpaA_	Alignment	not modelled	42.6	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** 1.5 angstrom crystal structure of human occludin fragment2 413-522
37	c1xzqA_	Alignment	not modelled	40.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
38	c2xdjF_	Alignment	not modelled	40.8	12	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
39	c2js5B_	Alignment	not modelled	40.1	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
40	d1u5pa1	Alignment	not modelled	39.7	16	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
41	c2fxmB_	Alignment	not modelled	38.5	10	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
42	c1deqD_	Alignment	not modelled	38.3	17	**PDB header:** **PDB COMPND:**
43	c2j375_	Alignment	not modelled	38.1	16	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein l35; **PDBTitle:** model of mammalian srp bound to 80s rncs
44	c2eqbC_	Alignment	not modelled	38.0	13	**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
45	d1u5pa2	Alignment	not modelled	37.8	14	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
46	c3kbtA_	Alignment	not modelled	37.4	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin beta chain, erythrocyte; **PDBTitle:** crystal structure of the ankyrin binding domain of human erythroid2 beta spectrin (repeats 13-15) in complex with the spectrin binding3 domain of human erythroid ankyrin (zu5-ank)
47	d1s35a1	Alignment	not modelled	36.4	9	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
48	d1cxzb_	Alignment	not modelled	36.3	14	**Fold:**Long alpha-hairpin **Superfamily:**HR1 repeat **Family:**HR1 repeat
49	c3hizB_	Alignment	not modelled	36.2	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
50	c2oszA_	Alignment	not modelled	35.8	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
51	c2c5iT_	Alignment	not modelled	35.7	20	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**t-snare affecting a late golgi compartment **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
52	c2p2uA_	Alignment	not modelled	35.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**host-nuclease inhibitor protein gam, putative; **PDBTitle:** crystal structure of putative host-nuclease inhibitor2 protein gam from desulfovibrio vulgaris
						PDB header:ribosomal protein/rna

53	c2zkrv_	Alignment	not modelled	34.2	11	**Chain:** V: **PDB Molecule:**rna expansion segment es9 part2; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
54	c3csxA_	Alignment	not modelled	33.4	18	**PDB header:**metal binding protein,unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structural characterization of a protein in the duf6832 family- crystal structure of cce_0567 from the3 cyanobacterium cyanothece 51142.
55	d1st6a3	Alignment	not modelled	32.3	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
56	c3ol1A_	Alignment	not modelled	30.7	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
57	d1uklc_	Alignment	not modelled	30.6	22	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
58	d1olma1	Alignment	not modelled	29.8	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
59	c3f31B_	Alignment	not modelled	29.4	17	**PDB header:**actin binding, structural protein **Chain:** B: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** crystal structure of the n-terminal region of alphaii-spectrin2 tetramerization domain
60	c3m0dC_	Alignment	not modelled	29.4	13	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**tnf receptor-associated factor 1; **PDBTitle:** crystal structure of the traf1:traf2:ciap2 complex
61	c2ihr1_	Alignment	not modelled	28.8	26	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
62	c3gehA_	Alignment	not modelled	28.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
63	c3hfdA_	Alignment	not modelled	28.6	9	**PDB header:**chaperone, protein transport **Chain:** A: **PDB Molecule:**nucleosome assembly protein 1; **PDBTitle:** nucleosome assembly protein 1 from plasmodium knowlesi
64	c2j8pA_	Alignment	not modelled	27.9	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
65	c3fs3A_	Alignment	not modelled	27.3	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**nucleosome assembly protein 1, putative; **PDBTitle:** crystal structure of malaria parasite nucleosome assembly protein2 (nap)
66	c2an7A_	Alignment	not modelled	26.9	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
67	c3ni0A_	Alignment	not modelled	26.9	20	**PDB header:**immune system **Chain:** A: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of mouse bst-2/tetherin ectodomain
68	c1xawA_	Alignment	not modelled	26.6	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
69	c1s35A_	Alignment	not modelled	26.4	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin beta chain, erythrocyte; **PDBTitle:** crystal structure of repeats 8 and 9 of human erythroid2 spectrin
70	d1st6a4	Alignment	not modelled	26.0	27	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
71	d1ydxa1	Alignment	not modelled	25.6	13	**Fold:**DNA methylase specificity domain **Superfamily:**DNA methylase specificity domain **Family:**Type I restriction modification DNA specificity domain
72	c3bhpA_	Alignment	not modelled	25.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
73	d1akha_	Alignment	not modelled	25.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	c3ghgD_	Alignment	not modelled	25.0	15	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
75	d1lvaa3	Alignment	not modelled	24.7	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
76	c2no2A_	Alignment	not modelled	24.5	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
77	c3u59C_	Alignment	not modelled	24.3	10	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
78	c3gh9A_	Alignment	not modelled	23.9	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2;

						PDBTitle: human liprin-beta2 coiled-coil
79	d1ykhb1	Alignment	not modelled	23.7	16	**Fold:**Mediator hinge subcomplex-like **Superfamily:**Mediator hinge subcomplex-like **Family:**CSE2-like
80	d1hcia4	Alignment	not modelled	23.5	12	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
81	c3m5gD_	Alignment	not modelled	22.4	16	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of a h7 influenza virus hemagglutinin
82	c2nrjA_	Alignment	not modelled	22.2	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hbl b protein; **PDBTitle:** crystal structure of hemolysin binding component from2 bacillus cereus
83	c3a7mA_	Alignment	not modelled	21.9	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**flagellar protein flit; **PDBTitle:** structure of flit, the flagellar type iii chaperone for flid
84	c2q9qC_	Alignment	not modelled	21.9	16	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna replication complex gins protein psf1; **PDBTitle:** the crystal structure of full length human gins complex
85	c2jeeA_	Alignment	not modelled	21.8	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
86	c2xusA_	Alignment	not modelled	21.6	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**breast cancer metastasis-suppressor 1; **PDBTitle:** crystal structure of the brms1 n-terminal region
87	c1jccC_	Alignment	not modelled	21.5	11	**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
88	d2e9xa1	Alignment	not modelled	21.5	16	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**PSF1 N-terminal domain-like
89	c2v6lI_	Alignment	not modelled	21.3	20	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**mxih; **PDBTitle:** molecular model of a type iii secretion system needle
90	c1gk6B_	Alignment	not modelled	21.3	10	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
91	c1m1jA_	Alignment	not modelled	21.2	17	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
92	c1avyA_	Alignment	not modelled	20.0	30	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)
93	c3geiB_	Alignment	not modelled	19.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
94	d2hgq11	Alignment	not modelled	19.7	13	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
95	c1cunC_	Alignment	not modelled	19.7	16	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein (alpha spectrin); **PDBTitle:** crystal structure of repeats 16 and 17 of chicken brain2 alpha spectrin
96	c3b7qA_	Alignment	not modelled	19.4	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**uncharacterized protein ykl091c; **PDBTitle:** crystal structure of yeast sec14 homolog sfh1 in complex with2 phosphatidylcholine
97	c1ox3A_	Alignment	not modelled	19.2	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** crystal structure of mini-fibritin
98	c1stzB_	Alignment	not modelled	18.7	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
99	c1jsdB_	Alignment	not modelled	18.6	18	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**haemagglutinin (ha2 chain); **PDBTitle:** crystal structure of swine h9 haemagglutinin