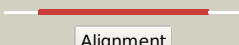
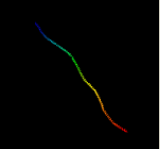

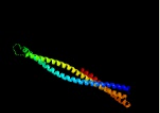
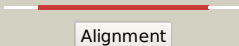
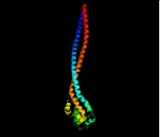
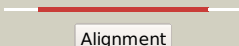
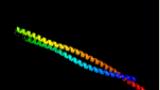

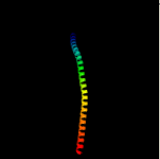
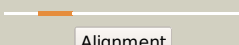
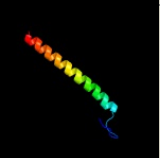
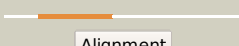
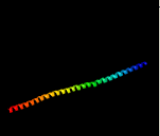
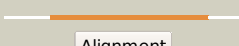
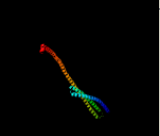

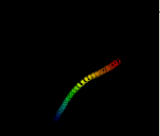

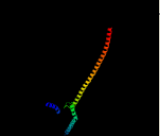

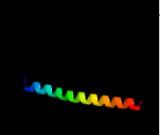


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1682_(-)_1906410_1907327
Date	Fri Aug 2 13:30:28 BST 2019
Unique Job ID	0698d50772f16874

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c1gA_	 Alignment		97.2	11	PDB header: contractile protein Chain: A; PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
2	c4c9kA_	 Alignment		96.8	9	PDB header: cell cycle Chain: A; PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus pneumoniae
3	c3wuqA_	 Alignment		95.4	7	PDB header: motor protein Chain: A; PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: structure of the entire stalk region of the dynein motor domain
4	c6ewyA_	 Alignment		93.3	18	PDB header: structural protein Chain: A; PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
5	c3q8tB_	 Alignment		88.8	11	PDB header: apoptosis Chain: B; PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
6	c6gqaD_	 Alignment		88.7	30	PDB header: cell cycle Chain: D; PDB Molecule: cell cycle protein gpsb; PDBTitle: cell division regulator s. pneumoniae gpsb
7	c3u59C_	 Alignment		88.6	14	PDB header: contractile protein Chain: C; PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
8	c1ciiA_	 Alignment		87.1	14	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
9	c6e2jB_	 Alignment		86.5	10	PDB header: protein fibril Chain: B; PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s231l mutation and wild-type human keratin 10 coil 1b
10	c3ojaB_	 Alignment		86.4	10	PDB header: protein binding Chain: B; PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
11	c4ug1A_	 Alignment		86.0	31	PDB header: cell cycle Chain: A; PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain

12	c4zryA_	Alignment		84.8	9	PDB header: protein fibril Chain: A; PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
13	c3ghgK_	Alignment		84.3	10	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
14	c5xg2A_	Alignment		84.0	12	PDB header: dna binding protein Chain: A; PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of a coiled-coil segment (residues 345-468 and 694-2 814) of pyrococcus yayanosii smc
15	c2wukD_	Alignment		83.0	24	PDB header: cell cycle Chain: D; PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
16	c2d3eD_	Alignment		81.0	6	PDB header: contractile protein Chain: D; PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
17	c5lm2B_	Alignment		80.4	7	PDB header: hydrolase Chain: B; PDB Molecule: tyrosine-protein phosphatase non-receptor type 23; PDBTitle: crystal structure of hd-ptp phosphatase
18	c5wjba_	Alignment		79.9	13	PDB header: actin/dna binding protein Chain: A; PDB Molecule: capsid assembly scaffolding protein,myosin-7; PDBTitle: crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
19	c3tnuB_	Alignment		79.1	16	PDB header: cytosolic protein Chain: B; PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
20	c6djlE_	Alignment		76.8	13	PDB header: signaling protein/protein transport Chain: E; PDB Molecule: sh3 domain-binding protein 5; PDBTitle: crystal structure of the rab11 gef sh3bp5 bound to nucleotide free2 rab11a
21	c1deqO_	Alignment	not modelled	75.0	13	PDB header: blood clotting Chain: O; PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
22	c2gl2B_	Alignment	not modelled	71.6	7	PDB header: cell adhesion Chain: B; PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
23	c1ei3E_	Alignment	not modelled	70.9	4	PDB header: blood clotting Chain: E; PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
24	c5ew5C_	Alignment	not modelled	70.4	7	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
25	c6gapB_	Alignment	not modelled	70.3	9	PDB header: viral protein Chain: B; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
26	c3swkB_	Alignment	not modelled	69.2	9	PDB header: structural protein Chain: B; PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
27	c5mg8B_	Alignment	not modelled	66.8	15	PDB header: recombination Chain: B; PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
28	c5bu8A_	Alignment	not modelled	65.7	11	PDB header: viral protein Chain: A; PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
						PDB header: motor protein Chain: D; PDB Molecule: gp7-myh7(1173-1238)-eb1 chimera

29	c4xa1D_	Alignment	not modelled	65.3	7	protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 1 of myh7
30	c5nnvD_	Alignment	not modelled	65.2	9	PDB header: cell cycle Chain: D: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of a bacillus subtilis smc coiled coil middle fragment
31	c3tnuA_	Alignment	not modelled	64.7	23	PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
32	c6a9pD_	Alignment	not modelled	64.4	9	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
33	c3wolB_	Alignment	not modelled	63.5	8	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
34	c3ojaA_	Alignment	not modelled	62.6	13	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
35	c6f1tx_	Alignment	not modelled	62.5	14	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1,bicd family-like cargo PDBTitle: cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
36	c6f1tX_	Alignment	not modelled	61.3	9	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1,bicd family-like cargo PDBTitle: cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
37	c1degF_	Alignment	not modelled	60.6	5	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
38	c3hnbW_	Alignment	not modelled	60.3	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
39	c1yvlB_	Alignment	not modelled	59.8	7	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
40	c6ianA_	Alignment	not modelled	58.1	9	PDB header: cytosolic protein Chain: A: PDB Molecule: intraflagellar transport protein 74; PDBTitle: t. brucei ift22/74/81 gtp-bound crystal structure
41	c3o11A_	Alignment	not modelled	58.1	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
42	c3na7A_	Alignment	not modelled	55.6	9	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
43	c5oi7A_	Alignment	not modelled	54.1	15	PDB header: protein binding Chain: A: PDB Molecule: centrosomal protein of 85 kda; PDBTitle: human cep85 - coiled coil domain 4
44	c6ec0A_	Alignment	not modelled	54.1	7	PDB header: protein fibril Chain: A: PDB Molecule: keratin 1; PDBTitle: crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10)
45	c6gajA_	Alignment	not modelled	53.6	9	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail (iodide)
46	c5cj1B_	Alignment	not modelled	53.5	14	PDB header: motor protein Chain: B: PDB Molecule: gp7-myh7-(1526-1571) chimera protein; PDBTitle: crystal structure of the coiled coil of myh7 residues 1526 to 15712 fused to gp7
47	c4ug3C_	Alignment	not modelled	53.4	26	PDB header: cell cycle Chain: C: PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb n-terminal domain
48	c4ll8E_	Alignment	not modelled	51.4	8	PDB header: motor protein/transport protein Chain: E: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: complex of carboxy terminal domain of myo4p and she3p middle fragment
49	c2qa7C_	Alignment	not modelled	51.2	13	PDB header: actin binding Chain: C: 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)
50	c6o7xa_	Alignment	not modelled	50.2	8	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
51	c4iloA_	Alignment	not modelled	48.8	7	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
52	c5t58B_	Alignment	not modelled	48.2	13	PDB header: cell cycle Chain: B: PDB Molecule: klla0e05809p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
53	c4fmyE_	Alignment	not modelled	47.4	11	PDB header: viral protein Chain: E: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystal form i

54	c2eqbC	Alignment	not modelled	47.2	18	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
55	c1bf5A	Alignment	not modelled	46.2	7	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
56	c1bg1A	Alignment	not modelled	45.9	7	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
57	c5yz0C	Alignment	not modelled	43.1	10	PDB header: cell cycle Chain: C: PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrip complex
58	c3ghgI	Alignment	not modelled	40.6	4	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
59	c3vkgA	Alignment	not modelled	40.5	10	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
60	c1hciB	Alignment	not modelled	40.3	9	PDB header: triple-helix coiled coil Chain: B: PDB Molecule: alpha-actinin 2; PDBTitle: crystal structure of the rod domain of alpha-actinin
61	c5nmoA	Alignment	not modelled	39.9	11	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
62	c4i1bB	Alignment	not modelled	39.4	23	PDB header: signaling protein/transferase/inhibitor Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha complexed with nish2 of p85alpha
63	c5j1iA	Alignment	not modelled	38.9	12	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: structure of the spectrin repeats 7, 8, and 9 of the plakin domain of2 plectin
64	c2fxmB	Alignment	not modelled	37.5	6	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
65	c4a7fB	Alignment	not modelled	37.4	14	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
66	c6o7ua	Alignment	not modelled	36.6	7	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
67	c2xdjC	Alignment	not modelled	34.5	9	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
68	c5cwsC	Alignment	not modelled	33.1	10	PDB header: protein transport Chain: C: PDB Molecule: nucleoporin nsp1; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
69	c4xa3A	Alignment	not modelled	32.9	10	PDB header: motor protein Chain: A: PDB Molecule: gp7-myh7(1361-1425)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 2 of myh7
70	c5ijnT	Alignment	not modelled	31.4	5	PDB header: transport protein Chain: T: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
71	c2jeeA	Alignment	not modelled	29.7	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein zapb; PDBTitle: xray structure of e. coli yjiu
72	c3o0zD	Alignment	not modelled	28.5	9	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
73	c4jzlA	Alignment	not modelled	27.8	16	PDB header: apoptosis, transport protein Chain: A: PDB Molecule: b-cell receptor-associated protein 31; PDBTitle: crystal structure of bap31 vded at alkaline ph
74	c1s1jB	Alignment	not modelled	26.9	10	PDB header: contractile protein Chain: B: PDB Molecule: actinin; PDBTitle: cryo-em structure of chicken gizzard smooth muscle alpha-actinin
75	c1deqD	Alignment	not modelled	25.4	8	PDB header: blood clotting Chain: D: PDB Molecule: fibrinogen (alpha chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
76	c5jxpA	Alignment	not modelled	24.6	8	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
77	c2efrB	Alignment	not modelled	24.5	14	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
78	c6flnE	Alignment	not modelled	22.5	9	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and

						pyspry domains
79	c5l5k_B	Alignment	not modelled	22.4	12	PDB header: cell cycle Chain: B: PDB Molecule: polyamine-modulated factor 1; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
80	c1gd2G	Alignment	not modelled	22.3	10	PDB header: transcription/dna Chain: G: PDB Molecule: transcription factor pap1; PDBTitle: crystal structure of bzfp transcription factor pap1 bound2 to dna
81	c3a7pB	Alignment	not modelled	22.3	21	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg16
82	c2b9cA	Alignment	not modelled	21.8	15	PDB header: contractile protein Chain: A: PDB Molecule: striated-muscle alpha tropomyosin; PDBTitle: structure of tropomyosin's mid-region: bending and binding sites for2 actin
83	c1jchC	Alignment	not modelled	21.7	9	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
84	c6gaoC	Alignment	not modelled	21.5	8	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail and body
85	c3u1aC	Alignment	not modelled	21.2	10	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
86	c5k7bA	Alignment	not modelled	20.2	10	PDB header: apoptosis Chain: A: PDB Molecule: beclin-2; PDBTitle: beclin 2 ccd homodimer
87	c1ei3C	Alignment	not modelled	19.3	8	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
88	c4pxjB	Alignment	not modelled	18.7	20	PDB header: protein binding Chain: B: PDB Molecule: c-jun-amino-terminal kinase-interacting protein 3; PDBTitle: crystallographic structure of the lzii fragment (anti-parallel2 orientation) from jip3
89	c3cveC	Alignment	not modelled	18.4	23	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
90	c3m9bK	Alignment	not modelled	17.9	12	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
91	c4rsiB	Alignment	not modelled	17.1	15	PDB header: cell cycle Chain: B: PDB Molecule: structural maintenance of chromosomes protein 4; PDBTitle: yeast smc2-smc4 hinge domain with extended coiled coils
92	c2v71A	Alignment	not modelled	16.8	11	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
93	c2no2A	Alignment	not modelled	16.2	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
94	c4h22A	Alignment	not modelled	16.1	12	PDB header: transcription Chain: A: PDB Molecule: leucine-rich repeat flightless-interacting protein 1; PDBTitle: crystal structure of the dimeric coiled-coil domain of the cytosolic2 nucleic acid sensor lrrfp1
95	c3m06F	Alignment	not modelled	14.9	11	PDB header: protein binding Chain: F: PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2
96	c2qa7B	Alignment	not modelled	14.9	20	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)
97	c5tvbB	Alignment	not modelled	14.8	8	PDB header: transferase Chain: B: PDB Molecule: nucleoprotein tpr; PDBTitle: structure of the tpr oligomerization domain
98	c2xdjF	Alignment	not modelled	14.4	10	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
99	d1an2a	Alignment	not modelled	14.0	24	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain