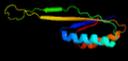
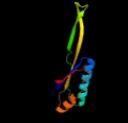
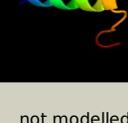


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0700\_(rpsj)\_800490\_800795  
 Date Fri Jul 26 01:50:27 BST 2019  
 Unique Job ID 9e945d9f431fd548

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o5jl_</a>	Alignment		100.0	98	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	<a href="#">d2qalj1</a>	Alignment		100.0	61	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S10 <b>Family:</b> Ribosomal protein S10
3	<a href="#">d2uubj1</a>	Alignment		100.0	58	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S10 <b>Family:</b> Ribosomal protein S10
4	<a href="#">c3bbnj_</a>	Alignment		100.0	53	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> ribosomal protein s10; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
5	<a href="#">c3zeyQ_</a>	Alignment		100.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> ribosomal protein s20, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
6	<a href="#">c3j20L_</a>	Alignment		100.0	35	<b>PDB header:</b> ribosome <b>Chain:</b> L; <b>PDB Molecule:</b> 30s ribosomal protein s10p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
7	<a href="#">c2xznj_</a>	Alignment		100.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> ribosomal protein s10 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
8	<a href="#">c3j6vj_</a>	Alignment		100.0	25	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 28s ribosomal protein s10, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
9	<a href="#">c2zkaj_</a>	Alignment		100.0	25	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> J; <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
10	<a href="#">c1s1hj_</a>	Alignment		100.0	29	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 40s ribosomal protein s20; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
11	<a href="#">c3iz6j_</a>	Alignment		100.0	26	<b>PDB header:</b> ribosome <b>Chain:</b> J; <b>PDB Molecule:</b> 40s ribosomal protein s20 (s10p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

12	<a href="#">c5xyiU</a>	Alignment		100.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> ribosomal protein s10p/s20e, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
13	<a href="#">c4v1ak</a>	Alignment		99.9	20	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
14	<a href="#">c2mewA</a>	Alignment		99.9	70	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> solution structure of nuse (s10) from thermotoga maritima
15	<a href="#">c3r2cj</a>	Alignment		99.9	57	<b>PDB header:</b> transcription/rna <b>Chain:</b> J: <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> crystal structure of antitermination factors nusB and nuse in complex with boxA rna
16	<a href="#">c3j7yf</a>	Alignment		99.3	17	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> ul4; <b>PDBTitle:</b> structure of the large ribosomal subunit from human mitochondria
17	<a href="#">d1xbpg1</a>	Alignment		35.4	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
18	<a href="#">c3cjqB</a>	Alignment		27.6	38	<b>PDB header:</b> transferase/ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> ribosomal protein l11 methyltransferase (prma) in complex with 2 dimethylated ribosomal protein l11 in space group p212121
19	<a href="#">c4hub1</a>	Alignment		21.1	24	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l11p; <b>PDBTitle:</b> the re-refined crystal structure of the haloarcula marismortui large 2 ribosomal subunit at 2.4 angstrom resolution: more complete structure 3 of the l7/l12 and l1 stalk, l5 and lx proteins
20	<a href="#">c5colB</a>	Alignment		19.5	19	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> ribosomal protein l11 from methanococcus jannaschii
21	<a href="#">d1fnoa3</a>	Alignment	not modelled	18.7	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
22	<a href="#">d1hc8a</a>	Alignment	not modelled	16.9	37	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
23	<a href="#">d1mmsa1</a>	Alignment	not modelled	16.8	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
24	<a href="#">c3ai4A</a>	Alignment	not modelled	15.7	23	<b>PDB header:</b> fluorescent protein, replication protein,dna polymerase <b>Chain:</b> A: <b>PDB Molecule:</b> yeast enhanced green fluorescent protein,dna polymerase <b>PDBTitle:</b> crystal structure of yeast enhanced green fluorescent protein - mouse2 polymerase iota ubiquitin binding motif fusion protein
25	<a href="#">c3j39K</a>	Alignment	not modelled	15.5	19	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 60s ribosomal protein l12; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
26	<a href="#">c1s1iK</a>	Alignment	not modelled	14.9	21	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 60s ribosomal protein l12; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
27	<a href="#">c2kl8A</a>	Alignment	not modelled	13.8	14	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> or15; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
						<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein rol14 (l14e):

28	<a href="#">c3zcn_</a>	Alignment	not modelled	13.7	20	<b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome <b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l11p; <b>PDBTitle:</b> the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
29	<a href="#">c1vq8l_</a>	Alignment	not modelled	13.4	21	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> kvap channel; <b>PDBTitle:</b> solution structure of vstx
30	<a href="#">c1s6xA_</a>	Alignment	not modelled	11.4	36	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> I: <b>PDB Molecule:</b> rna expansion segment es15 part i; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
31	<a href="#">c2zkri_</a>	Alignment	not modelled	11.1	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0907 protein; <b>PDBTitle:</b> solution structure of the kh domain in kiaa0907 protein
32	<a href="#">c2yqrA_</a>	Alignment	not modelled	11.0	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed ferredoxin-ferredoxin domain insertion <b>PDBTitle:</b> crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
33	<a href="#">c5cw9A_</a>	Alignment	not modelled	10.9	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
34	<a href="#">d1dbda_</a>	Alignment	not modelled	10.9	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
35	<a href="#">d2bopa_</a>	Alignment	not modelled	10.6	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
36	<a href="#">c4ky3A_</a>	Alignment	not modelled	10.5	10	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein or327; <b>PDBTitle:</b> three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
37	<a href="#">d1iwga2</a>	Alignment	not modelled	10.4	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
38	<a href="#">c2ko4A_</a>	Alignment	not modelled	10.0	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 15; <b>PDBTitle:</b> complex structure of the activation domain of gcn4 bound to the2 mediator co-activator domain of gal11/med15
39	<a href="#">c1jqmA_</a>	Alignment	not modelled	9.8	26	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid
40	<a href="#">c2k6nA_</a>	Alignment	not modelled	9.7	36	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> supervillin; <b>PDBTitle:</b> solution structure of human supervillin headpiece, minimized2 average
41	<a href="#">c3j46n_</a>	Alignment	not modelled	9.6	33	<b>PDB header:</b> ribosome/protein transport <b>Chain:</b> N: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the secy protein translocation channel in action
42	<a href="#">c3zf7y_</a>	Alignment	not modelled	9.4	15	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> 60s ribosomal protein l24, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
43	<a href="#">c5o60j_</a>	Alignment	not modelled	9.4	42	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
44	<a href="#">c3bboK_</a>	Alignment	not modelled	9.2	26	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> ribosomal protein l11; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
45	<a href="#">c2vhml_</a>	Alignment	not modelled	9.2	33	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l11; <b>PDBTitle:</b> structure of pdf binding helix in complex with the ribosome2 (part 1 of 4)
46	<a href="#">c4a1eE_</a>	Alignment	not modelled	9.2	11	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
47	<a href="#">c3lpeF_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> dna-directed rna polymerase subunit e''; <b>PDBTitle:</b> crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
48	<a href="#">c4p1zD_</a>	Alignment	not modelled	8.8	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> piwi-like protein 1; <b>PDBTitle:</b> structure of the mid domain from miwi
49	<a href="#">d1vqoe2</a>	Alignment	not modelled	8.5	21	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
50	<a href="#">c4g0mB_</a>	Alignment	not modelled	8.5	11	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> protein argonaute 2; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana ago2 mid domain
51	<a href="#">c2kwvA_</a>	Alignment	not modelled	8.1	40	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iota; <b>PDBTitle:</b> solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
						<b>Fold:</b> Ribonuclease H-like motif

52	<a href="#">d1yvua2</a>	Alignment	not modelled	8.1	5	<b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> PIWI domain
53	<a href="#">c3iz5F_</a>	Alignment	not modelled	7.9	22	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l9 (l6p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
54	<a href="#">c2hxgB_</a>	Alignment	not modelled	7.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-arabinose isomerase; <b>PDBTitle:</b> crystal structure of mn2+ bound ecai
55	<a href="#">d1vqoi1</a>	Alignment	not modelled	7.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
56	<a href="#">c5h2wD_</a>	Alignment	not modelled	7.4	14	<b>PDB header:</b> protein transport/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like-specific protease 1; <b>PDBTitle:</b> crystal structure of the karyopherin kap60p bound to the sumo protease2 ulp1p (150-340)
57	<a href="#">c5h2xB_</a>	Alignment	not modelled	7.4	14	<b>PDB header:</b> protein transport/hydrogenase <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like-specific protease 1; <b>PDBTitle:</b> crystal structure of the karyopherin kap60p bound to the sumo protease2 ulp1p (150-172)
58	<a href="#">c3j39H_</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
59	<a href="#">c2ln3A_</a>	Alignment	not modelled	7.0	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein or135; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, if3-like fold,2 northeast structural genomics consortium target or135 (casd target)
60	<a href="#">c6amgA_</a>	Alignment	not modelled	6.7	8	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p460; <b>PDBTitle:</b> cyt p460 of nitrosomonas sp. al212
61	<a href="#">d2q79a1</a>	Alignment	not modelled	6.6	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
62	<a href="#">c2mulA_</a>	Alignment	not modelled	6.6	50	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase huwe1; <b>PDBTitle:</b> solution structure of the ubm1 domain of human huwe1/arf-bp1
63	<a href="#">c3zf7M_</a>	Alignment	not modelled	6.3	16	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l12, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
64	<a href="#">c2l3xA_</a>	Alignment	not modelled	6.3	56	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ablim2 protein; <b>PDBTitle:</b> villin head piece domain of human ablim2
65	<a href="#">c3ccmE_</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein l6p; <b>PDBTitle:</b> structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2611u
66	<a href="#">c3f41B_</a>	Alignment	not modelled	6.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
67	<a href="#">c5an9B_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> 60s ribosomal protein l9; <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit
68	<a href="#">d1yu5x1</a>	Alignment	not modelled	5.8	71	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
69	<a href="#">c3b0vD_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
70	<a href="#">d1a7ge_</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
71	<a href="#">d1j2jb_</a>	Alignment	not modelled	5.4	32	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> GAT-like domain <b>Family:</b> GAT domain
72	<a href="#">c4bduC_</a>	Alignment	not modelled	5.4	24	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> green fluorescent protein, apoptosis regulator bax; <b>PDBTitle:</b> bax bh3-in-groove dimer (gfp)
73	<a href="#">d1pbya3</a>	Alignment	not modelled	5.4	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
74	<a href="#">d1f9fa_</a>	Alignment	not modelled	5.3	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
75	<a href="#">c5o60W_</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l25; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
76	<a href="#">d1r8ha_</a>	Alignment	not modelled	5.2	4	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Viral DNA-binding domain <b>Family:</b> Viral DNA-binding domain
77	<a href="#">d1qzpa_</a>	Alignment	not modelled	5.1	57	<b>Fold:</b> VHP, Villin headpiece domain <b>Superfamily:</b> VHP, Villin headpiece domain <b>Family:</b> VHP, Villin headpiece domain
78	<a href="#">c5vntA_</a>	Alignment	not modelled	5.1	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> villin-4; <b>PDBTitle:</b> solution nmr structure of the c-terminal headpiece

