
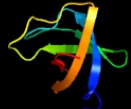





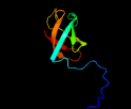


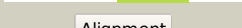

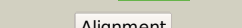
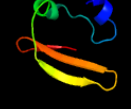
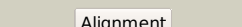

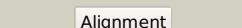
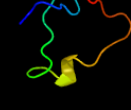
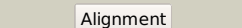
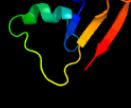





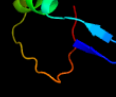







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1487_(-)_1676947_1677381
Date	Fri Aug 2 13:30:07 BST 2019
Unique Job ID	238b6a18283855c4

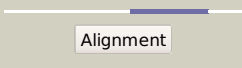
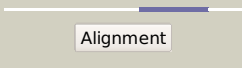
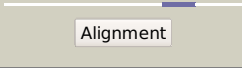
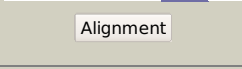
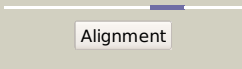
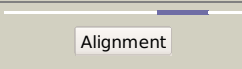
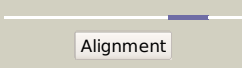
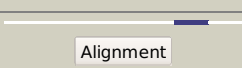
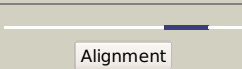
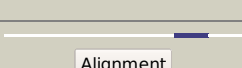
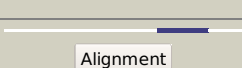
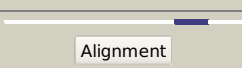
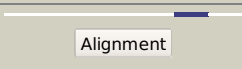
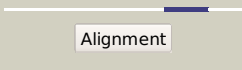
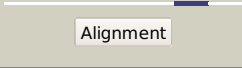
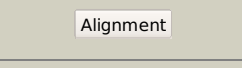
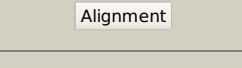
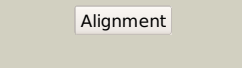
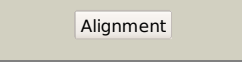
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cp0A_</a>	 Alignment		99.5	43	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein implicated in regulation of membrane <b>PDBTitle:</b> crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
2	<a href="#">c2k5hA_</a>	 Alignment		99.5	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein; <b>PDBTitle:</b> solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
3	<a href="#">c3wvvvA_</a>	 Alignment		99.4	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stomatin operon partner protein; <b>PDBTitle:</b> c-terminal domain of stomatin operon partner protein 1510-c from2 pyrococcus horikoshii
4	<a href="#">d2exda1</a>	 Alignment		99.4	32	<b>Fold:</b> OB-fold <b>Superfamily:</b> NfeD domain-like <b>Family:</b> NfeD domain-like
5	<a href="#">c2k14A_</a>	 Alignment		99.0	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yuaf protein; <b>PDBTitle:</b> solution structure of the soluble domain of the nfeD2 protein yuaf from bacillus subtilis
6	<a href="#">c4xi7A_</a>	 Alignment		65.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase mib1; <b>PDBTitle:</b> crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
7	<a href="#">c4tseA_</a>	 Alignment		57.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase mib1; <b>PDBTitle:</b> crystal structure of the mib repeat domain of mind bomb 1
8	<a href="#">d1tkeal</a>	 Alignment		53.1	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
9	<a href="#">c5z81A_</a>	 Alignment		35.0	40	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 15; <b>PDBTitle:</b> trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
10	<a href="#">d1dm9a_</a>	 Alignment		34.5	29	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
11	<a href="#">c1dm9A_</a>	 Alignment		34.5	29	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic <b>PDBTitle:</b> heat shock protein 15 kd

12	<a href="#">d1k25a2</a>	Alignment		33.3	3	<b>Fold:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Superfamily:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Family:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain
13	<a href="#">d1nyra2</a>	Alignment		32.1	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
14	<a href="#">c1ywkE</a>	Alignment		31.7	14	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-1-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
15	<a href="#">c3e0eA</a>	Alignment		30.4	23	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a; <b>PDBTitle:</b> crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 target mrr110b
16	<a href="#">d1vioa2</a>	Alignment		29.6	15	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsuA N-terminal domain
17	<a href="#">c6i52B</a>	Alignment		28.3	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> replication factor a protein 2; <b>PDBTitle:</b> yeast rpa bound to ssdna
18	<a href="#">d1v43a2</a>	Alignment		27.7	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
19	<a href="#">d1ywka1</a>	Alignment		26.1	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Kdul-like
20	<a href="#">d1xrua1</a>	Alignment		25.5	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Kdul-like
21	<a href="#">d1nnxa</a>	Alignment	not modelled	23.4	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Hypothetical protein YgiW <b>Family:</b> Hypothetical protein YgiW
22	<a href="#">d1tygb</a>	Alignment	not modelled	20.4	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/This <b>Family:</b> This
23	<a href="#">c1wwtA</a>	Alignment	not modelled	19.8	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the tgs domain from human threonyl-2 trna synthetase
24	<a href="#">c2k6pA</a>	Alignment	not modelled	19.7	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp_1423; <b>PDBTitle:</b> solution structure of hypothetical protein, hp1423
25	<a href="#">c2rcnA</a>	Alignment	not modelled	19.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
26	<a href="#">c2kmmA</a>	Alignment	not modelled	18.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> guanosine-3',5'-bis(diphosphate) 3'- <b>PDBTitle:</b> solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
27	<a href="#">d1p9ka</a>	Alignment	not modelled	18.5	35	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ybcj-like
28	<a href="#">d1qbaa2</a>	Alignment	not modelled	17.8	22	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Bacterial chitinase, n-terminal domain

29	<a href="#">c2yv5A_</a>	Alignment	not modelled	16.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yjeq protein; <b>PDBTitle:</b> crystal structure of yjeq from aquifex aeolicus
30	<a href="#">c3fjsC_</a>	Alignment	not modelled	16.6	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein with rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
31	<a href="#">c2nv4A_</a>	Alignment	not modelled	16.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0066 protein af_0241; <b>PDBTitle:</b> crystal structure of upf0066 protein af0241 in complex with2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
32	<a href="#">c1tygG_</a>	Alignment	not modelled	15.9	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> yjbs; <b>PDBTitle:</b> structure of the thiazole synthase/this complex
33	<a href="#">d2gcxa1</a>	Alignment	not modelled	15.8	13	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
34	<a href="#">d1oxk1</a>	Alignment	not modelled	15.6	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
35	<a href="#">c2d49A_</a>	Alignment	not modelled	15.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase c; <b>PDBTitle:</b> solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
36	<a href="#">d1psea_</a>	Alignment	not modelled	15.4	21	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
37	<a href="#">d1ydl1</a>	Alignment	not modelled	15.0	19	<b>Fold:</b> TFB5-like <b>Superfamily:</b> TFB5-like <b>Family:</b> TFB5-like
38	<a href="#">d1g2914</a>	Alignment	not modelled	15.0	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
39	<a href="#">c4y2wA_</a>	Alignment	not modelled	14.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> crystal structure of a thermostable alanine racemase from2 thermoanaerobacter tengcongensis mb4
40	<a href="#">c5uz4Z_</a>	Alignment	not modelled	14.4	24	<b>PDB header:</b> ribosome/hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> small ribosomal subunit biogenesis gtpase rsga; <b>PDBTitle:</b> the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
41	<a href="#">d1kk8a1</a>	Alignment	not modelled	14.0	43	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Myosin S1 fragment, N-terminal domain <b>Family:</b> Myosin S1 fragment, N-terminal domain
42	<a href="#">c4n6eB_</a>	Alignment	not modelled	13.9	13	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> this/moad family protein; <b>PDBTitle:</b> crystal structure of amycolatopsis orientalis bexx/cyso complex
43	<a href="#">d1tq5a1</a>	Alignment	not modelled	13.8	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Pirin-like
44	<a href="#">d1zud21</a>	Alignment	not modelled	13.6	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Moad/ThiS <b>Family:</b> ThiS
45	<a href="#">c4gopB_</a>	Alignment	not modelled	13.4	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
46	<a href="#">d1j3ta_</a>	Alignment	not modelled	13.2	15	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
47	<a href="#">d1u0la1</a>	Alignment	not modelled	13.2	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
48	<a href="#">d1goia1</a>	Alignment	not modelled	13.2	33	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
49	<a href="#">c2lcIA_</a>	Alignment	not modelled	13.0	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator rfah; <b>PDBTitle:</b> solution structure of rfah carboxyterminal domain
50	<a href="#">c2kl0A_</a>	Alignment	not modelled	12.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiamin biosynthesis this; <b>PDBTitle:</b> solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
51	<a href="#">c2kncA_</a>	Alignment	not modelled	12.9	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
52	<a href="#">d1ueba3</a>	Alignment	not modelled	12.8	36	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
53	<a href="#">d1jb0e_</a>	Alignment	not modelled	12.8	14	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
54	<a href="#">c1zuyB_</a>	Alignment	not modelled	12.6	8	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin-5 isoform;

						<b>PDBTitle:</b> high-resolution structure of yeast myo5 sh3 domain
55	<a href="#">d2c35b1</a>	Alignment	not modelled	12.6	5	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
56	<a href="#">c2jvvA</a>	Alignment	not modelled	12.3	50	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of e. coli nusg carboxyterminal domain
57	<a href="#">c2kvqG</a>	Alignment	not modelled	12.3	50	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> solution structure of nuse:nusg-ctd complex
58	<a href="#">d2fo0a1</a>	Alignment	not modelled	12.2	10	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
59	<a href="#">d1aiwa</a>	Alignment	not modelled	12.1	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
60	<a href="#">c5xg9A</a>	Alignment	not modelled	12.0	19	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin ib; <b>PDBTitle:</b> crystal structure of peg-bound sh3 domain of myosin ib from entamoeba2 histolytica
61	<a href="#">c3cwiA</a>	Alignment	not modelled	11.8	33	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-biosynthesis protein this; <b>PDBTitle:</b> crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
62	<a href="#">d2v1ra1</a>	Alignment	not modelled	11.5	8	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
63	<a href="#">d1wgka</a>	Alignment	not modelled	11.4	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> C9orf74 homolog
64	<a href="#">d1yfba1</a>	Alignment	not modelled	11.4	14	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> AbrB N-terminal domain-like
65	<a href="#">d2pi2a1</a>	Alignment	not modelled	11.3	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
66	<a href="#">d1lr5a</a>	Alignment	not modelled	11.3	6	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmIC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
67	<a href="#">c3ilaG</a>	Alignment	not modelled	11.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> G: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
68	<a href="#">c1ri9A</a>	Alignment	not modelled	10.9	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> fyn-binding protein; <b>PDBTitle:</b> structure of a helically extended sh3 domain of the t cell2 adapter protein adap
69	<a href="#">d1ri9a</a>	Alignment	not modelled	10.9	28	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
70	<a href="#">c3dh3C</a>	Alignment	not modelled	10.8	48	<b>PDB header:</b> isomerase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase f; <b>PDBTitle:</b> crystal structure of rluf in complex with a 22 nucleotide rna2 substrate
71	<a href="#">c2p0pA</a>	Alignment	not modelled	10.8	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alr1010 protein; <b>PDBTitle:</b> calcium binding protein in the free form
72	<a href="#">c2pi2A</a>	Alignment	not modelled	10.8	18	<b>PDB header:</b> replication, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a 32 kda subunit; <b>PDBTitle:</b> full-length replication protein a subunits rpa14 and rpa32
73	<a href="#">d1qp3a</a>	Alignment	not modelled	10.8	14	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Photosystem I accessory protein E (PsaE)
74	<a href="#">c6hwhX</a>	Alignment	not modelled	10.8	14	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
75	<a href="#">c2mrnB</a>	Alignment	not modelled	10.7	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin maze; <b>PDBTitle:</b> structure of truncated ecmaze
76	<a href="#">c2vldA</a>	Alignment	not modelled	10.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease nucs; <b>PDBTitle:</b> crystal structure of a repair endonuclease from pyrococcus abyssi
77	<a href="#">c4esnB</a>	Alignment	not modelled	10.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1312 family protein (rumgna_02503) from2 ruminococcus gnavus atcc 29149 at 2.20 a resolution
78	<a href="#">c2k9xA</a>	Alignment	not modelled	10.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of urm1 from trypanosoma brucei
79	<a href="#">c5o5jl</a>	Alignment	not modelled	10.6	50	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 30s ribosomal protein s9; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
80	<a href="#">d1nppa2</a>	Alignment	not modelled	10.5	55	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain

81	<a href="#">c2nchA</a>		Alignment	not modelled	10.4	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi
82	<a href="#">c1pyuD</a>		Alignment	not modelled	10.3	22	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartate 1-decarboxylase alfa chain; <b>PDBTitle:</b> processed aspartate decarboxylase mutant with ser25 mutated to cys
83	<a href="#">c2rtsA</a>		Alignment	not modelled	10.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> chitin binding domain1
84	<a href="#">c2istA</a>		Alignment	not modelled	10.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal large subunit pseudouridine synthase d; <b>PDBTitle:</b> crystal structure of rlud from e. coli
85	<a href="#">c3j20K</a>		Alignment	not modelled	10.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 30s ribosomal protein s9p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
86	<a href="#">c2qjIA</a>		Alignment	not modelled	10.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-related modifier 1; <b>PDBTitle:</b> crystal structure of urm1
87	<a href="#">c2lx7A</a>		Alignment	not modelled	10.0	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> growth arrest-specific protein 7; <b>PDBTitle:</b> solution nmr structure of sh3 domain of growth arrest-specific protein2 7 (gas7) (fragment 1-60) from homo sapiens, northeast structural3 genomics consortium (nesg) target hr8574a
88	<a href="#">d2h3ja1</a>		Alignment	not modelled	9.9	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
89	<a href="#">c3hvxB</a>		Alignment	not modelled	9.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
90	<a href="#">c3okxA</a>		Alignment	not modelled	9.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yaeb-like protein rpa0152; <b>PDBTitle:</b> crystal structure of yaeb-like protein from rhodospseudomonas palustris
91	<a href="#">d1xo3a</a>		Alignment	not modelled	9.8	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> C9orf74 homolog
92	<a href="#">d1mvfd</a>		Alignment	not modelled	9.8	10	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/PemI addiction antidote
93	<a href="#">d1nz9a</a>		Alignment	not modelled	9.7	55	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> N-utilization substance G protein NusG, C-terminal domain
94	<a href="#">d1pyya2</a>		Alignment	not modelled	9.6	10	<b>Fold:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Superfamily:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Family:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain
95	<a href="#">d2do3a1</a>		Alignment	not modelled	9.6	42	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
96	<a href="#">d1uhfa</a>		Alignment	not modelled	9.4	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
97	<a href="#">d2cdea1</a>		Alignment	not modelled	9.4	30	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
98	<a href="#">c4a1cS</a>		Alignment	not modelled	9.3	20	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> rpl26; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
99	<a href="#">c5xyiQ</a>		Alignment	not modelled	9.3	29	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 40s ribosomal protein s16, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome