Phyre^2

Email	l.a.kelley@imperial.ac.uk
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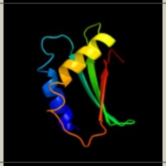
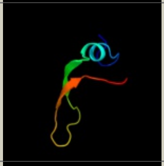
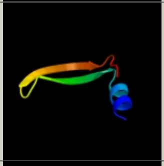
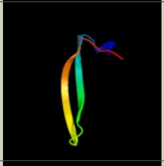
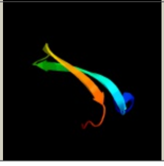
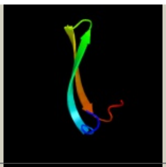
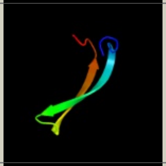
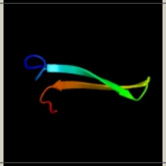
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ib8A_	Alignment		100.0	32	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**conserved protein sp14.3; **PDBTitle:** solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
2	d1ib8a2	Alignment		99.9	37	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**YhbC-like, N-terminal domain **Family:**YhbC-like, N-terminal domain
3	d1ib8a1	Alignment		99.4	28	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
4	c1y96C_	Alignment		88.7	11	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**gem-associated protein 6; **PDBTitle:** crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
5	c3cw15_	Alignment		85.0	22	**PDB header:**splicing **Chain:** 5: **PDB Molecule:**small nuclear ribonucleoprotein g; **PDB Fragment:**residues 1-215; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
6	d1h641_	Alignment		83.9	24	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
7	d1th7a1	Alignment		83.0	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
8	d1i8fa_	Alignment		80.8	18	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
9	d1m5q1_	Alignment		79.4	37	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
10	d1mgqa_	Alignment		77.4	25	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
11	c3bw1A_	Alignment		77.1	29	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm3; **PDBTitle:** crystal structure of homomeric yeast lsm3 exhibiting novel octameric2 ring organisation

12	d1b34a_	Alignment		76.3	32	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
13	c1b34A_	Alignment		76.3	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d1); **PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
14	d1jbma_	Alignment		76.2	25	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
15	c3swnT_	Alignment		75.8	21	**PDB header:**rna binding protein **Chain:** T: **PDB Molecule:**u6 snrna-associated sm-like protein lsm6; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
16	c3cw1Z_	Alignment		74.9	25	**PDB header:**splicing **Chain:** Z: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
17	c1n9sH_	Alignment		74.9	21	**PDB header:**translation **Chain:** H: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of yeast smf in spacegroup p43212
18	c3swnA_	Alignment		74.8	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
19	c2fwkB_	Alignment		74.3	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** crystal structure of cryptosporidium parvum u6 snrna-associated sm-2 like protein lsm5
20	d1ljoa_	Alignment		74.2	17	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
21	d1d3bl_	Alignment	not modelled	74.1	17	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
22	c3swnC_	Alignment	not modelled	73.7	20	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**u6 snrna-associated sm-like protein lsm7; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
23	d1n9ra_	Alignment	not modelled	73.5	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
24	d1d3ba_	Alignment	not modelled	72.6	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
25	d1n9sc_	Alignment	not modelled	72.5	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
26	d1biaa2	Alignment	not modelled	71.6	16	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
27	d1i4k1_	Alignment	not modelled	71.3	20	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
28	c2ewnA_	Alignment	not modelled	71.2	19	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
						PDB header:transcription

29	c2e70A_	Alignment	not modelled	70.9	13	**Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the fifth kow motif of human2 transcription elongation factor spt5
30	d1d3bb_	Alignment	not modelled	69.5	28	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
31	c2kvqG_	Alignment	not modelled	68.4	30	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
32	c2jvvA_	Alignment	not modelled	68.4	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
33	d1ycya1	Alignment	not modelled	67.8	27	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**PF1955-like
34	c3pgwQ_	Alignment	not modelled	67.2	27	**PDB header:**splicing/dna/rna **Chain:** Q: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
35	d1nz9a_	Alignment	not modelled	66.8	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
36	d2fwka1	Alignment	not modelled	66.5	17	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
37	c3pgwB_	Alignment	not modelled	64.3	26	**PDB header:**splicing/dna/rna **Chain:** B: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
38	c2ej9A_	Alignment	not modelled	61.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative biotin ligase; **PDBTitle:** crystal structure of biotin protein ligase from2 methanococcus jannaschii
39	c3cw1A_	Alignment	not modelled	58.8	27	**PDB header:**splicing **Chain:** A: **PDB Molecule:**small nuclear ribonucleoprotein-associated proteins b and **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
40	c2rm4A_	Alignment	not modelled	56.7	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cg6311-pb; **PDBTitle:** solution structure of the lsm domain of dm edc3 (enhancer2 of decapping 3)
41	d1r5pa_	Alignment	not modelled	52.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
42	c2cghB_	Alignment	not modelled	52.5	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin ligase; **PDBTitle:** crystal structure of biotin ligase from mycobacterium2 tuberculosis
43	c3cw1D_	Alignment	not modelled	51.5	14	**PDB header:**splicing **Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
44	c2e6zA_	Alignment	not modelled	47.4	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
45	d2pi2e1	Alignment	not modelled	43.5	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
46	c2pqaB_	Alignment	not modelled	42.0	26	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
47	d1qd1a1	Alignment	not modelled	40.3	17	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
48	c2pt7G_	Alignment	not modelled	39.2	17	**PDB header:**hydrolase/protein binding **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
49	c2eayB_	Alignment	not modelled	38.3	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin [acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from aquifex2 aeolicus
50	d1nppa2	Alignment	not modelled	36.4	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
51	d1kk8a1	Alignment	not modelled	35.4	21	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
52	d1h9aa1	Alignment	not modelled	34.7	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	c2vc8A_	Alignment	not modelled	34.5	24	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of the lsm domain of human edc3 (enhancer2 of decapping 3)
54	d1qkia1	Alignment	not modelled	31.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						Fold: OmpH-like

55	d1u2ma_	Alignment	not modelled	31.3	13	**Superfamily:**OmpH-like **Family:**OmpH-like
56	c2hbpA_	Alignment	not modelled	29.1	12	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
57	c1tt9B_	Alignment	not modelled	28.3	17	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
58	d1b34b_	Alignment	not modelled	26.9	35	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
59	c1b34B_	Alignment	not modelled	26.9	35	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d2); **PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
60	d1wina_	Alignment	not modelled	25.4	15	**Fold:**EF-Ts domain-like **Superfamily:**Band 7/SPFH domain **Family:**Band 7/SPFH domain
61	d1sg5a1	Alignment	not modelled	22.4	19	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**Rof-like
62	c1gshA_	Alignment	not modelled	22.3	16	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
63	c1h9aA_	Alignment	not modelled	22.1	18	**PDB header:**oxidoreductase (choh(d) - nad(p)) **Chain:** A: **PDB Molecule:**glucose 6-phosphate 1-dehydrogenase; **PDBTitle:** complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
64	d1ug7a_	Alignment	not modelled	20.9	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain from hypothetical 2610208m17rik protein **Family:**Domain from hypothetical 2610208m17rik protein
65	c3cw1W_	Alignment	not modelled	20.5	21	**PDB header:**splicing **Chain:** W: **PDB Molecule:**small nuclear ribonucleoprotein e; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
66	c1qkiE_	Alignment	not modelled	20.0	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
67	c3ic8D_	Alignment	not modelled	20.0	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
68	c2zy3A_	Alignment	not modelled	18.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
69	d1t4za_	Alignment	not modelled	17.5	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
70	d3bypa1	Alignment	not modelled	17.2	11	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
71	d1kuta_	Alignment	not modelled	17.1	25	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**SAICAR synthase
72	c2bhlB_	Alignment	not modelled	16.8	15	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
73	c3dexA_	Alignment	not modelled	16.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sav_2001; **PDBTitle:** crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
74	c2iruA_	Alignment	not modelled	16.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
75	d1h8la1	Alignment	not modelled	15.2	20	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
76	c1qd1A_	Alignment	not modelled	15.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formiminotransferase-cyclodeaminase; **PDBTitle:** the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
77	c1zq1B_	Alignment	not modelled	15.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
78	c1bknA_	Alignment	not modelled	14.9	28	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
79	d2bu1a1	Alignment	not modelled	14.8	26	**Fold:**RNA bacteriophage capsid protein **Superfamily:**RNA bacteriophage capsid protein **Family:**RNA bacteriophage capsid protein
						Fold: Prealbumin-like

80	d1uwya1	Alignment	not modelled	14.8	36	**Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
81	c2gqsA_	Alignment	not modelled	14.5	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** saicar synthetase complexed with cair-mg2+ and adp
82	c3kreA_	Alignment	not modelled	14.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
83	c1m1gB_	Alignment	not modelled	14.2	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
84	c2z02A_	Alignment	not modelled	14.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** crystal structure of2 phosphoribosylaminoimidazolesuccinocarboxamide synthase3 wit atp from methanocaldococcus jannaschii
85	c2ywvB_	Alignment	not modelled	13.7	4	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole succinocarboxamide synthetase; **PDBTitle:** crystal structure of saicar synthetase from geobacillus kaustophilus
86	c2faoB_	Alignment	not modelled	13.5	14	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**probable atp-dependent dna ligase; **PDBTitle:** crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
87	c3d0fA_	Alignment	not modelled	13.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
88	c2h31A_	Alignment	not modelled	13.3	18	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
89	c3nuaB_	Alignment	not modelled	13.3	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from clostridium perfringens
90	c2kz0A_	Alignment	not modelled	13.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bola family protein; **PDBTitle:** solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
91	c3qiiA_	Alignment	not modelled	12.7	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
92	c3kbqA_	Alignment	not modelled	12.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
93	c2p0gB_	Alignment	not modelled	12.3	6	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**selenoprotein w-related protein; **PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
94	c2ojlB_	Alignment	not modelled	12.0	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
95	c3bfmA_	Alignment	not modelled	11.9	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**biotin protein ligase-like protein of unknown function; **PDBTitle:** crystal structure of a biotin protein ligase-like protein of unknown2 function (tm1040_0394) from silicibacter sp. tm1040 at 1.70 a3 resolution
96	c2ckkA_	Alignment	not modelled	11.3	20	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**kin17; **PDBTitle:** high resolution crystal structure of the human kin172 c-terminal domain containing a kow motif3 kin17.
97	d3bpda1	Alignment	not modelled	11.3	8	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
98	d1utya_	Alignment	not modelled	10.9	39	**Fold:**BTV NS2-like ssRNA-binding domain **Superfamily:**BTV NS2-like ssRNA-binding domain **Family:**BTV NS2-like ssRNA-binding domain
99	c1utyA_	Alignment	not modelled	10.9	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 2; **PDBTitle:** crystal structure of the rna binding domain of bluetongue2 virus non-structural protein 2(ns2)