Phyre2

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Description	P0A6X3
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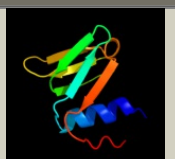
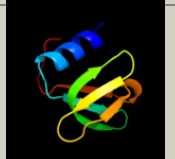
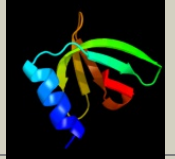
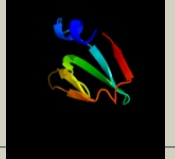
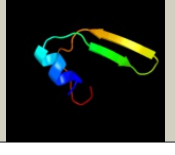
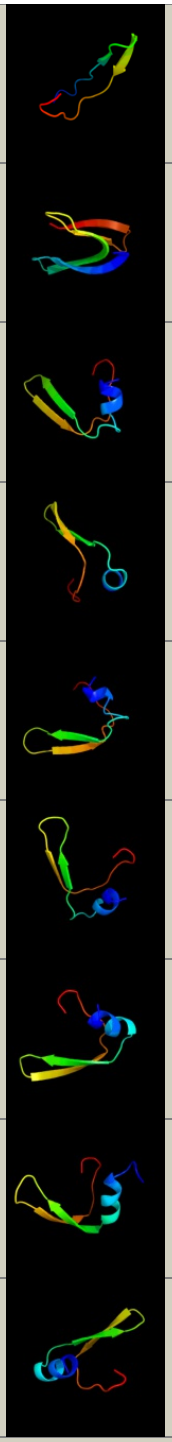
Unique Job ID	7e5497423abd56be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qhsD_	Alignment		100.0	100	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of full-length hfq from escherichia coli
2	d1u1sa1	Alignment		100.0	92	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
3	d1hk9a_	Alignment		100.0	100	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
4	c3hsbB_	Alignment		100.0	45	**PDB header:**rna binding protein/rna **Chain:** B: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
5	c1kq1W_	Alignment		100.0	32	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
6	d1kq1a_	Alignment		100.0	33	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
7	c2qtxL_	Alignment		97.4	30	**PDB header:**rna binding protein **Chain:** L: **PDB Molecule:**uncharacterized protein mj1435; **PDBTitle:** crystal structure of an hfq-like protein from methanococcus2 jannaschii
8	c3hfoC_	Alignment		96.8	29	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**ssr3341 protein; **PDBTitle:** crystal structure of an hfq protein from synechocystis sp.
9	c3hfnA_	Alignment		96.5	26	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**asl2047 protein; **PDBTitle:** crystal structure of an hfq protein from anabaena sp.
10	d1b34b_	Alignment		96.0	26	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
11	c1b34B_	Alignment		96.0	26	**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

12	c3cw1W_	Alignment		92.3	29	**PDB header:**splicing **Chain:** W: **PDB Molecule:**small nuclear ribonucleoprotein e; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
13	c2x4jA_	Alignment		91.2	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hypothetical protein orf137; **PDBTitle:** crystal structure of orf137 from pyrobaculum spherical2 virus
14	d1th7a1	Alignment		91.0	22	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
15	d1h641_	Alignment		90.8	16	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
16	c2fwkB_	Alignment		90.6	10	**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
17	c3swnA_	Alignment		90.4	13	**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
18	d1d3ba_	Alignment		90.0	16	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
19	d1jbma_	Alignment		89.8	26	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
20	d1i4k1_	Alignment		89.6	25	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
21	d1ljoa_	Alignment	not modelled	88.9	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
22	c3cw1Z_	Alignment	not modelled	88.0	38	**PDB header:**splicing **Chain:** Z: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
23	d1mgqa_	Alignment	not modelled	87.6	29	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
24	d2fwka1	Alignment	not modelled	87.4	10	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
25	c3swnT_	Alignment	not modelled	85.9	29	**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
26	d1i8fa_	Alignment	not modelled	85.6	32	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
27	c3cw15_	Alignment	not modelled	85.5	30	**PDB header:**splicing **Chain:** 5: **PDB Molecule:**small nuclear ribonucleoprotein g; **PDB Fragment:**residues 1-215; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
28	d1n9sc_	Alignment	not modelled	84.8	25	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
						PDB header:translation

29	c1n9sH_	Alignment	not modelled	83.8	25	**Chain:** H: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of yeast smf in spacegroup p43212
30	d1n9ra_	Alignment	not modelled	83.7	25	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
31	c3bw1A_	Alignment	not modelled	83.5	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
32	c3swnC_	Alignment	not modelled	82.4	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
33	d1b34a_	Alignment	not modelled	81.5	33	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
34	c1b34A_	Alignment	not modelled	81.5	33	**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
35	d1d3bl_	Alignment	not modelled	80.0	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
36	d1m5q1_	Alignment	not modelled	78.7	24	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
37	d1d3bb_	Alignment	not modelled	77.3	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
38	c3cw1D_	Alignment	not modelled	75.5	16	**PDB header:**splicing **Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
39	c3pgwQ_	Alignment	not modelled	75.2	20	**PDB header:**splicing/dna/rna **Chain:** Q: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
40	c3cw1A_	Alignment	not modelled	71.8	20	**PDB header:**splicing **Chain:** A: **PDB Molecule:**small nuclear ribonucleoprotein-associated proteins b and **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
41	c1y96C_	Alignment	not modelled	64.2	23	**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
42	d2bo9b2	Alignment	not modelled	60.5	24	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
43	c3pgwB_	Alignment	not modelled	60.0	21	**PDB header:**splicing/dna/rna **Chain:** B: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
44	c2bo9B_	Alignment	not modelled	54.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**human latexin; **PDBTitle:** human carboxypeptidase a4 in complex with human latexin.
45	d1ycya1	Alignment	not modelled	41.4	46	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**PF1955-like
46	d1914a2	Alignment	not modelled	33.4	35	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
47	d1f15a_	Alignment	not modelled	18.5	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
48	d2diga1	Alignment	not modelled	16.8	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
49	d1e8ob_	Alignment	not modelled	16.2	40	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
50	d1wlfa1	Alignment	not modelled	14.1	22	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
51	d1tpna_	Alignment	not modelled	11.6	21	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
52	d1g40a1	Alignment	not modelled	11.4	23	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
53	c1vjqB_	Alignment	not modelled	11.3	29	**PDB header:**structural genomics, de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
						PDB header:nucleic acid binding protein

54	c2kcmA_	Alignment	not modelled	9.7	20	**Chain:** A: **PDB Molecule:**cold shock domain family protein; **PDBTitle:** solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
55	c1f15C_	Alignment	not modelled	8.9	31	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** cucumber mosaic virus (strain fny)
56	d1sg5a1	Alignment	not modelled	8.0	19	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**Rof-like
57	d1f15b_	Alignment	not modelled	8.0	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
58	d2c71a1	Alignment	not modelled	7.8	21	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
59	c2gtiA_	Alignment	not modelled	7.4	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** mutation of mhv coronavirus non-structural protein nsp15 (f307l)
60	c3lf4B_	Alignment	not modelled	7.1	17	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**fluorescent timer precursor blue102; **PDBTitle:** crystal structure of fluorescent timer precursor blue102
61	d2j13a1	Alignment	not modelled	6.4	21	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
62	d1g6pa_	Alignment	not modelled	6.4	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	d1rqpa1	Alignment	not modelled	6.1	31	**Fold:**Bacterial fluorinating enzyme, C-terminal domain **Superfamily:**Bacterial fluorinating enzyme, C-terminal domain **Family:**Bacterial fluorinating enzyme, C-terminal domain
64	c2g3dB_	Alignment	not modelled	6.0	14	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**green fluorescent protein; **PDBTitle:** structure of s65g y66a gfp variant after spontaneous2 peptide hydrolysis
65	c1914A_	Alignment	not modelled	5.7	35	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
66	d1j5ya2	Alignment	not modelled	5.5	21	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
67	c1wlfA_	Alignment	not modelled	5.3	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1; **PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
68	d2iuwa1	Alignment	not modelled	5.2	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**AlkB-like
69	c2iuwA_	Alignment	not modelled	5.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkylated repair protein alkb homolog 3; **PDBTitle:** crystal structure of human abh3 in complex with iron ion2 and 2-oxoglutarate
70	c3iv4A_	Alignment	not modelled	5.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** a putative oxidoreductase with a thioredoxin fold
71	d2g9hd2	Alignment	not modelled	5.1	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Superantigen toxins, C-terminal domain **Family:**Superantigen toxins, C-terminal domain