Phyre2

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Description	RVBD2785c_(rpsO)_3093489_3093758
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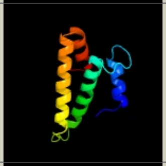
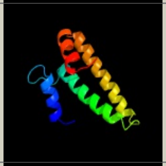
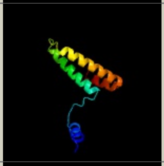
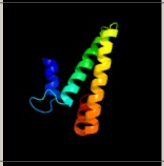
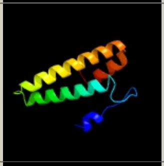
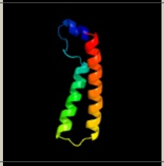
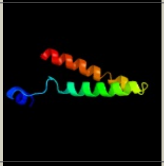
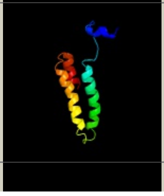
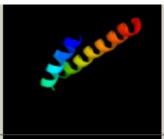
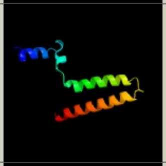
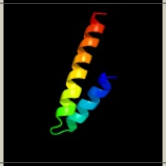
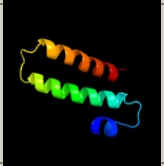
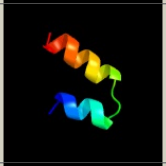
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jO_	Alignment		100.0	89	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**30s ribosomal protein s15; **PDBTitle:** structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	d1vs5o1	Alignment		100.0	52	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
3	d1g1xb_	Alignment		100.0	56	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
4	d1a32a_	Alignment		100.0	61	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
5	c3ulwA_	Alignment		100.0	51	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s15; **PDBTitle:** 30s ribosomal protein s15 from campylobacter jejuni
6	d1kuqa_	Alignment		100.0	57	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**Ribosomal protein S15
7	c3j6vO_	Alignment		100.0	26	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**28s ribosomal protein s15, mitochondrial; **PDBTitle:** cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
8	c3bbnO_	Alignment		99.9	39	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**ribosomal protein s15; **PDBTitle:** homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
9	c2xzmO_	Alignment		99.2	19	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rps13e; **PDBTitle:** 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 1
10	c5xyiN_	Alignment		99.1	27	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**40s ribosomal protein s13, putative; **PDBTitle:** small subunit of trichomonas vaginalis ribosome
11	c3izbO_	Alignment		99.1	14	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein rps13 (s15p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome

12	c3u5cN_	Alignment		98.8	26	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
13	c1yshE_	Alignment		97.9	25	**PDB header:**structural protein/rna **Chain:** E: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
14	c3zeyG_	Alignment		97.8	28	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**40s ribosomal protein s13, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
15	c3j20Q_	Alignment		96.2	43	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**30s ribosomal protein s15p/s13e; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
16	c1s1hO_	Alignment		96.0	19	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** 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.
17	c4ar9A_	Alignment		43.8	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**collagenase colt; **PDBTitle:** crystal structure of the peptidase domain of collagenase t2 from clostridium tetani at 1.69 angstrom resolution.
18	c4ar1A_	Alignment		38.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**colh protein; **PDBTitle:** crystal structure of the peptidase domain of collagenase h from2 clostridium histolyticum at 2.01 angstrom resolution.
19	d1y0ua_	Alignment		32.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
20	c2y50A_	Alignment		26.1	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**collagenase; **PDBTitle:** crystal structure of collagenase g from clostridium2 histolyticum at 2.80 angstrom resolution
21	c5ajaC_	Alignment	not modelled	22.4	38	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein; **PDBTitle:** crystal structure of mandrill samhd1 (amino acid residues 1-114)2 bound to vpx isolated from mandrill and human dcaf1 (amino3 acid residues 1058-1396)
22	c5dukA_	Alignment	not modelled	21.7	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative dna binding protein; **PDBTitle:** n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
23	c2ke4A_	Alignment	not modelled	21.5	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
24	d1sxjd1	Alignment	not modelled	21.0	15	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
25	c2zvnF_	Alignment	not modelled	17.6	11	**PDB header:**signaling protein/transcription **Chain:** F: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cozi domain incomplex with diubiquitin in p212121 space group
26	c3uosH_	Alignment	not modelled	15.2	25	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**50s ribosomal protein l10; **PDBTitle:** crystal structure of release factor rf3 trapped in the gtp state on a2 rotated conformation of the ribosome (without viomycin)
27	c5frgA_	Alignment	not modelled	13.7	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**formin-binding protein 1-like; **PDBTitle:** the nmr structure of the cdc42-interacting region of toca1
28	c2lhuA_	Alignment	not modelled	13.5	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain

29	c3f1iH_	Alignment	not modelled	11.3	17	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
30	c4kmfA_	Alignment	not modelled	11.2	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**interferon-inducible and double-stranded-dependent eif- **PDBTitle:** crystal structure of zalpha domain from carassius auratus pkz in2 complex with z-dna
31	c2vogB_	Alignment	not modelled	10.8	67	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-modifying factor; **PDBTitle:** structure of mouse a1 bound to the bmf bh3-domain
32	c4wyhA_	Alignment	not modelled	10.7	35	**PDB header:**replication **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of prix from the hyperthermophilic archaeon2 sulfolobus solfataricus
33	c2hjqA_	Alignment	not modelled	10.4	21	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein yqbf; **PDBTitle:** nmr structure of bacillus subtilis protein yqbf, northeast2 structural genomics target sr449
34	c2v4hA_	Alignment	not modelled	9.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
35	c4lb6B_	Alignment	not modelled	9.6	16	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**protein kinase containing z-dna binding domains; **PDBTitle:** crystal structure of pkz zalpha in complex with ds(cg)6 (tetragonal2 form)
36	c3nqwB_	Alignment	not modelled	8.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
37	c1ye9E_	Alignment	not modelled	8.7	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of proteolytically truncated catalase2 hpii from e. coli
38	c5tzqD_	Alignment	not modelled	8.5	67	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**bcl-2-modifying factor; **PDBTitle:** crystal structure of fpv039:bmf bh3 complex
39	c5tzqC_	Alignment	not modelled	8.5	67	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**bcl-2-modifying factor; **PDBTitle:** crystal structure of fpv039:bmf bh3 complex
40	c2ymyB_	Alignment	not modelled	8.3	83	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**ras association domain-containing protein 5; **PDBTitle:** structure of the murine nore1-sarah domain
41	c2khnA_	Alignment	not modelled	8.3	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** nmr solution structure of the eh 1 domain from human2 intersectin-1 protein. northeast structural genomics3 consortium target hr3646e.
42	c3rj1Q_	Alignment	not modelled	8.2	13	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 8; **PDBTitle:** architecture of the mediator head module
43	d2jdia1	Alignment	not modelled	8.1	13	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
44	d3bj1b1	Alignment	not modelled	7.3	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
45	c2f5xC_	Alignment	not modelled	7.3	17	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
46	c3cuoB_	Alignment	not modelled	6.9	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
47	c4bj5A_	Alignment	not modelled	6.7	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein rif2; **PDBTitle:** crystal structure of rif2 in complex with the c-terminal domain of2 rap1 (rap1-rct)
48	c5d1vB_	Alignment	not modelled	6.7	9	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**globin; **PDBTitle:** crystal structure and thermal stability of hemoglobin from2 thermophilic phototrophic bacterium chloroflexus aurantiacus
49	d1sxjb1	Alignment	not modelled	6.6	19	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
50	c3qkuC_	Alignment	not modelled	6.6	16	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** mre11 rad50 binding domain in complex with rad50 and amp-pnp
51	d1fx0a1	Alignment	not modelled	6.4	10	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
52	d3crda_	Alignment	not modelled	6.4	8	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
						Fold: Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1

53	d2f43a1	Alignment	not modelled	6.2	13	ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
54	d1biaa1	Alignment	not modelled	6.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
55	c3katA_	Alignment	not modelled	5.9	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**nacht, lrr and pyd domains-containing protein 1; **PDBTitle:** crystal structure of the card domain of the human nlrp1 protein,2 northeast structural genomics consortium target hr3486e
56	d2zjrw1	Alignment	not modelled	5.6	27	**Fold:**Ribosomal protein L30p/L7e **Superfamily:**Ribosomal protein L30p/L7e **Family:**Ribosomal protein L30p/L7e
57	d1spgb_	Alignment	not modelled	5.5	24	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
58	c1m7lA_	Alignment	not modelled	5.5	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
59	c3qkrC_	Alignment	not modelled	5.5	16	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** mre11 rad50 binding domain bound to rad50
60	c3ac6A_	Alignment	not modelled	5.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
61	c2b19A_	Alignment	not modelled	5.3	50	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**neuropeptide k; **PDBTitle:** solution structure of mammalian tachykinin peptide,2 neuropeptide k
62	d1gyza_	Alignment	not modelled	5.2	10	**Fold:**PABP domain-like **Superfamily:**Ribosomal protein L20 **Family:**Ribosomal protein L20
63	c2nz7A_	Alignment	not modelled	5.2	12	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**caspase recruitment domain-containing protein 4; **PDBTitle:** crystal structure analysis of caspase-recruitment domain2 (card) of nod1
64	d2jxca1	Alignment	not modelled	5.2	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
65	c3j3vY_	Alignment	not modelled	5.2	33	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**50s ribosomal protein l30; **PDBTitle:** atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
66	c3m20A_	Alignment	not modelled	5.1	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
67	d2b7ea1	Alignment	not modelled	5.1	36	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
68	c3piwA_	Alignment	not modelled	5.1	14	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**type i interferon 2; **PDBTitle:** zebrafish interferon 2
69	c5o60a_	Alignment	not modelled	5.1	27	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**23s rrna; **PDBTitle:** structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
70	c6dlcA_	Alignment	not modelled	5.1	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein dhd1:234_a; **PDBTitle:** designed protein dhd1:234_a, designed protein dhd1:234_b
71	d1skyb1	Alignment	not modelled	5.1	9	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
72	c2l4aA_	Alignment	not modelled	5.1	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
73	d1x4ta1	Alignment	not modelled	5.0	20	**Fold:**Long alpha-hairpin **Superfamily:**ISY1 domain-like **Family:**ISY1 N-terminal domain-like