Phyre2

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Description	RVBD0717_(rpsN)_812630_812815
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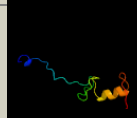
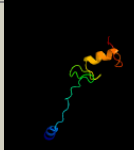
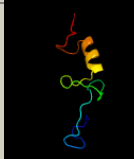
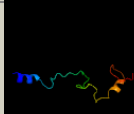
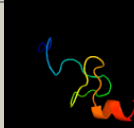
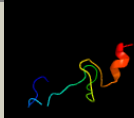
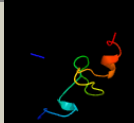
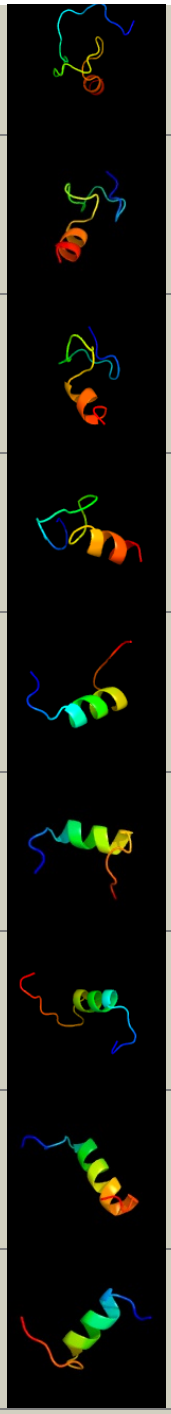
Unique Job ID	3ae17c405a39d3e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2uubn1	Alignment		100.0	70	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein S14
2	c6dzkN_	Alignment		100.0	54	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**30s ribosomal protein s14; **PDBTitle:** cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
3	c3bbnN_	Alignment		100.0	48	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**ribosomal protein s14; **PDBTitle:** homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
4	d2qaln1	Alignment		100.0	46	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein S14
5	c2gy9N_	Alignment		100.0	49	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**30s ribosomal subunit protein s14; **PDBTitle:** cryo-em structure of the 30s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
6	c3j6vN_	Alignment		99.9	37	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**28s ribosomal protein s14, mitochondrial; **PDBTitle:** cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
7	c5xyid_	Alignment		96.2	38	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s3, putative; **PDBTitle:** small subunit of trichomonas vaginalis ribosome
8	c3jyvN_	Alignment		96.1	31	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**40s ribosomal protein s29(a); **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
9	c3j20P_	Alignment		96.0	39	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**30s ribosomal protein s14p type z; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
10	c2xznN_	Alignment		95.9	31	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**rps29e; **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 2
11	c5xxud_	Alignment		95.9	28	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein us3; **PDBTitle:** small subunit of toxoplasma gondii ribosome

12	c2zkqn_	Alignment		95.8	29	**PDB header:**ribosomal protein/rna **Chain:** N: **PDB Molecule:** **PDBTitle:** 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
13	c3zey8_	Alignment		95.3	43	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**ribosomal protein s29, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
14	c6az1S_	Alignment		95.1	39	**PDB header:**ribosome/antibiotic **Chain:** S: **PDB Molecule:**ribosomal protein s14; **PDBTitle:** cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
15	c1s1hN_	Alignment		85.3	38	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**40s ribosomal protein s29-b; **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.
16	c4j2nB_	Alignment		27.8	27	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
17	c4j2nA_	Alignment		25.8	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
18	c6amaO_	Alignment		23.7	19	**PDB header:**dna binding protein/dna **Chain:** O: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
19	d2bmfa1	Alignment		18.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
20	c4lhfA_	Alignment		11.5	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**regulatory protein cox; **PDBTitle:** crystal structure of a dna binding protein from phage p2
21	c5ntbB_	Alignment	not modelled	11.2	30	**PDB header:**protease inhibitor **Chain:** B: **PDB Molecule:**papain inhibitor; **PDBTitle:** streptomyces papain inhibitor (spi)
22	c2zhhA_	Alignment	not modelled	11.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
23	c1yuzB_	Alignment	not modelled	7.9	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
24	c2xzm8_	Alignment	not modelled	7.7	32	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**rps25e,; **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
25	d1n10a2	Alignment	not modelled	7.4	25	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Pollen allergen PHL P 1 N-terminal domain
26	c3zeyU_	Alignment	not modelled	7.1	26	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s25, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
27	d2ieaa3	Alignment	not modelled	7.1	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
28	c2fugC_	Alignment	not modelled	6.8	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
						Fold: Putative DNA-binding domain

29	d1r8da_	Alignment	not modelled	6.5	12	**Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
30	c1y6uA_	Alignment	not modelled	6.2	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
31	c3izbV_	Alignment	not modelled	6.2	36	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**40s ribosomal protein rps25 (s25e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
32	c4ivvA_	Alignment	not modelled	5.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**autolysin; **PDBTitle:** catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumaniae
33	c1z4hA_	Alignment	not modelled	5.7	18	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
34	c3iz6V_	Alignment	not modelled	5.7	23	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**40s ribosomal protein s25 (s25e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
35	c5jyxB_	Alignment	not modelled	5.5	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archeaosine synthase quef-like; **PDBTitle:** crystal structure of the covalent thioimide intermediate of the2 archaeosine synthase quef-like
36	c3gpvA_	Alignment	not modelled	5.3	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
37	c3j3aZ_	Alignment	not modelled	5.3	32	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**40s ribosomal protein s25; **PDBTitle:** structure of the human 40s ribosomal proteins