


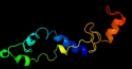




















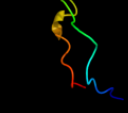








Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AG59
Date	Thu Jan 5 11:28:11 GMT 2012
Unique Job ID	8f434d413bd1fa17

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qaln1	 Alignment		100.0	100	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Ribosomal protein S14
2	c3bbnN_	 Alignment		100.0	40	PDB header: ribosome Chain: N: PDB Molecule: ribosomal protein s14; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
3	c2gy9N_	 Alignment		99.9	100	PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal subunit protein s14; PDBTitle: structure of the 30s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
4	d2uubn1	 Alignment		99.9	41	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Ribosomal protein S14
5	c3jyvN_	 Alignment		93.8	32	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
6	c2xznN_	 Alignment		93.7	32	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
7	c2zkgN_	 Alignment		91.8	33	PDB header: ribosomal protein/rna Chain: N: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by fitting homology models of the rna3 and proteins into an 8.7 a cryo-em map
8	c1s1hN_	 Alignment		75.3	35	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29-b; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
9	d2bmfa1	 Alignment		21.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
10	c2zhbA_	 Alignment		20.1	12	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
11	d1r8da_	 Alignment		14.5	8	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators

12	d2ieaa3	Alignment		13.4	24	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
13	c3gpvA_	Alignment		13.0	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
14	c1qw1A_	Alignment		12.9	12	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: solution structure of the c-terminal domain of dbxr2 residues 110-226
15	c1yuzB_	Alignment		12.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
16	c3izbV_	Alignment		11.0	35	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
17	c1y6uA_	Alignment		10.3	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
18	c2xzm8_	Alignment		9.9	27	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
19	d2cp5a1	Alignment		9.8	30	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
20	c3iz6V_	Alignment		9.1	26	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
21	d1n10a2	Alignment	not modelled	8.7	17	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: Pollen allergen PHL P 1 N-terminal domain
22	d1nj1a2	Alignment	not modelled	8.7	17	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
23	c3bboY_	Alignment	not modelled	7.8	38	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein l28; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
24	d1kcf1	Alignment	not modelled	7.4	25	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
25	c1z4hA_	Alignment	not modelled	7.3	14	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
26	c2fugC_	Alignment	not modelled	7.1	38	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
27	d2qamz1	Alignment	not modelled	6.8	38	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
28	d1e0ea_	Alignment	not modelled	6.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
						Fold: Another 3-helical bundle

29	d1s7za_	Alignment	not modelled	6.4	33	Superfamily: B-form DNA mimic Ocr Family: B-form DNA mimic Ocr
30	c3hh0C_	Alignment	not modelled	6.3	4	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
31	d1whha_	Alignment	not modelled	6.2	17	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
32	d1wg2a_	Alignment	not modelled	5.9	28	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
33	d1whja_	Alignment	not modelled	5.5	30	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
34	d1k6ya1	Alignment	not modelled	5.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
35	d2coza1	Alignment	not modelled	5.4	25	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
36	c2k0aA_	Alignment	not modelled	5.3	21	PDB header: metal binding protein Chain: A: PDB Molecule: pre-mrna-splicing factor rds3; PDBTitle: 1h, 15n and 13c chemical shift assignments for rds3 protein
37	d1wjfa_	Alignment	not modelled	5.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
38	d2coya1	Alignment	not modelled	5.2	21	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain