

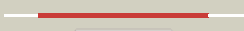














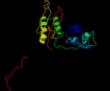

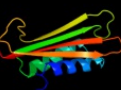









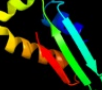

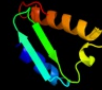










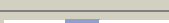


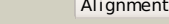

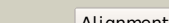



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qbfC	 Alignment		100.0	100	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: crystal structure of the bacterial ribosome from escherichia2 coli in complex with ribosome recycling factor (rrf). this3 file contains the 30s subunit of the second 70s ribosome.4 the entire crystal structure contains two 70s ribosomes and5 is described in remark 400.
2	c1pnxC	 Alignment		100.0	52	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: crystal structure of the wild type ribosome from e. coli,2 30s subunit of 70s ribosome. this file, 1pnx, contains3 only molecules of the 30s ribosomal subunit. the 50s4 subunit is in the pdb file 1pny.
3	c2gy9C	 Alignment		100.0	100	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal subunit protein s3; 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	c1hnwC	 Alignment		100.0	52	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: structure of the thermus thermophilus 30s ribosomal subunit2 in complex with tetracycline
5	c3bbnC	 Alignment		100.0	42	PDB header: ribosome Chain: C: PDB Molecule: ribosomal protein s3; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
6	c2xznC	 Alignment		100.0	21	PDB header: ribosome Chain: C: PDB Molecule: kh domain containing protein; 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	c2zkqc	 Alignment		100.0	25	PDB header: ribosomal protein/rna Chain: C: PDB Molecule: rna expansion segment es4; PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
8	c1s1hC	 Alignment		100.0	25	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s3; 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	c3izbB	 Alignment		100.0	26	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein rps3 (s3p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
10	d2uubc2	 Alignment		100.0	62	Fold: Ribosomal protein S3 C-terminal domain Superfamily: Ribosomal protein S3 C-terminal domain Family: Ribosomal protein S3 C-terminal domain
11	d2qalc2	 Alignment		100.0	100	Fold: Ribosomal protein S3 C-terminal domain Superfamily: Ribosomal protein S3 C-terminal domain Family: Ribosomal protein S3 C-terminal domain

12	d2qalc1	 Alignment		100.0	100	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
13	d2uubc1	 Alignment		100.0	43	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
14	d1wh9a_	 Alignment		99.4	22	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
15	c3gkuB_	 Alignment		94.2	18	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
16	c2pt7G_	 Alignment		92.7	15	PDB header: hydrolase/protein binding Chain: G: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
17	d1hh2p3	 Alignment		58.2	26	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
18	d2asba3	 Alignment		53.9	21	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
19	d1tuaa1	 Alignment		32.8	18	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
20	c2hh3A_	 Alignment		27.3	32	PDB header: rna binding protein Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the third kh domain of ksrp
21	c2hh2A_	 Alignment	not modelled	26.2	33	PDB header: rna binding protein Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the fourth kh domain of ksrp
22	c2cy1A_	 Alignment	not modelled	26.1	22	PDB header: transcription Chain: A: PDB Molecule: nusa protein homolog; PDBTitle: crystal structure of ape1850
23	d2axya1	 Alignment	not modelled	26.1	43	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
24	c2asbA_	 Alignment	not modelled	22.7	21	PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex
25	d1dt4a_	 Alignment	not modelled	22.6	15	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
26	d1j4wa1	 Alignment	not modelled	21.4	39	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
27	c2anrA_	 Alignment	not modelled	19.7	33	PDB header: rna-binding protein/rna Chain: A: PDB Molecule: neuro-oncological ventral antigen 1; PDBTitle: crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin
28	d1j4wa2	 Alignment	not modelled	19.3	26	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
29	d1dtja_	 Alignment	not modelled	18.4	15	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I)

					Family: Eukaryotic type KH-domain (KH-domain type I)
30	d1khma_	Alignment	not modelled	17.8	30 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
31	d1ec6a_	Alignment	not modelled	17.6	15 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
32	d1wf3a2	Alignment	not modelled	17.4	17 Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
33	d1we8a_	Alignment	not modelled	16.2	19 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
34	c1j4wA_	Alignment	not modelled	15.5	41 PDB header: transcription/dna Chain: A: PDB Molecule: fuse binding protein; PDBTitle: complex of the kh3 and kh4 domains of fbp with a2 single stranded 29mer dna oligonucleotide from the fuse3 element of the c-myc oncogene
35	c1ztgD_	Alignment	not modelled	15.3	44 PDB header: dna, rna binding protein/dna Chain: D: PDB Molecule: poly(rc)-binding protein 1; PDBTitle: human alpha polyc binding protein kh1
36	d1wvna1	Alignment	not modelled	15.2	26 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
37	d1viga_	Alignment	not modelled	15.0	16 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
38	d1zzka1	Alignment	not modelled	14.0	33 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
39	d1x4na1	Alignment	not modelled	13.9	19 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
40	c1tuaA_	Alignment	not modelled	13.7	31 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ape0754; PDBTitle: 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix
41	c2jvfA_	Alignment	not modelled	13.7	19 PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
42	d2ctla1	Alignment	not modelled	13.2	25 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
43	d2ba0a3	Alignment	not modelled	12.7	39 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
44	d1x4ma1	Alignment	not modelled	12.3	33 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
45	c2dgrA_	Alignment	not modelled	12.1	26 PDB header: rna binding protein Chain: A: PDB Molecule: ring finger and kh domain-containing protein 1; PDBTitle: solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
46	c1k0rB_	Alignment	not modelled	11.8	21 PDB header: transcription Chain: B: PDB Molecule: nusa; PDBTitle: crystal structure of mycobacterium tuberculosis nusa
47	d2ctja1	Alignment	not modelled	11.6	22 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
48	c3af5A_	Alignment	not modelled	11.2	19 PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
49	c3krmB_	Alignment	not modelled	11.1	33 PDB header: rna binding protein Chain: B: PDB Molecule: insulin-like growth factor 2 mrna-binding protein PDBTitle: imp1 kh34
50	c1hh2P_	Alignment	not modelled	11.1	26 PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
51	d2ctea1	Alignment	not modelled	10.6	33 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
52	d2cmea1	Alignment	not modelled	10.6	50 Fold: SARS ORF9b-like Superfamily: SARS ORF9b-like Family: SARS ORF9b-like
53	c2fenA_	Alignment	not modelled	10.6	43 PDB header: isomerase Chain: A: PDB Molecule: 3-carboxy-cis,cis-muconate lactonizing enzyme; PDBTitle: 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
54	c2qndA_	Alignment	not modelled	10.3	24 PDB header: rna binding protein Chain: A: PDB Molecule: fmr1 protein; PDBTitle: crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein
55	d2ctka1	Alignment	not modelled	10.1	27 Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)

56	c2jzxA	Alignment	not modelled	9.8	46	PDB header: rna binding protein Chain: A: PDB Molecule: poly(rc)-binding protein 2; PDBTitle: pcbp2 kh1-kh2 domains
57	c2jvzA	Alignment	not modelled	9.3	36	PDB header: splicing Chain: A: PDB Molecule: far upstream element-binding protein 2; PDBTitle: solution nmr structure of the second and third kh domains2 of ksrp
58	c1l2fA	Alignment	not modelled	9.3	26	PDB header: transcription Chain: A: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
59	c2w2rA	Alignment	not modelled	9.1	15	PDB header: viral protein Chain: A: PDB Molecule: matrix protein; PDBTitle: structure of the vesicular stomatitis virus matrix protein
60	d1hsta	Alignment	not modelled	8.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
61	d2ctma1	Alignment	not modelled	8.6	19	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
62	d1egaa2	Alignment	not modelled	8.2	25	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
63	d1myna	Alignment	not modelled	8.1	42	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Insect defensins
64	c1egaB	Alignment	not modelled	7.6	18	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
65	d2gysa1	Alignment	not modelled	7.5	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
66	d1c3ca	Alignment	not modelled	7.4	43	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
67	c1qysA	Alignment	not modelled	7.3	13	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
68	c2pfmA	Alignment	not modelled	7.2	43	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
69	d2ctfa1	Alignment	not modelled	6.9	26	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
70	c3gtdB	Alignment	not modelled	6.7	57	PDB header: lyase Chain: B: PDB Molecule: fumarate hydratase class ii; PDBTitle: 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
71	d1tj7a	Alignment	not modelled	6.7	50	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
72	d1lg7a	Alignment	not modelled	6.6	12	Fold: VSV matrix protein Superfamily: VSV matrix protein Family: VSV matrix protein
73	d1tjva	Alignment	not modelled	6.1	50	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
74	d2fmra	Alignment	not modelled	6.0	38	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
75	c3ocfB	Alignment	not modelled	6.0	57	PDB header: lyase Chain: B: PDB Molecule: fumarate lyase:delta crystallin; PDBTitle: crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
76	c3ej9D	Alignment	not modelled	5.9	44	PDB header: hydrolase Chain: D: PDB Molecule: beta-subunit of trans-3-chloroacrylic acid dehalogenase; PDBTitle: structural and mechanistic analysis of trans-3-chloroacrylic acid2 dehalogenase activity
77	d1f1oa	Alignment	not modelled	5.4	43	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
78	d1eu3a2	Alignment	not modelled	5.3	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Superantigen toxins, C-terminal domain Family: Superantigen toxins, C-terminal domain
79	c3no9C	Alignment	not modelled	5.3	43	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
80	d1ldofa	Alignment	not modelled	5.2	14	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
81	c3e04C	Alignment	not modelled	5.1	57	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
82	d1yfma	Alignment	not modelled	5.0	57	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase