

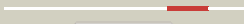





























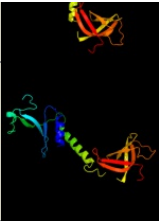
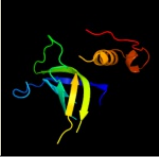
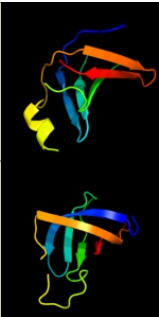
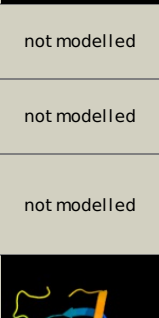
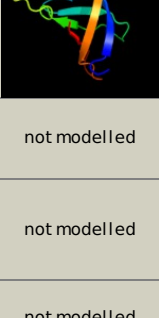


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3go5A_	 Alignment		100.0	20	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
2	c1yz6A_	 Alignment		99.8	26	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
3	c2khjA_	 Alignment		99.8	100	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
4	c1q46A_	 Alignment		99.8	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
5	c2k4kA_	 Alignment		99.8	43	PDB header: rna binding protein Chain: A: PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis
6	c1q8kA_	 Alignment		99.8	23	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2
7	d3bzka4	 Alignment		99.8	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
8	c2khiA_	 Alignment		99.8	29	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
9	d1q46a2	 Alignment		99.7	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
10	d1sroa_	 Alignment		99.7	38	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
11	c2k52A_	 Alignment		99.7	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1198; PDBTitle: structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b

12	c2cqoA	Alignment		99.7	23	PDB header: ribosome Chain: A: PDB Molecule: nucleolar protein of 40 kda; PDBTitle: solution structure of the s1 rna binding domain of human2 hypothetical protein flj11067
13	c2oceA	Alignment		99.7	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
14	d1go3e1	Alignment		99.7	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
15	c2ahoB	Alignment		99.7	21	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp
16	d1wi5a	Alignment		99.7	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
17	c3psiA	Alignment		99.7	18	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
18	d2ba0a1	Alignment		99.7	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
19	c1kl9A	Alignment		99.6	20	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 subunit 1; PDBTitle: crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
20	c2eqsA	Alignment		99.6	31	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dhx8; PDBTitle: solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
21	d1kl9a2	Alignment	not modelled	99.6	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
22	d2z0sa1	Alignment	not modelled	99.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
23	d2je6i1	Alignment	not modelled	99.6	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	d2ahob2	Alignment	not modelled	99.6	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
25	d1y14b1	Alignment	not modelled	99.5	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
26	d2nn6h1	Alignment	not modelled	99.5	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
27	c2z0sA	Alignment	not modelled	99.5	17	PDB header: rna binding protein Chain: A: PDB Molecule: probable exosome complex rna-binding protein 1; PDBTitle: crystal structure of putative exosome complex rna-binding2 protein
28	c1l2fA	Alignment		99.4	12	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
29	c1hh2P_	Alignment		99.4	13 PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
30	c2ba0A_	Alignment	not modelled	99.3	26 PDB header: rna binding protein Chain: A: PDB Molecule: archaeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core
31	d1hh2p1	Alignment	not modelled	99.3	23 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
32	d2nn6i1	Alignment	not modelled	99.3	26 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
33	c1go3E_	Alignment	not modelled	99.3	27 PDB header: transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex
34	c2je6l_	Alignment	not modelled	99.2	29 PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome
35	d2c35b1	Alignment	not modelled	99.2	23 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
36	c2pmzE_	Alignment	not modelled	99.1	30 PDB header: translation, transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
37	c2ba1B_	Alignment	not modelled	99.1	23 PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
38	c2nn6l_	Alignment	not modelled	99.1	26 PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
39	c2c35F_	Alignment	not modelled	99.1	21 PDB header: polymerase Chain: F: PDB Molecule: dna-directed rna polymerase ii 19 kda PDBTitle: subunits rpb4 and rpb7 of human rna polymerase ii
40	c2b8kG_	Alignment	not modelled	98.9	19 PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda PDBTitle: 12-subunit rna polymerase ii
41	c3h0gS_	Alignment	not modelled	98.8	21 PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase ii subunit rpb7; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
42	d1smxa_	Alignment	not modelled	98.7	26 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
43	c1nt9G_	Alignment	not modelled	98.6	18 PDB header: transcription, transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kd polypeptide; PDBTitle: complete 12-subunit rna polymerase ii
44	c2ix1A_	Alignment	not modelled	98.5	25 PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant
45	c2bh8B_	Alignment	not modelled	98.5	18 PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11
46	c2ckzB_	Alignment	not modelled	98.3	19 PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase iii 25 kd PDBTitle: x-ray structure of rna polymerase iii subcomplex c17-c25.
47	d2asba1	Alignment	not modelled	98.1	28 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
48	c3ayhB_	Alignment	not modelled	98.1	16 PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase iii subunit rpc8; PDBTitle: crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
49	c2wp8J_	Alignment	not modelled	98.0	28 PDB header: hydrolase Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease
50	c2asba_	Alignment		98.0	20 PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex

51	c2nn6H_	Alignment		97.9	19	PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
52	d2nn6g1	Alignment		97.9	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
53	c2vnuD_	Alignment	not modelled	97.8	30	PDB header: hydrolase/rna Chain: D: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: crystal structure of sc rrp44
54	d2ja9a1	Alignment	not modelled	97.5	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
55	c2rf4A_	Alignment	not modelled	97.5	11	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
56	c2nn6G_	Alignment		97.5	24	PDB header: hydrolase/transferase Chain: G: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
57	c2ja9A_	Alignment	not modelled	97.5	17	PDB header: rna-binding protein Chain: A: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the n-terminal deletion of yeast exosome2 component rrp40
58	c2r7fA_	Alignment	not modelled	97.3	11	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease ii family protein; PDBTitle: crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
59	c1k0rB_	Alignment	not modelled	97.2	19	PDB header: transcription Chain: B: PDB Molecule: nusa; PDBTitle: crystal structure of mycobacterium tuberculosis nusa
60	c2c4rL_	Alignment	not modelled	97.2	29	PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnase e
61	d2ix0a3	Alignment	not modelled	96.4	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
62	d1jiga_	Alignment	not modelled	91.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
63	d1luza_	Alignment	not modelled	90.5	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
64	c3i4oA_	Alignment	not modelled	89.6	19	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
65	d1ah9a_	Alignment	not modelled	89.2	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
66	c3d0fA_	Alignment	not modelled	88.7	14	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
67	d1k3ra1	Alignment	not modelled	84.6	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain
68	d1e3pa2	Alignment	not modelled	82.3	31	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
69	c1h9mB_	Alignment	not modelled	78.9	19	PDB header: binding protein Chain: B: PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
70	c3dlmA_	Alignment	not modelled	74.8	19	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
71	d1hr0w_	Alignment	not modelled	66.7	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
72	d1wfga_	Alignment	not modelled	63.9	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
PDB header: replication						

73	c3dm3A_	Alignment	not modelled	62.8	20	Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
74	d2vnud2	Alignment	not modelled	62.1	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	d1krta_	Alignment	not modelled	60.8	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
76	d1h95a_	Alignment	not modelled	58.8	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
77	d1bbua1	Alignment	not modelled	47.5	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
78	c2bkdN_	Alignment	not modelled	46.8	19	PDB header: nuclear protein Chain: N: PDB Molecule: fragile x mental retardation 1 protein; PDBTitle: structure of the n-terminal domain of fragile x mental2 retardation protein
79	d2ix0a2	Alignment	not modelled	46.1	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
80	d1e1oa1	Alignment	not modelled	45.8	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
81	c1ng2A_	Alignment	not modelled	41.9	16	PDB header: oxidoreductase activator Chain: A: PDB Molecule: neutrophil cytosolic factor 1; PDBTitle: structure of autoinhibited p47phox
82	c2kcmA_	Alignment	not modelled	41.3	12	PDB header: nucleic acid binding protein 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.
83	d1jt8a_	Alignment	not modelled	39.2	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
84	c2k75A_	Alignment	not modelled	38.9	16	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ta0387; PDBTitle: solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
85	d1fr3a_	Alignment	not modelled	38.8	18	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
86	c2ytyA_	Alignment	not modelled	38.1	16	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein)
87	c2ytvA_	Alignment	not modelled	33.7	17	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein)
88	c2ytxA_	Alignment	not modelled	33.1	23	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
89	c1ssfA_	Alignment	not modelled	32.4	23	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
90	c1x65A_	Alignment	not modelled	32.3	16	PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
91	d1nz9a_	Alignment	not modelled	31.5	20	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
92	c1ov3A_	Alignment	not modelled	30.7	12	PDB header: oxidoreductase activator Chain: A: PDB Molecule: neutrophil cytosol factor 1; PDBTitle: structure of the p22phox-p47phox complex
93	d2ot2a1	Alignment	not modelled	30.0	22	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
94	c2h5xA_	Alignment	not modelled	29.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
95	d2do3a1	Alignment	not modelled	28.0	16	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
96	c2qqsb_	Alignment	not modelled	26.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjdc domain-containing histone demethylation PDBTitle: jmjcd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
97	d1nppa2	Alignment	not modelled	26.5	24	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
98	c1xni1_	Alignment	not modelled	26.1	23	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
						PDB header: translation

99	c2oqkA_	Alignment	not modelled	25.8	20	Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
100	c3kygB_	Alignment	not modelled	24.1	8	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein vca0042; PDBTitle: crystal structure of vca0042 (I135r) complexed with c-di-gmp
101	dlixra2	Alignment	not modelled	24.1	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
102	dla8pa1	Alignment	not modelled	24.1	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
103	dlwjja_	Alignment	not modelled	23.5	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
104	dlyeza1	Alignment	not modelled	23.0	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
105	cle22A_	Alignment	not modelled	22.7	21	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
106	dlfdra1	Alignment	not modelled	20.8	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
107	dlri9a_	Alignment	not modelled	20.8	11	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
108	clri9A_	Alignment	not modelled	20.8	11	PDB header: signaling protein Chain: A: PDB Molecule: fyn-binding protein; PDBTitle: structure of a helically extended sh3 domain of the t cell12 adapter protein adap