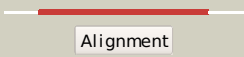
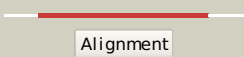
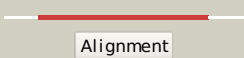
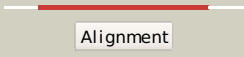
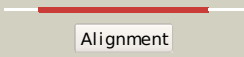
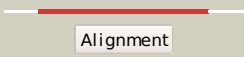
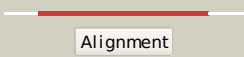
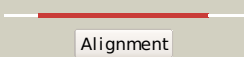
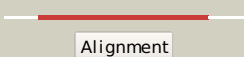
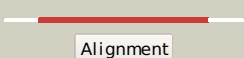
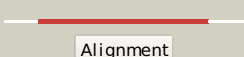


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mjca_	 Alignment		99.9	72	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
2	d1h95a_	 Alignment		99.9	45	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
3	d1c9oa_	 Alignment		99.9	63	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
4	d2es2a1	 Alignment		99.9	59	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
5	c3camB_	 Alignment		99.8	55	PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis
6	c3a0jB_	 Alignment		99.8	55	PDB header: transcription Chain: B: PDB Molecule: cold shock protein; PDBTitle: crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
7	d1g6pa_	 Alignment		99.8	55	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
8	c2k5nA_	 Alignment		99.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cold-shock protein; PDBTitle: solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a
9	c2kcmA_	 Alignment		99.8	30	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.
10	c3aqqD_	 Alignment		99.8	30	PDB header: dna binding protein Chain: D: PDB Molecule: calcium-regulated heat stable protein 1; PDBTitle: crystal structure of human crhsp-24
11	c3trzE_	 Alignment		99.8	37	PDB header: rna binding protein/rna Chain: E: PDB Molecule: protein lin-28 homolog a; PDBTitle: mouse lin28a in complex with let-7d microRNA pre-element

12	c2ytyA_	Alignment		99.7	27	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)
13	d1wfga_	Alignment		99.7	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
14	c2ytxA_	Alignment		99.7	29	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)
15	c1x65A_	Alignment		99.6	29	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)
16	c2bh8B_	Alignment		99.6	67	PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11
17	c2yvtA_	Alignment		99.5	35	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)
18	d2ix0a2	Alignment		97.6	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
19	c2ix1A_	Alignment		96.9	21	PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant
20	d1a62a2	Alignment		96.6	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
21	c2a8vA_	Alignment	not modelled	96.6	23	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
22	d1smxa_	Alignment	not modelled	95.4	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
23	d1kl9a2	Alignment	not modelled	92.4	7	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	c2k52A_	Alignment	not modelled	91.9	10	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
25	d2ix0a1	Alignment	not modelled	91.7	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
26	c2vnuD_	Alignment	not modelled	90.9	17	PDB header: hydrolase/rna Chain: D: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: crystal structure of sc rrp44
27	c3go5A_	Alignment	not modelled	89.7	11	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
28	d1y14b1	Alignment	not modelled	89.7	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like

29	c1xpUB_	Alignment	not modelled	89.0	27	PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
30	d1u0la1	Alignment	not modelled	88.6	9	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
31	d2c35b1	Alignment	not modelled	86.3	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
32	d1hh2p1	Alignment	not modelled	86.2	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
33	c1hh2P_	Alignment	not modelled	82.9	10	PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
34	c1u0lB_	Alignment	not modelled	81.0	9	PDB header: hydrolase Chain: B: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima
35	c2cqoA_	Alignment	not modelled	81.0	22	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
36	c1l2fA_	Alignment	not modelled	80.3	10	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
37	d2z0sa1	Alignment	not modelled	80.1	5	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
38	c2oceA_	Alignment	not modelled	78.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
39	c2khiA_	Alignment	not modelled	78.0	21	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
40	d2nn6h1	Alignment	not modelled	76.3	9	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
41	c2l55A_	Alignment	not modelled	76.2	21	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
42	c1zeqX_	Alignment	not modelled	74.7	17	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
43	d1wi5a_	Alignment	not modelled	73.8	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	c2c4rL_	Alignment	not modelled	71.0	21	PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnase e
45	c3l0oB_	Alignment	not modelled	70.4	26	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
46	d2ba0a1	Alignment	not modelled	68.8	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
47	d3bzka4	Alignment	not modelled	68.0	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
48	c2khjA_	Alignment	not modelled	66.8	17	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
49	d1q46a2	Alignment	not modelled	64.2	4	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
50	c1q46A_	Alignment	not modelled	64.0	5	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
51	c3h0gS_	Alignment	not modelled	61.9	23	PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase ii subunit rpb7; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
52	c1yz6A_	Alignment	not modelled	61.7	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
53	c2wp8l_	Alignment	not modelled	61.5	15	PDB header: hydrolase Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease
54	c2k4kA_	Alignment	not modelled	60.2	19	PDB header: rna binding protein Chain: A: PDB Molecule: general stress protein 13;

					PDBTitle: solution structure of gsp13 from bacillus subtilis
55	c2eqsA	Alignment	not modelled	57.0	13 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
56	d2je6i1	Alignment	not modelled	56.6	17 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
57	c2ahoB	Alignment	not modelled	51.9	22 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
58	c2z0sA	Alignment	not modelled	51.4	6 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
59	d1go3e1	Alignment	not modelled	51.4	20 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
60	c2c35F	Alignment	not modelled	48.5	19 PDB header: polymerase Chain: F: PDB Molecule: dna-directed rna polymerase ii 19 kda PDBTitle: subunits rpb4 and rpb7 of human rna polymerase ii
61	d1h9ma2	Alignment	not modelled	44.0	20 Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
62	c3psiA	Alignment	not modelled	43.4	12 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)
63	d2ahob2	Alignment	not modelled	41.2	22 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
64	c2b8kG	Alignment	not modelled	38.6	25 PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda PDBTitle: 12-subunit rna polymerase ii
65	c1nt9G	Alignment	not modelled	37.6	20 PDB header: transcription, transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kd polypeptide; PDBTitle: complete 12-subunit rna polymerase ii
66	c2pmzE	Alignment	not modelled	37.6	20 PDB header: translation, transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
67	c1q8kA	Alignment	not modelled	36.9	8 PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2
68	d1j6qa	Alignment	not modelled	36.7	19 Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
69	c1j6qA	Alignment	not modelled	36.7	19 PDB header: chaperone Chain: A: PDB Molecule: cytochrome c maturation protein e; PDBTitle: solution structure and characterization of the heme2 chaperone ccme
70	d1tp5a1	Alignment	not modelled	35.9	17 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
71	c2xngA	Alignment	not modelled	35.7	37 PDB header: rna binding protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein 3; PDBTitle: structural insights into cis element recognition of non-2 polyadenylated rnas by the nab3-rrm
72	c2dhxA	Alignment	not modelled	33.3	21 PDB header: rna binding protein Chain: A: PDB Molecule: poly (adp-ribose) polymerase family, member 10 PDBTitle: solution structure of the rrm domain in the human poly (adp-2 ribose) polymerase family, member 10 variant
73	d1sroa	Alignment	not modelled	30.7	26 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
74	c2opgB	Alignment	not modelled	30.4	12 PDB header: structural protein Chain: B: PDB Molecule: multiple pdz domain protein; PDBTitle: the crystal structure of the 10th pdz domain of mpdz
75	d1u1sa1	Alignment	not modelled	29.3	25 Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq
76	d1be9a	Alignment	not modelled	29.2	17 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
77	d1ueqa	Alignment	not modelled	29.1	15 Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
78	c3soeA	Alignment	not modelled	28.9	19 PDB header: signaling protein Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: crystal structure of the 3rd pdz domain of the human membrane-2 associated guanylate kinase, ww and pdz domain-containing protein 33 (magi3)
79	d1t9ha1	Alignment	not modelled	28.5	20 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like

80	d2asba1	Alignment	not modelled	28.3	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
81	d1h9ma1	Alignment	not modelled	28.3	13	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
82	d1fr3a_	Alignment	not modelled	27.7	19	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
83	c1go3E_	Alignment	not modelled	25.9	25	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
84	d1hk9a_	Alignment	not modelled	25.8	25	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq
85	c2qt7B_	Alignment	not modelled	25.7	25	PDB header: hydrolase Chain: B: PDB Molecule: receptor-type tyrosine-protein phosphatase-like PDBTitle: crystallographic structure of the mature ectodomain of the2 human receptor-type protein-tyrosine phosphatase ia-2 at3 1.30 angstroms
86	c3qhsD_	Alignment	not modelled	25.5	25	PDB header: rna binding protein Chain: D: PDB Molecule: protein hfq; PDBTitle: crystal structure of full-length hfq from escherichia coli
87	d1guta_	Alignment	not modelled	25.1	12	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
88	c2q3gA_	Alignment	not modelled	24.8	10	PDB header: structural genomics Chain: A: PDB Molecule: pdz and lim domain protein 7; PDBTitle: structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
89	c2dc2A_	Alignment	not modelled	24.2	11	PDB header: structural protein Chain: A: PDB Molecule: golgi associated pdz and coiled-coil motif PDBTitle: solution structure of pdz domain
90	c3bpuA_	Alignment	not modelled	23.8	21	PDB header: transferase Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant
91	c2gu1A_	Alignment	not modelled	22.7	20	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
92	c1h9mB_	Alignment	not modelled	22.1	20	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
93	d1ujva_	Alignment	not modelled	21.9	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
94	c2asbA_	Alignment	not modelled	21.3	7	PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex
95	c3ggeA_	Alignment	not modelled	21.2	17	PDB header: protein binding Chain: A: PDB Molecule: pdz domain-containing protein gipc2; PDBTitle: crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
96	c2rcnA_	Alignment	not modelled	21.2	14	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
97	d1kq1a_	Alignment	not modelled	20.3	18	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq
98	c2i04B_	Alignment	not modelled	19.9	16	PDB header: peptide binding protein Chain: B: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: x-ray crystal structure of magi-1 pdz1 bound to the c-2 terminal peptide of hpv18 e6
99	c3hsbB_	Alignment	not modelled	19.4	36	PDB header: rna binding protein/rna Chain: B: PDB Molecule: protein hfq; PDBTitle: crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer