Phyre2

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Description	P0A976
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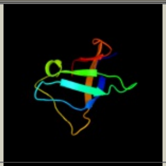
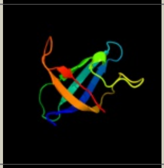
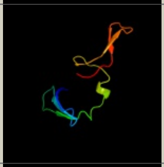
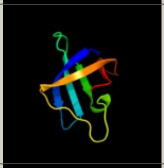
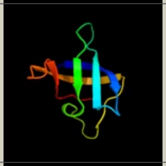
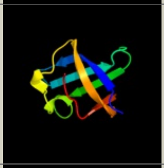
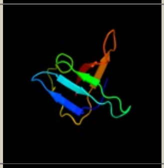
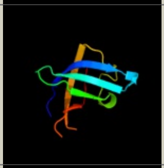
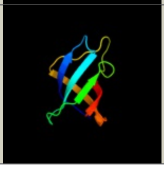
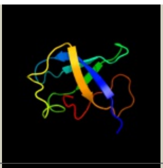
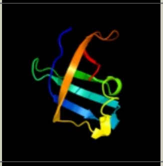
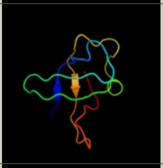
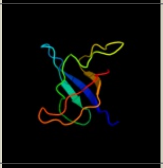
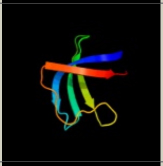
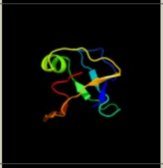
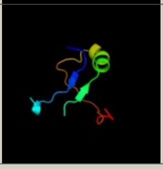
Unique Job ID	b4b4f39ee676617d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h95a_	Alignment		99.9	34	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
2	d1mjca_	Alignment		99.9	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
3	c3camB_	Alignment		99.9	40	**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
4	d2es2a1	Alignment		99.9	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
5	c2kcmA_	Alignment		99.9	29	**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.
6	c3a0jB_	Alignment		99.9	34	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
7	c2k5nA_	Alignment		99.9	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
8	d1g6pa_	Alignment		99.9	42	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	d1c9oa_	Alignment		99.8	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	c3aqqD_	Alignment		99.8	27	**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	28	**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	24	**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	d1wfqa_	Alignment		99.7	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2ytxA_	Alignment		99.7	26	**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	22	**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		99.5	45	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
17	c2ytvA_	Alignment		99.4	30	**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		97.5	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
19	c2ix1A_	Alignment		96.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
20	c2a8vA_	Alignment		96.0	18	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
21	d1a62a2	Alignment	not modelled	95.9	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	d1smxa_	Alignment	not modelled	93.9	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	c2vnuD_	Alignment	not modelled	91.2	21	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
24	d2ix0a1	Alignment	not modelled	91.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	c2cqoA_	Alignment	not modelled	89.0	21	**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
26	c1hh2P_	Alignment	not modelled	88.5	22	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
27	c2k52A_	Alignment	not modelled	88.3	13	**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
28	d1hh2p1	Alignment	not modelled	88.1	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						Fold:OB-fold

29	d1u0la1	Alignment	not modelled	86.7	18	**Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
30	c1zeqX_	Alignment	not modelled	85.1	22	**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
31	c1xpuB_	Alignment	not modelled	82.4	18	**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)
32	c3go5A_	Alignment	not modelled	78.2	10	**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
33	d1kl9a2	Alignment	not modelled	76.2	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
34	c2l55A_	Alignment	not modelled	73.8	20	**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
35	c1u0lB_	Alignment	not modelled	71.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
36	c2wp8J_	Alignment	not modelled	66.3	13	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
37	d2c35b1	Alignment	not modelled	66.1	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
38	d1y14b1	Alignment	not modelled	63.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c1l2fA_	Alignment	not modelled	61.2	19	**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
40	d1wi5a_	Alignment	not modelled	57.6	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	d2z0sa1	Alignment	not modelled	57.6	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c3l0oB_	Alignment	not modelled	55.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
43	c2oceA_	Alignment	not modelled	53.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
44	d2nn6h1	Alignment	not modelled	51.8	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
45	d3bzka4	Alignment	not modelled	49.5	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d2ba0a1	Alignment	not modelled	48.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	c2c4rL_	Alignment	not modelled	48.1	11	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
48	d2asba1	Alignment	not modelled	47.3	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
49	c3h0gS_	Alignment	not modelled	42.9	20	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
50	d1t9ha1	Alignment	not modelled	38.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	c2khiA_	Alignment	not modelled	37.5	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
52	c2asbA_	Alignment	not modelled	36.8	17	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
53	c2k4kA_	Alignment	not modelled	36.7	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
54	d1h9ma2	Alignment	not modelled	35.9	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
						PDB header:rna binding protein

55	c2xnqA_	Alignment	not modelled	34.4	25	**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
56	d2je6i1	Alignment	not modelled	32.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
57	c2khjA_	Alignment	not modelled	29.9	23	**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
58	d1go3e1	Alignment	not modelled	28.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
59	c1j6qA_	Alignment	not modelled	27.6	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
60	d1j6qa_	Alignment	not modelled	27.6	12	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
61	c2dhxA_	Alignment	not modelled	26.4	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
62	d1q46a2	Alignment	not modelled	25.0	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c2b8kG_	Alignment	not modelled	24.3	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
64	c1q46A_	Alignment	not modelled	21.3	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
65	c2c35F_	Alignment	not modelled	20.6	12	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
66	c2eqsA_	Alignment	not modelled	20.6	17	**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
67	d1h9ma1	Alignment	not modelled	19.4	13	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
68	c2opgB_	Alignment	not modelled	19.0	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 10th pdz domain of mpdz
69	d2vnud3	Alignment	not modelled	18.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
70	d2bs2b2	Alignment	not modelled	18.5	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
71	d1guta_	Alignment	not modelled	18.2	9	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
72	d1fr3a_	Alignment	not modelled	17.8	13	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
73	c1nt9G_	Alignment	not modelled	16.9	17	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide; **PDBTitle:** complete 12-subunit rna polymerase ii
74	c1go3E_	Alignment	not modelled	16.2	22	**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
75	d1wf1a_	Alignment	not modelled	15.7	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
76	d1kq1a_	Alignment	not modelled	15.3	27	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
77	c2dc2A_	Alignment	not modelled	14.8	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**golgi associated pdz and coiled-coil motif **PDBTitle:** solution structure of pdz domain
78	d1n7ea_	Alignment	not modelled	14.8	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
79	c2kviA_	Alignment	not modelled	14.5	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nuclear polyadenylated rna-binding protein 3; **PDBTitle:** structure of nab3 rrm
80	d1whxa_	Alignment	not modelled	14.5	6	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
						Fold:PDZ domain-like

81	d1qaua_	Alignment	not modelled	14.1	15	**Superfamily:**PDZ domain-like **Family:**PDZ domain
82	d1hk9a_	Alignment	not modelled	14.0	36	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
83	c3qhsD_	Alignment	not modelled	13.9	36	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of full-length hfq from escherichia coli
84	c3hsbB_	Alignment	not modelled	13.7	45	**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
85	c2g18K_	Alignment	not modelled	13.3	2	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**phycocyanobilin:ferredoxin oxidoreductase; **PDBTitle:** crystal structure of nostoc sp. 7120 phycocyanobilin:ferredoxin2 oxidoreductase (pcya) apoprotein
86	c2kjdA_	Alignment	not modelled	13.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchange regulatory cofactor nhe- **PDBTitle:** solution structure of extended pdz2 domain from nherf1 (150-2 270)
87	c1yz6A_	Alignment	not modelled	13.1	20	**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
88	c1kq1W_	Alignment	not modelled	13.1	27	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
89	c1h9mB_	Alignment	not modelled	13.0	17	**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
90	d2o14a1	Alignment	not modelled	13.0	36	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**YxiM N-terminal domain-like
91	c2qt7B_	Alignment	not modelled	13.0	19	**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
92	c3ggeA_	Alignment	not modelled	12.8	14	**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
93	c2z0sA_	Alignment	not modelled	12.6	8	**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
94	c2pmzE_	Alignment	not modelled	12.0	22	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
95	c1q8kA_	Alignment	not modelled	11.5	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
96	c3psiA_	Alignment	not modelled	11.5	14	**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)
97	d1rgwa_	Alignment	not modelled	11.5	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
98	c2iwnA_	Alignment	not modelled	11.3	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
99	d1be9a_	Alignment	not modelled	11.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain