Phyre2

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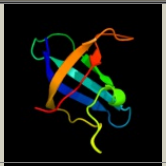
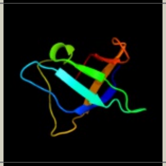
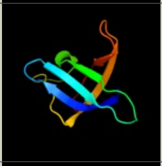
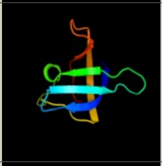
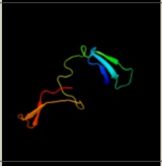
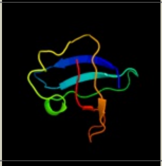
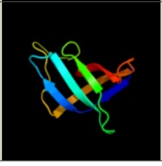
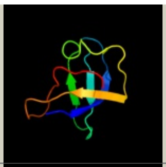
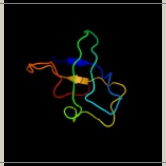
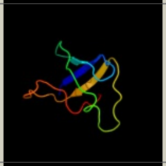
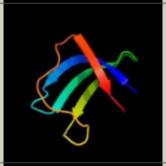
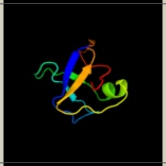
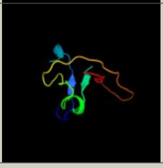
Description	P0A9Y6
Date	Wed Jan 25 15:20:20 GMT 2012
Unique Job ID	17c758006835dc6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mjca_	Alignment		99.9	69	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
2	d1h95a_	Alignment		99.9	47	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
3	d2es2a1	Alignment		99.9	66	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
4	d1c9oa_	Alignment		99.9	61	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
5	c3a0jB_	Alignment		99.9	56	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
6	c3camB_	Alignment		99.9	59	**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
7	d1g6pa_	Alignment		99.9	62	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
8	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
9	c2kcmA_	Alignment		99.8	31	**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	39	**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	46	**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	29	**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	c2ytxA_	Alignment		99.7	35	**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)
14	d1wfqa_	Alignment		99.7	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
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	60	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
17	c2ytvA_	Alignment		99.5	33	**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	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
19	c2ix1A_	Alignment		97.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
20	d1a62a2	Alignment		96.3	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	c2a8vA_	Alignment	not modelled	96.2	28	**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	95.9	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	d2ix0a1	Alignment	not modelled	95.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
24	c2k52A_	Alignment	not modelled	92.4	14	**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	d1kl9a2	Alignment	not modelled	92.0	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c2vnuD_	Alignment	not modelled	90.5	18	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
27	d1y14b1	Alignment	not modelled	86.6	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	c3go5A_	Alignment	not modelled	86.4	14	**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
29	c1xpuB_	Alignment	not modelled	85.3	34	**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	84.5	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	c2cqoA_	Alignment	not modelled	84.0	16	**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
32	c2l55A_	Alignment	not modelled	83.4	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
33	d1hh2p1	Alignment	not modelled	82.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
34	d2c35b1	Alignment	not modelled	82.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	d2z0sa1	Alignment	not modelled	81.7	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
36	c1hh2P_	Alignment	not modelled	81.6	15	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
37	c1l2fA_	Alignment	not modelled	80.3	15	**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
38	c2c4rL_	Alignment	not modelled	78.8	24	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
39	d1wi5a_	Alignment	not modelled	78.6	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
40	c1u0lB_	Alignment	not modelled	77.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
41	c1zeqX_	Alignment	not modelled	76.0	12	**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
42	d2nn6h1	Alignment	not modelled	74.1	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
43	c2khiA_	Alignment	not modelled	70.6	23	**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
44	c2oceA_	Alignment	not modelled	70.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
45	d2ba0a1	Alignment	not modelled	68.7	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d2je6i1	Alignment	not modelled	68.5	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	c3l0oB_	Alignment	not modelled	63.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
48	c2khjA_	Alignment	not modelled	62.8	16	**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	60.0	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
50	c1q46A_	Alignment	not modelled	59.8	11	**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	c2wp8J_	Alignment	not modelled	58.6	19	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
52	d1t9ha1	Alignment	not modelled	58.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
53	d3bzka4	Alignment	not modelled	56.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
54	c3h0gS_	Alignment	not modelled	54.8	27	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe

55	d1go3e1	Alignment	not modelled	54.2	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
56	c1yz6A_	Alignment	not modelled	47.0	19	**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
57	c2ahoB_	Alignment	not modelled	45.8	20	**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	c2k4kA_	Alignment	not modelled	45.3	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
59	c2eqsA_	Alignment	not modelled	43.1	19	**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
60	d2ahob2	Alignment	not modelled	42.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
61	d2asba1	Alignment	not modelled	40.5	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
62	c2c35F_	Alignment	not modelled	40.5	18	**PDB header:**polymerase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii
63	c2z0sA_	Alignment	not modelled	39.0	9	**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
64	c1nt9G_	Alignment	not modelled	38.5	20	**PDB header:**transcription, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide; **PDBTitle:** complete 12-subunit rna polymerase ii
65	d1j6qa_	Alignment	not modelled	37.5	21	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
66	c1j6qA_	Alignment	not modelled	37.5	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
67	c2xnqA_	Alignment	not modelled	33.8	32	**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
68	c3psiA_	Alignment	not modelled	33.7	13	**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)
69	c2je6I_	Alignment	not modelled	32.7	17	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
70	c2asbA_	Alignment	not modelled	32.1	11	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
71	c2dhxA_	Alignment	not modelled	31.3	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
72	c1q8kA_	Alignment	not modelled	30.8	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
73	c2i38A_	Alignment	not modelled	29.4	29	**PDB header:**rna binding protein/chimera **Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g- **PDBTitle:** solution structure of the rrm of srp20
74	c2yv5A_	Alignment	not modelled	26.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
75	c2b8kG_	Alignment	not modelled	26.6	20	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
76	c2pmzE_	Alignment	not modelled	25.4	22	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
77	c2qt7B_	Alignment	not modelled	23.5	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
78	d1tp5a1	Alignment	not modelled	23.1	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
						PDB header:signaling protein **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase,

79	c3soeA_	Alignment	not modelled	23.0	19	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)
80	d1sroa_	Alignment	not modelled	23.0	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
81	d1h9ma2	Alignment	not modelled	22.1	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
82	c2gu1A_	Alignment	not modelled	20.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
83	c2ba0A_	Alignment	not modelled	20.5	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
84	c2dc2A_	Alignment	not modelled	19.6	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**golgi associated pdz and coiled-coil motif **PDBTitle:** solution structure of pdz domain
85	c3bpuA_	Alignment	not modelled	18.7	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
86	d1ueqa_	Alignment	not modelled	18.0	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
87	c1go3E_	Alignment	not modelled	17.5	33	**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
88	c2kviA_	Alignment	not modelled	17.1	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nuclear polyadenylated rna-binding protein 3; **PDBTitle:** structure of nab3 rrm
89	d2f3ga_	Alignment	not modelled	17.0	36	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
90	d2vpaa1	Alignment	not modelled	16.8	14	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
91	d1ujva_	Alignment	not modelled	16.3	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	d1be9a_	Alignment	not modelled	16.3	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
93	d1wf1a_	Alignment	not modelled	16.1	26	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
94	d1glaf_	Alignment	not modelled	15.8	36	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
95	d2vgna1	Alignment	not modelled	15.0	20	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
96	c2kjdA_	Alignment	not modelled	15.0	12	**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)
97	c2i04B_	Alignment	not modelled	14.8	22	**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
98	d2vnud3	Alignment	not modelled	14.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
99	c1kq1W_	Alignment	not modelled	14.2	17	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq