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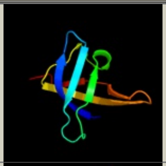
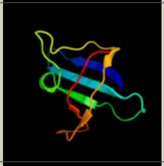
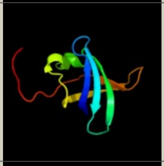
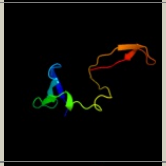
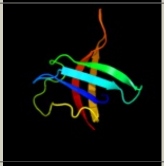
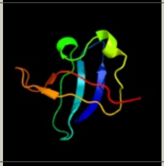
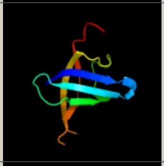
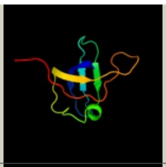
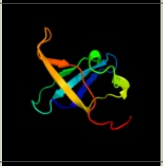
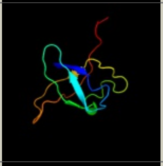
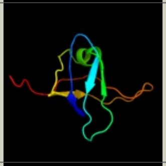
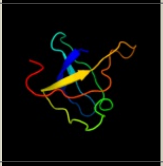
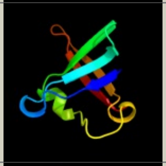
Description	P0A968
Date	Thu Jan 5 11:09:29 GMT 2012
Unique Job ID	be120deaa52293b1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a0jB_	Alignment		99.9	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
2	d1c9oa_	Alignment		99.9	52	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
3	d2es2a1	Alignment		99.9	45	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
4	d1h95a_	Alignment		99.9	40	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
5	d1mjca_	Alignment		99.9	49	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
6	c2k5nA_	Alignment		99.9	28	**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
7	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
8	d1g6pa_	Alignment		99.9	49	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	c2kcmA_	Alignment		99.8	36	**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	31	**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	31	**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	23	**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	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2ytxA_	Alignment		99.6	24	**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	c2ytvA_	Alignment		99.6	26	**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)
16	c1x65A_	Alignment		99.6	28	**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)
17	c2bh8B_	Alignment		99.5	38	**PDB header:**transcription **Chain:** B: **PDB Molecule:**1b11; **PDBTitle:** combinatorial protein 1b11
18	d2ix0a2	Alignment		97.0	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
19	d1a62a2	Alignment		96.7	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
20	c2ix1A_	Alignment		96.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exoribonuclease 2; **PDBTitle:** rnase ii d209n mutant
21	c2a8vA_	Alignment	not modelled	96.4	24	**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	94.1	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	c3go5A_	Alignment	not modelled	92.1	15	**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
24	c2vnuD_	Alignment	not modelled	89.0	13	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp44; **PDBTitle:** crystal structure of sc rrp44
25	c2k52A_	Alignment	not modelled	87.0	12	**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
26	c1xpuB_	Alignment	not modelled	87.0	24	**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)
27	d2ix0a1	Alignment	not modelled	85.8	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						Fold:OB-fold

28	d1t9ha1	Alignment	not modelled	82.2	20	**Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
29	d1u0la1	Alignment	not modelled	81.6	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
30	d1y14b1	Alignment	not modelled	80.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	c1u0lB_	Alignment	not modelled	75.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
32	c1hh2P_	Alignment	not modelled	73.0	17	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
33	c2l55A_	Alignment	not modelled	72.6	24	**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
34	d1hh2p1	Alignment	not modelled	70.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	c2cqoA_	Alignment	not modelled	69.7	14	**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	c2c4rL_	Alignment	not modelled	69.6	18	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
37	d1kl9a2	Alignment	not modelled	66.7	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
38	d2c35b1	Alignment	not modelled	66.2	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c1zeqX_	Alignment	not modelled	66.2	16	**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
40	c1j6qA_	Alignment	not modelled	64.9	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
41	d1j6qa_	Alignment	not modelled	64.9	19	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
42	c2wp8J_	Alignment	not modelled	62.5	11	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3; **PDBTitle:** yeast rrp44 nuclease
43	c1l2fA_	Alignment	not modelled	61.7	17	**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
44	c3l0oB_	Alignment	not modelled	61.5	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
45	d2nn6h1	Alignment	not modelled	58.4	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	d2z0sa1	Alignment	not modelled	58.2	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	c2yv5A_	Alignment	not modelled	49.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
48	d2ba0a1	Alignment	not modelled	47.0	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
49	c2eqsA_	Alignment	not modelled	43.0	21	**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
50	c2xnqA_	Alignment	not modelled	41.5	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
51	c2oceA_	Alignment	not modelled	40.0	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
52	c2qt7B_	Alignment	not modelled	39.5	18	**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
53	d2je6i1	Alignment	not modelled	37.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						PDB header:rna binding protein

54	c2dhxA_	Alignment	not modelled	35.5	16	**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
55	c1t9hA_	Alignment	not modelled	35.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
56	d3bzka4	Alignment	not modelled	35.1	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
57	d1tp5a1	Alignment	not modelled	34.7	31	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
58	d1be9a_	Alignment	not modelled	34.0	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
59	c2gu1A_	Alignment	not modelled	33.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
60	d1sr3a_	Alignment	not modelled	33.0	20	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
61	d1wi5a_	Alignment	not modelled	32.7	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
62	c2khiA_	Alignment	not modelled	31.3	18	**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
63	c2k4kA_	Alignment	not modelled	31.0	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**general stress protein 13; **PDBTitle:** solution structure of gsp13 from bacillus subtilis
64	d1go3e1	Alignment	not modelled	26.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
65	c3h0gS_	Alignment	not modelled	26.3	21	**PDB header:**transcription **Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
66	c2dc2A_	Alignment	not modelled	26.2	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**golgi associated pdz and coiled-coil motif **PDBTitle:** solution structure of pdz domain
67	d1glaf_	Alignment	not modelled	25.8	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
68	c2khjA_	Alignment	not modelled	24.6	21	**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
69	c3ggeA_	Alignment	not modelled	24.5	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
70	d2vpaa1	Alignment	not modelled	24.4	11	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
71	d1qaua_	Alignment	not modelled	23.9	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
72	c3bpuA_	Alignment	not modelled	22.8	28	**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
73	d2f3ga_	Alignment	not modelled	22.8	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
74	d1q46a2	Alignment	not modelled	22.6	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
75	c2kjdA_	Alignment	not modelled	22.1	17	**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)
76	c2c35F_	Alignment	not modelled	21.6	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
77	c3soeA_	Alignment	not modelled	21.5	21	**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)
78	c2b8kG_	Alignment	not modelled	20.3	17	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda **PDBTitle:** 12-subunit rna polymerase ii
79	d2vnud3	Alignment	not modelled	20.0	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins

						Family: Cold shock DNA-binding domain-like
80	c2kviA_	Alignment	not modelled	19.9	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nuclear polyadenylated rna-binding protein 3; **PDBTitle:** structure of nab3 rrm
81	c2kctA_	Alignment	not modelled	19.5	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccme; **PDBTitle:** solution nmr structure of the ob-fold domain of heme2 chaperone ccme from desulfovibrio vulgaris. northeast3 structural genomics target dvr115g.
82	d1wf1a_	Alignment	not modelled	19.2	26	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
83	d1wi2a_	Alignment	not modelled	19.0	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	d1ueqa_	Alignment	not modelled	18.7	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	c2q3gA_	Alignment	not modelled	18.2	19	**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
86	c2pmzE_	Alignment	not modelled	17.5	30	**PDB header:**translation, transferase **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
87	c2ba0A_	Alignment	not modelled	17.3	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
88	c1go3E_	Alignment	not modelled	17.3	29	**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
89	d2gpra_	Alignment	not modelled	16.7	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
90	d2fura1	Alignment	not modelled	15.8	25	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
91	c2q9vA_	Alignment	not modelled	15.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the c890s mutant of the 4th pdz domain of human2 membrane associated guanylate kinase
92	c2je6I_	Alignment	not modelled	15.5	15	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
93	c2vwrA_	Alignment	not modelled	15.5	9	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**ligand of numb protein x 2; **PDBTitle:** crystal structure of the second pdz domain of numb-binding2 protein 2
94	c1q46A_	Alignment	not modelled	15.5	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
95	d1gpra_	Alignment	not modelled	14.9	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
96	d1ujva_	Alignment	not modelled	14.9	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	d1rgwa_	Alignment	not modelled	14.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
98	c2pkuA_	Alignment	not modelled	14.7	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** solution structure of pick1 pdz in complex with the2 carboxyl tail peptide of glur2
99	c2iwoA_	Alignment	not modelled	14.6	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 12th pdz domain of multiple pdz domain protein mpdz (casp2 target)