




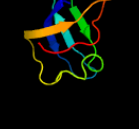





Phyre2

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 Description RVBD3648c_cspA_4088507_4088710
 Date Fri Aug 9 18:20:33 BST 2019
 Unique Job ID 1f2412cb54a6794f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xv9A_	Alignment		99.9	57	PDB header: rna binding protein Chain: A; PDB Molecule: cold-shock dna-binding domain family protein; PDBTitle: solution structure of cold shock protein from colwellia2 psychrerythraea
2	c5o6fA_	Alignment		99.9	84	PDB header: dna binding protein Chain: A; PDB Molecule: cold-shock protein; PDBTitle: nmr structure of cold shock protein a from corynebacterium2 pseudotuberculosis
3	d1c9oa_	Alignment		99.9	62	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
4	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
5	d2es2a1	Alignment		99.9	60	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
6	d1mjca_	Alignment		99.9	60	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
7	c3camB_	Alignment		99.9	47	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	c2lssA_	Alignment		99.9	39	PDB header: rna binding protein, dna binding protein Chain: A; PDB Molecule: cold shock-like protein; PDBTitle: solution structure of the r. rickettsii cold shock-like protein
9	d1h95a_	Alignment		99.9	43	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
10	c4a4iA_	Alignment		99.9	45	PDB header: rna binding protein Chain: A; PDB Molecule: protein lin-28 homolog b; PDBTitle: crystal structure of the human lin28b cold shock domain
11	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 protein eca15802 from erwinia carotovora, northeast structural genomics consortium3 target ewr156a

12	c2mqhA_	Alignment		99.9	55	PDB header: dna binding protein Chain: A: PDB Molecule: nucleic acid binding protein; PDBTitle: solution structure of the chlamydomonas reinhardtii nab1 cold shock2 domain, csd1
13	d1g6pa_	Alignment		99.9	53	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
14	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.
15	c3aaqD_	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
16	c3trzE_	Alignment		99.8	42	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
17	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)
18	c2ytxA_	Alignment		99.7	38	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)
19	d1wfga_	Alignment		99.7	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
20	c1x65A_	Alignment		99.6	27	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)
21	c2yvtA_	Alignment	not modelled	99.5	29	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)
22	c2bh8B_	Alignment	not modelled	99.5	48	PDB header: transcription Chain: B: PDB Molecule: 1b11; PDBTitle: combinatorial protein 1b11
23	d2ix0a2	Alignment	not modelled	96.7	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	d1a62a2	Alignment	not modelled	96.3	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
25	c2a8vA_	Alignment	not modelled	96.3	23	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
26	c2ix1A_	Alignment	not modelled	96.1	23	PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant
27	d1smxa_	Alignment	not modelled	93.6	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
28	c3l0oA_	Alignment	not modelled	89.8	22	PDB header: hydrolase Chain: A: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding

29	c3go5A	Alignment	not modelled	89.7	10	domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
30	c4pmwB	Alignment	not modelled	89.7	15	PDB header: hydrolase/rna Chain: B: PDB Molecule: dis3-like exonuclease 2; PDBTitle: structure of mouse dis3l2 in complex with oligou rna substrate
31	c2k52A	Alignment	not modelled	87.9	8	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
32	c6qh2A	Alignment	not modelled	87.1	24	PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of2 exosomal polynucleotide phosphorylase at 298k compiled using the3 comand method
33	c1xpuB	Alignment	not modelled	87.0	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)
34	d2ix0a1	Alignment	not modelled	86.6	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
35	c4aimA	Alignment	not modelled	86.4	23	PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna e2 recognition peptide
36	c1zeqX	Alignment	not modelled	85.1	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
37	c2vnuD	Alignment	not modelled	84.8	22	PDB header: hydrolase/rna Chain: D: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: crystal structure of sc rrp44
38	d1t9ha1	Alignment	not modelled	83.4	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
39	c5xguB	Alignment	not modelled	82.7	31	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease r; PDBTitle: escherichia coli. rnae r
40	c4oxpA	Alignment	not modelled	82.0	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease e; PDBTitle: x-ray crystal structure of the s1 and 5'-sensor domains of rnae e2 from caulobacter crescentus
41	d1u0la1	Alignment	not modelled	81.8	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
42	c2I55A	Alignment	not modelled	80.0	17	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
43	d1y14b1	Alignment	not modelled	76.5	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	c2cqoA	Alignment	not modelled	75.1	18	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
45	c1u0lB	Alignment	not modelled	73.4	11	PDB header: hydrolase Chain: B: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima
46	d2c35b1	Alignment	not modelled	72.8	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
47	c3l0oB	Alignment	not modelled	70.0	23	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
48	d1hh2p1	Alignment	not modelled	68.8	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
49	d1kl9a2	Alignment	not modelled	67.0	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
50	c1hh2P	Alignment	not modelled	63.3	14	PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a; PDBTitle: crystal structure of nusa from thermotoga maritima
51	c5lm7A	Alignment	not modelled	62.6	10	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex
52	c3sluB	Alignment	not modelled	61.6	9	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
53	c5x50G	Alignment	not modelled	59.8	24	PDB header: transferase Chain: G: PDB Molecule: rna polymerase ii subunit; PDBTitle: rna polymerase ii from komagataella pastoris (type-2 crystal)
54	c2c4rL	Alignment	not modelled	56.3	19	PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e;

						PDBTitle: catalytic domain of e. coli rnase e
55	c2yv5A_	Alignment	not modelled	55.9	9	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
56	d2z0sa1	Alignment	not modelled	53.9	7	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
57	c2oceA_	Alignment	not modelled	53.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
58	c1t9hA_	Alignment	not modelled	53.2	21	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
59	d2nn6h1	Alignment	not modelled	49.6	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
60	c2mf1A_	Alignment	not modelled	48.7	20	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 2 of e. coli ribosomal protein s1
61	d2ba0a1	Alignment	not modelled	48.6	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
62	c1l2fA_	Alignment	not modelled	47.9	14	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
63	d1wi5a_	Alignment	not modelled	46.3	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
64	c1j6qA_	Alignment	not modelled	42.3	17	PDB header: chaperone Chain: A: PDB Molecule: cytochrome c maturation protein e; PDBTitle: solution structure and characterization of the heme2 chaperone ccme
65	d1j6qa_	Alignment	not modelled	42.3	17	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
66	c2wp8J_	Alignment	not modelled	42.0	17	PDB header: hydrolase Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease
67	c3uz0D_	Alignment	not modelled	41.9	21	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiih and spoiiq complex
68	d1tp5a1	Alignment	not modelled	38.9	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
69	c5c0wJ_	Alignment	not modelled	36.4	17	PDB header: hydrolase/rna Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to single-2 stranded rna substrates
70	c2khiA_	Alignment	not modelled	35.5	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
71	c2xnqA_	Alignment	not modelled	34.5	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
72	d2je6i1	Alignment	not modelled	32.9	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
73	d3bzka4	Alignment	not modelled	32.1	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
74	c2dhxA_	Alignment	not modelled	31.3	16	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
75	c4nnkA_	Alignment	not modelled	31.3	14	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
76	c2k4kA_	Alignment	not modelled	29.2	20	PDB header: rna binding protein Chain: A: PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis
77	c2m0tA_	Alignment	not modelled	28.3	16	PDB header: protein binding Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf1; PDBTitle: structural characterization of the extended pdz1 domain from nherf1
78	c4rnzA_	Alignment	not modelled	26.7	24	PDB header: hydrolase Chain: A: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd3 from the hexagonal crystal
79	c2gu1A_	Alignment	not modelled	26.4	18	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
80	c3h0gS_	Alignment	not modelled	26.0	28	PDB header: transcription Chain: S: PDB Molecule: dna-directed rna polymerase ii subunit rpb7;

						PDBTitle: rna polymerase ii from schizosaccharomyces pombe
81	c2dc2A_	Alignment	not modelled	24.8	14	PDB header: structural protein Chain: A: PDB Molecule: golgi associated pdz and coiled-coil motif PDBTitle: solution structure of pdz domain
82	c3bpuA_	Alignment	not modelled	24.4	22	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
83	c2i38A_	Alignment	not modelled	24.2	27	PDB header: rna binding protein/chimera Chain: A: PDB Molecule: fusion protein consists of immunoglobulin g-binding protein PDBTitle: solution structure of the rrm of srp20
84	c4wjiA_	Alignment	not modelled	24.0	50	PDB header: transcription Chain: A: PDB Molecule: splicing factor, proline- and glutamine-rich; PDBTitle: human splicing factor, construct 1
85	c2kjdA_	Alignment	not modelled	23.5	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)
86	c2qt7B_	Alignment	not modelled	23.3	23	PDB header: hydrolase Chain: B: PDB Molecule: receptor-type tyrosine-protein phosphatase-like n; PDBTitle: crystallographic structure of the mature ectodomain of the human2 receptor-type protein-tyrosine phosphatase ia-2 at 1.30 angstroms
87	c5n7gA_	Alignment	not modelled	23.2	20	PDB header: signaling protein Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: magi-1 complexed with a synthetic prsk1 peptide
88	c2pmzE_	Alignment	not modelled	23.1	24	PDB header: translation, transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
89	c3ggeA_	Alignment	not modelled	22.4	19	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
90	c2c35F_	Alignment	not modelled	21.5	15	PDB header: transferase Chain: F: PDB Molecule: dna-directed rna polymerase ii 19 kda polypeptide; PDBTitle: subunits rpb4 and rpb7 of human rna polymerase ii
91	d1be9a_	Alignment	not modelled	21.4	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
92	d1qaua_	Alignment	not modelled	20.2	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
93	c2b8kG_	Alignment	not modelled	20.2	23	PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda polypeptide; PDBTitle: 12-subunit rna polymerase ii
94	c2khjA_	Alignment	not modelled	19.7	18	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
95	d1ueqa_	Alignment	not modelled	19.3	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
96	d1rgwa_	Alignment	not modelled	19.0	11	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
97	c3zh6B_	Alignment	not modelled	19.0	20	PDB header: cell adhesion Chain: B: PDB Molecule: protein e; PDBTitle: the structure of haemophilus influenzae se_met form of protein e
98	c3fm3B_	Alignment	not modelled	17.8	24	PDB header: hydrolase Chain: B: PDB Molecule: methionine aminopeptidase 2; PDBTitle: crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
99	c2i04B_	Alignment	not modelled	17.8	20	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