
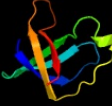









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3462c_(infA)_3880611_3880832
Date	Fri Aug 9 18:20:13 BST 2019
Unique Job ID	4642ac4f795dc5f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6c00A_	Alignment		100.0	68	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor 1 from clostridium2 difficile
2	c4ql5A_	Alignment		100.0	68	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4
3	d1ah9a_	Alignment		100.0	69	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
4	c2nchA_	Alignment		100.0	49	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi
5	c3i4oA_	Alignment		100.0	100	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
6	d1hr0w_	Alignment		100.0	66	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
7	d1jt8a_	Alignment		99.9	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
8	c4bpp0_	Alignment		99.9	22	PDB header: ribosome Chain: 0: PDB Molecule: translation initiation factor eif-1a family protein; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
9	d1d7qa_	Alignment		99.9	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
10	c3j81i_	Alignment		99.9	24	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
11	c2oqkA_	Alignment		99.9	33	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a

12	c4mnoA	Alignment		99.8	33	PDB header: translation Chain: A; PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
13	c2dgyA	Alignment		99.7	21	PDB header: translation Chain: A; PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
14	d1u0la1	Alignment		97.8	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
15	d1t9ha1	Alignment		97.4	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
16	c1u0lB	Alignment		97.1	33	PDB header: hydrolase Chain: B; PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima
17	c2yv5A	Alignment		96.9	24	PDB header: hydrolase Chain: A; PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
18	c5uz4Z	Alignment		96.3	23	PDB header: ribosome/hydrolase Chain: Z; PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
19	c6h4dA	Alignment		96.1	23	PDB header: rna binding protein Chain: A; PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: crystal structure of rsga from pseudomonas aeruginosa
20	c2rcnA	Alignment		96.0	24	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.
21	c1t9ha	Alignment	not modelled	95.4	21	PDB header: hydrolase Chain: A; PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
22	c4a2iV	Alignment	not modelled	94.8	23	PDB header: ribosome/hydrolase Chain: V; PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
23	c4aimA	Alignment	not modelled	93.5	23	PDB header: transferase/peptide Chain: A; PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnae2 recognition peptide
24	c3fp9E	Alignment	not modelled	92.3	14	PDB header: hydrolase Chain: E; PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
25	c1q46A	Alignment	not modelled	90.3	19	PDB header: translation Chain: A; PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
26	c2k52A	Alignment	not modelled	89.7	17	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
27	d1k19a2	Alignment	not modelled	89.4	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
28	c5zwwA	Alignment	not modelled	88.6	13	PDB header: gene regulation Chain: A; PDB Molecule: agenet domain-containing protein; PDBTitle: crystal structure of arabidopsis thaliana agdp1 agd34

29	c6qh2A	Alignment	not modelled	88.5	25	PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of 2' exosomal polynucleotide phosphorylase at 298k compiled using the3 comand method
30	c5xguB	Alignment	not modelled	88.4	17	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease r; PDBTitle: escherichia coli. rnase r
31	c1zn1L	Alignment	not modelled	88.0	23	PDB header: biosynthetic/structural protein/rna Chain: L: PDB Molecule: 30s ribosomal protein s12; PDBTitle: coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
32	c5zwxB	Alignment	not modelled	87.4	16	PDB header: gene regulation Chain: B: PDB Molecule: duf724 domain-containing protein 6-like; PDBTitle: crystal structure of raphanus sativus agdp1 agd12 in complex with an2 h3k9me2 peptide
33	d2uubl1	Alignment	not modelled	86.4	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
34	c1xnil	Alignment	not modelled	86.2	14	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
35	d1y14b1	Alignment	not modelled	84.7	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
36	c3j20N	Alignment	not modelled	83.0	37	PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal protein s12p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
37	c3m9bK	Alignment	not modelled	82.8	11	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
38	c4nnkA	Alignment	not modelled	82.6	31	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: structural basis for targeting the ribosomal protein s1 of 2 mycobacterium tuberculosis by pyrazinamide
39	c3j6vL	Alignment	not modelled	82.4	23	PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
40	c2xzmL	Alignment	not modelled	82.3	27	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s12; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
41	c1ssfA	Alignment	not modelled	81.2	14	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
42	c2oceA	Alignment	not modelled	80.1	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
43	c5x50G	Alignment	not modelled	79.5	14	PDB header: transferase Chain: G: PDB Molecule: rna polymerase ii subunit; PDBTitle: rna polymerase ii from komagataella pastoris (type-2 crystal)
44	c3u5gX	Alignment	not modelled	79.4	30	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
45	c2r7fA	Alignment	not modelled	79.3	17	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease ii family protein; PDBTitle: crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
46	c1s1hL	Alignment	not modelled	79.0	30	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s23; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
47	d1i94I	Alignment	not modelled	78.9	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
48	c5xyiX	Alignment	not modelled	78.1	33	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
49	c3zeyS	Alignment	not modelled	78.0	30	PDB header: ribosome Chain: S: PDB Molecule: 40s ribosomal protein s23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
50	d2qall1	Alignment	not modelled	77.8	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
51	c4dapA	Alignment	not modelled	77.5	15	PDB header: dna binding protein Chain: A: PDB Molecule: sugar fermentation stimulation protein a; PDBTitle: the structure of escherichia coli sfsa
52	c2k4kA	Alignment	not modelled	73.5	22	PDB header: rna binding protein Chain: A: PDB Molecule: general stress protein 13; PDBTitle: solution structure of gsp13 from bacillus subtilis
						PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2

53	c1kl9A_	Alignment	not modelled	71.9	18	subunit 1; PDBTitle: crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha
54	d1g2914	Alignment	not modelled	71.8	14	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
55	d1go3e1	Alignment	not modelled	71.6	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
56	c1go3E_	Alignment	not modelled	71.5	28	PDB header: transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: structure of an archeal homolog of the eukaryotic rna polymerase ii2 rpb4/rpb7 complex
57	c2pmzE_	Alignment	not modelled	71.4	27	PDB header: translation, transferase Chain: E: PDB Molecule: dna-directed rna polymerase subunit e; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
58	c2mflA_	Alignment	not modelled	71.4	17	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 2 of e. coli ribosomal protein s1
59	c2c35F_	Alignment	not modelled	70.9	16	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
60	c5x8r8_	Alignment	not modelled	69.0	31	PDB header: ribosome Chain: 8: PDB Molecule: 30s ribosomal protein s1, chloroplastic; PDBTitle: structure of the 30s small subunit of chloroplast ribosome from2 spinach
61	c2ix1A_	Alignment	not modelled	67.8	13	PDB header: hydrolase Chain: A: PDB Molecule: exoribonuclease 2; PDBTitle: rnase ii d209n mutant
62	d2g3ra1	Alignment	not modelled	67.5	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
63	c3go5A_	Alignment	not modelled	66.4	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
64	c1yz6A_	Alignment	not modelled	66.4	24	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
65	d2ahob2	Alignment	not modelled	66.2	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
66	c2khjA_	Alignment	not modelled	66.1	19	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
67	c2khiA_	Alignment	not modelled	65.2	27	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
68	c2b8kG_	Alignment	not modelled	64.7	17	PDB header: transferase Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kda polypeptide; PDBTitle: 12-subunit rna polymerase ii
69	d1q46a2	Alignment	not modelled	64.5	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
70	c2wp8L_	Alignment	not modelled	63.6	17	PDB header: hydrolase Chain: J: PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease
71	c2zkql_	Alignment	not modelled	63.3	38	PDB header: ribosomal protein/rna Chain: L: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
72	c1h9mB_	Alignment	not modelled	62.9	13	PDB header: binding protein Chain: B: PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. peg-grown form with4 molybdate bound
73	d1guta_	Alignment	not modelled	62.5	16	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
74	c2equA_	Alignment	not modelled	61.6	10	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
75	c1q8kA_	Alignment	not modelled	59.4	19	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2 PDBTitle: solution structure of alpha subunit of human eif2
76	c5c0wL_	Alignment	not modelled	59.3	15	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
77	d1smxa_	Alignment	not modelled	58.9	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
						PDB header: transcription, transferase

78	c1nt9G_	Alignment	not modelled	58.5	17	Chain: G: PDB Molecule: dna-directed rna polymerase ii 19 kd polypeptide; PDBTitle: complete 12-subunit rna polymerase ii
79	d2z0sa1	Alignment	not modelled	55.8	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
80	c4xi7A_	Alignment	not modelled	54.3	12	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
81	c3p8dB_	Alignment	not modelled	53.9	8	PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
82	d1h9ma1	Alignment	not modelled	53.8	20	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
83	d1b12a_	Alignment	not modelled	53.2	45	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: Type 1 signal peptidase
84	d1sroa_	Alignment	not modelled	52.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
85	c1h9sA_	Alignment	not modelled	50.6	12	PDB header: transcription regulator Chain: A: PDB Molecule: molybdenum transport protein mode; PDBTitle: molybdate bound complex of dimop domain of mode from e.coli
86	c5ohoB_	Alignment	not modelled	50.3	24	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kowx-kow4 domain of human dsif
87	c4ytiB_	Alignment	not modelled	50.0	20	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
88	c3psiA_	Alignment	not modelled	49.7	8	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)
89	c5oikZ_	Alignment	not modelled	49.2	23	PDB header: transcription Chain: Z: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of an rna polymerase ii-dsif transcription elongation2 complex
90	c3qiiA_	Alignment	not modelled	49.2	8	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
91	c2wg6L_	Alignment	not modelled	49.1	18	PDB header: transcription,hydrolase Chain: L: PDB Molecule: general control protein gcn4, proteasome-activating PDBTitle: proteasome-activating nucleotidase (pan) n-domain (57-134) from2 archaeoglobus fulgidus fused to gcn4, p61a mutant
92	d2nn6g1	Alignment	not modelled	47.6	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
93	c2ahoB_	Alignment	not modelled	47.5	14	PDB header: translation Chain: B: PDB Molecule: translation initiation factor 2 alpha subunit; PDBTitle: structure of the archaeal initiation factor eif2 alpha-gamma2 heterodimer from sulfolobus solfataricus complexed with gdpnp
94	c4pmwB_	Alignment	not modelled	46.9	26	PDB header: hydrolase/rna Chain: B: PDB Molecule: dis3-like exonuclease 2; PDBTitle: structure of mouse dis3l2 in complex with oligou rna substrate
95	c4davA_	Alignment	not modelled	46.8	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: sugar fermentation stimulation protein homolog; PDBTitle: the structure of pyrococcus furiosus sfsa in complex with dna
96	d1h9ma2	Alignment	not modelled	46.3	11	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
97	c2pqaB_	Alignment	not modelled	45.8	19	PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
98	c4n31A_	Alignment	not modelled	44.5	14	PDB header: cell adhesion Chain: A: PDB Molecule: sipa; PDBTitle: structure and activity of streptococcus pyogenes sipa: a signal2 peptidase homologue essential for pilus polymerisation
99	c2l66B_	Alignment	not modelled	43.6	35	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, aabr family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-aabr2 superfamily from archaea.
100	c2ldmA_	Alignment	not modelled	43.5	7	PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
101	c2mfiA_	Alignment	not modelled	43.4	20	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: domain 1 of e. coli ribosomal protein s1
102	c2qqsB_	Alignment	not modelled	43.0	10	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
103	c2eqsA_	Alignment	not modelled	42.3	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
104	c5lm7A_	Alignment	not modelled	41.4	21	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex
105	c4qmgD_	Alignment	not modelled	40.0	23	PDB header: transcription Chain: D: PDB Molecule: staphylococcal nuclease domain-containing protein 1; PDBTitle: the structure of mtdh-snd1 complex reveals novel cancer-promoting2 interactions
106	d1v43a2	Alignment	not modelled	38.8	21	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
107	d2pi2e1	Alignment	not modelled	38.5	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
108	c6et9H_	Alignment	not modelled	38.1	33	PDB header: transferase Chain: H: PDB Molecule: pfam duf35; PDBTitle: structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
109	c4gopX_	Alignment	not modelled	37.4	9	PDB header: dna binding protein/dna Chain: X: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
110	c2z0sA_	Alignment	not modelled	37.4	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
111	c4k8wA_	Alignment	not modelled	37.0	14	PDB header: cell adhesion Chain: A: PDB Molecule: lepa; PDBTitle: an arm-swapped dimer of the s. pyogenes pilin specific assembly factor2 sipa
112	c6d6rK_	Alignment	not modelled	36.7	16	PDB header: hydrolase Chain: K: PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
113	c2nn6G_	Alignment	not modelled	36.5	11	PDB header: hydrolase/transferase Chain: G: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
114	c2ba0A_	Alignment	not modelled	35.7	10	PDB header: rna binding protein Chain: A: PDB Molecule: archaeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core
115	c2fhdA_	Alignment	not modelled	34.9	14	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9/crb2; PDBTitle: crystal structure of crb2 tandem tudor domains
116	d1h9ra1	Alignment	not modelled	34.3	12	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
117	d2gnra1	Alignment	not modelled	33.7	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
118	c2nn6I_	Alignment	not modelled	32.3	15	PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
119	d1e32a1	Alignment	not modelled	32.1	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
120	d3d31a1	Alignment	not modelled	32.0	15	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain