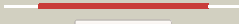
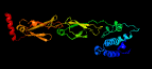


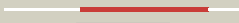
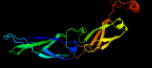

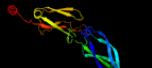

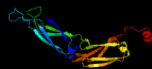

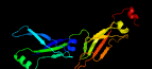



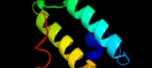

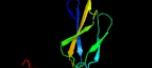

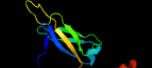

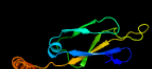

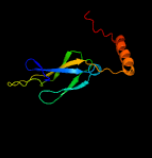

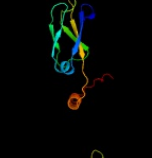



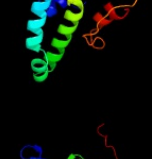
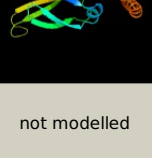


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0352_(dna)1_422452_423639
 Date Tue Jul 23 14:50:42 BST 2019
 Unique Job ID a248571bbb909aca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j80B_	 Alignment		100.0	37	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein dnaj 2; PDBTitle: thermus thermophilus dnaj
2	c1nltA_	 Alignment		100.0	32	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial protein import protein mas5; PDBTitle: the crystal structure of hsp40 ydj1
3	c3lz8A_	 Alignment		100.0	40	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
4	c2q2gA_	 Alignment		100.0	24	PDB header: chaperone Chain: A: PDB Molecule: heat shock 40 kda protein, putative (fragment); PDBTitle: crystal structure of dimerization domain of hsp40 from2 cryptosporidium parvum, cgd2_1800
5	c2qldA_	 Alignment		100.0	25	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 1; PDBTitle: human hsp40 hdj1
6	c2b26A_	 Alignment		100.0	29	PDB header: chaperone/protein transport Chain: A: PDB Molecule: sis1 protein; PDBTitle: the crystal structure of the protein complex of yeast hsp402 sis1 and hsp70 ssa1
7	c3i38D_	 Alignment		99.9	36	PDB header: chaperone Chain: D: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
8	c3apaB_	 Alignment		99.9	42	PDB header: oxidoreductase Chain: B: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of j-trx1 fragment of erdj5
9	c3i38K_	 Alignment		99.9	36	PDB header: chaperone Chain: K: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
10	c3i38G_	 Alignment		99.9	36	PDB header: chaperone Chain: G: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
11	c3i38A_	 Alignment		99.9	36	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578

12	c3i38J_	Alignment		99.9	37	PDB header: chaperone Chain: J: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
13	c3i38F_	Alignment		99.9	37	PDB header: chaperone Chain: F: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
14	c3i38B_	Alignment		99.9	37	PDB header: chaperone Chain: B: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
15	c3i38H_	Alignment		99.9	37	PDB header: chaperone Chain: H: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
16	c3i38L_	Alignment		99.9	38	PDB header: chaperone Chain: L: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
17	c3i38E_	Alignment		99.9	38	PDB header: chaperone Chain: E: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
18	c3i38C_	Alignment		99.9	38	PDB header: chaperone Chain: C: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
19	c4j7zC_	Alignment		99.9	45	PDB header: chaperone Chain: C: PDB Molecule: chaperone protein dnaj j- and g/f-domains PDBTitle: thermus thermophilus dnaj j- and g/f-domains
20	c3i38I_	Alignment		99.9	38	PDB header: chaperone Chain: I: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
21	c2ctqA_	Alignment	not modelled	99.9	28	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 12; PDBTitle: solution structure of j-domain from human dnaj subfamily c2 member 12
22	c2i6iA_	Alignment	not modelled	99.9	29	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
23	c2yuaA_	Alignment	not modelled	99.9	34	PDB header: chaperone Chain: A: PDB Molecule: williams-beuren syndrome chromosome region 18 PDBTitle: solution structure of the dnaj domain from human williams-2 beuren syndrome chromosome region 18 protein
24	c1fpoA_	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein hscb; PDBTitle: hsc20 (hscb), a j-type co-chaperone from e. coli
25	d1c3ga2	Alignment	not modelled	99.9	37	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
26	d1hdja_	Alignment	not modelled	99.9	49	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
27	c3hhoA_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb homolog; PDBTitle: chaperone hscb from vibrio cholerae
28	c2ctwA_	Alignment	not modelled	99.9	42	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 5; PDBTitle: solution structure of j-domain from mouse dnaj subfamily c2 member 5 PDB header: chaperone

29	c3bovA	Alignment	not modelled	99.9	18	Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
30	c2dmxA	Alignment	not modelled	99.8	49	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 8; PDBTitle: solution structure of the j domain of dnaj homolog2 subfamily b member 8
31	c2ctrA	Alignment	not modelled	99.8	39	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 9; PDBTitle: solution structure of j-domain from human dnaj subfamily b2 member 9
32	c5vsoA	Alignment	not modelled	99.8	50	PDB header: chaperone Chain: A: PDB Molecule: yeast dnaj protein 1; PDBTitle: nmr structure of ydj1 j-domain, a cytosolic hsp40 from <i>saccharomyces2 cerevisiae</i>
33	d1xbla	Alignment	not modelled	99.8	40	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
34	c1xaoA	Alignment	not modelled	99.8	21	PDB header: chaperone Chain: A: PDB Molecule: mitochondrial protein import protein mas5; PDBTitle: hsp40-ydj1 dimerization domain
35	c2cugA	Alignment	not modelled	99.8	43	PDB header: chaperone Chain: A: PDB Molecule: mkiaa0962 protein; PDBTitle: solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
36	c2kqxA	Alignment	not modelled	99.8	47	PDB header: chaperone binding protein Chain: A: PDB Molecule: curved dna-binding protein; PDBTitle: nmr structure of the j-domain (residues 2-72) in the2 <i>escherichia coli</i> cbpa
37	c2o37A	Alignment	not modelled	99.8	41	PDB header: chaperone Chain: A: PDB Molecule: protein sis1; PDBTitle: j-domain of sis1 protein, hsp40 co-chaperone from <i>saccharomyces2 cerevisiae</i> .
38	c2ctpA	Alignment	not modelled	99.8	49	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 12; PDBTitle: solution structure of j-domain from human dnaj subfamily b2 member 12
39	c5y88T	Alignment	not modelled	99.8	36	PDB header: splicing Chain: T: PDB Molecule: pre-mrna-splicing factor cwc23; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from <i>s.cerevisiae</i> at 3.5 angstrom
40	c2dn9A	Alignment	not modelled	99.8	47	PDB header: apoptosis, chaperone Chain: A: PDB Molecule: dnaj homolog subfamily a member 3; PDBTitle: solution structure of j-domain from the dnaj homolog, human2 tid1 protein
41	d1iura	Alignment	not modelled	99.8	26	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
42	c2lqwA	Alignment	not modelled	99.8	46	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 2; PDBTitle: solution structure of the j domain of hsj1a
43	d1gh6a	Alignment	not modelled	99.8	18	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
44	c1bq0A	Alignment	not modelled	99.8	40	PDB header: chaperone Chain: A: PDB Molecule: dnaj; PDBTitle: j-domain (residues 1-77) of the <i>escherichia coli</i> n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
45	c2qsaA	Alignment	not modelled	99.8	30	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog dnj-2; PDBTitle: crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 <i>c.elegans</i> .
46	d1wjza	Alignment	not modelled	99.8	28	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
47	c2ochA	Alignment	not modelled	99.8	51	PDB header: chaperone Chain: A: PDB Molecule: hypothetical protein dnj-12; PDBTitle: j-domain of dnj-12 from <i>caenorhabditis elegans</i>
48	c2ys8A	Alignment	not modelled	99.8	44	PDB header: protein binding Chain: A: PDB Molecule: rab-related gtp-binding protein rabj; PDBTitle: solution structure of the dnaj-like domain from human ras-2 associated protein rap1
49	c2pf4E	Alignment	not modelled	99.8	21	PDB header: hydrolase regulator/viral protein Chain: E: PDB Molecule: small t antigen; PDBTitle: crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha subunit
50	d1nlta2	Alignment	not modelled	99.7	28	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
51	c2cttA	Alignment	not modelled	99.7	37	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily a member 3; PDBTitle: solution structure of zinc finger domain from human dnaj2 subfamily a member 3
52	d1fpoa1	Alignment	not modelled	99.7	24	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
53	d1fafa	Alignment	not modelled	99.7	11	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
54	d1c3ga1	Alignment	not modelled	99.6	24	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
						Fold: Long alpha-hairpin

55	d1n4ca_	Alignment	not modelled	99.6	26	Superfamily: Chaperone J-domain Family: Chaperone J-domain
56	d1nz6a_	Alignment	not modelled	99.6	26	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
57	c2guzO_	Alignment	not modelled	99.5	24	PDB header: chaperone, protein transport Chain: O: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: structure of the tim14-tim16 complex of the mitochondrial protein2 import motor
58	c2y4tA_	Alignment	not modelled	99.4	40	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
59	c3apoA_	Alignment	not modelled	99.4	50	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of full-length erdj5
60	d1exka_	Alignment	not modelled	99.3	44	Fold: Dnaj/Hsp40 cysteine-rich domain Superfamily: Dnaj/Hsp40 cysteine-rich domain Family: Dnaj/Hsp40 cysteine-rich domain
61	d1nlta1_	Alignment	not modelled	99.3	36	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
62	c3ag7A_	Alignment	not modelled	99.3	18	PDB header: plant protein Chain: A: PDB Molecule: putative uncharacterized protein f9e10.5; PDBTitle: an auxilin-like j-domain containing protein, jac1 j-domain
63	c2guzD_	Alignment	not modelled	99.2	15	PDB header: chaperone, protein transport Chain: D: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: structure of the tim14-tim16 complex of the mitochondrial protein2 import motor
64	d1nlta3_	Alignment	not modelled	98.9	34	Fold: Dnaj/Hsp40 cysteine-rich domain Superfamily: Dnaj/Hsp40 cysteine-rich domain Family: Dnaj/Hsp40 cysteine-rich domain
65	c3uo2A_	Alignment	not modelled	98.8	21	PDB header: chaperone Chain: A: PDB Molecule: j-type co-chaperone jac1, mitochondrial; PDBTitle: jac1 co-chaperone from saccharomyces cerevisiae
66	c6ekbA_	Alignment	not modelled	97.8	34	PDB header: chaperone Chain: A: PDB Molecule: dnaj/hsp40 cysteine-rich domain superfamily protein; PDBTitle: crystal structure of the bsd2 homolog of arabidopsis thaliana
67	c6nd1A_	Alignment	not modelled	95.2	5	PDB header: protein transport Chain: A: PDB Molecule: protein translocation protein sec63; PDBTitle: cryoem structure of the sec complex from yeast
68	c4wb7B_	Alignment	not modelled	95.1	56	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: dnaj homolog subfamily b member 1,camp-dependent protein PDBTitle: crystal structure of a chimeric fusion of human dnaj (hsp40) and camp-2 dependent protein kinase a (catalytic alpha subunit)
69	c2k3vA_	Alignment	not modelled	95.0	22	PDB header: electron transport Chain: A: PDB Molecule: tetraheme cytochrome c-type; PDBTitle: solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
70	c3ld0Q_	Alignment	not modelled	92.4	39	PDB header: gene regulation Chain: Q: PDB Molecule: inhibitor of trap, regulated by t-box (trp) sequence rtpa; PDBTitle: crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
71	c4mo1B_	Alignment	not modelled	91.0	48	PDB header: transcription regulator Chain: B: PDB Molecule: antitermination protein q; PDBTitle: crystal structure of antitermination protein q from bacteriophage2 lambda. northeast structural genomics consortium target or18a.
72	d2fiya1_	Alignment	not modelled	80.8	15	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
73	c5z5mB_	Alignment	not modelled	79.2	27	PDB header: lyase Chain: B: PDB Molecule: predicted protein; PDBTitle: crystal structure of (s)-allantoin synthase
74	c2bx9J_	Alignment	not modelled	74.1	36	PDB header: transcription regulation Chain: J: PDB Molecule: tryptophan rna-binding attenuator protein-inhibitory PDBTitle: crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
75	c3pihA_	Alignment	not modelled	73.7	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
76	d2q37a1_	Alignment	not modelled	57.0	13	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
77	c2q37A_	Alignment	not modelled	57.0	13	PDB header: plant protein, lyase Chain: A: PDB Molecule: ohcu decarboxylase; PDBTitle: crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
78	c4kssC_	Alignment	not modelled	55.3	30	PDB header: protein transport Chain: C: PDB Molecule: type ii secretion system protein e, hemolysin-coregulated PDBTitle: crystal structure of vibrio cholerae atpase gspse hexamer
79	c4ptsB_	Alignment	not modelled	52.3	29	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a glutathione transferase from gordonia2 bronchialis dsm 43247, target efi-507405

80	c5ijlA	Alignment	not modelled	52.2	20	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
81	c3m1gC	Alignment	not modelled	51.0	29	PDB header: transferase Chain: C: PDB Molecule: putative glutathione s-transferase; PDBTitle: the structure of a putative glutathione s-transferase from <i>Corynebacterium glutamicum</i>
82	d1ug2a	Alignment	not modelled	50.0	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
83	c4m5dB	Alignment	not modelled	46.5	14	PDB header: rna binding protein Chain: B: PDB Molecule: ribosomal rna-processing protein 7; PDBTitle: crystal structure of the utp22 and rrp7 complex from <i>Saccharomyces cerevisiae</i>
84	c2qkdA	Alignment	not modelled	45.9	23	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
85	d2o8ia1	Alignment	not modelled	45.4	27	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
86	c6gbhA	Alignment	not modelled	41.7	21	PDB header: cell adhesion Chain: A: PDB Molecule: hopq; PDBTitle: helicobacter pylori adhesin hopq type ii bound to the n-terminal2 domain of human ceacam1
87	c6gzfB	Alignment	not modelled	41.4	32	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: xi class gst from <i>Natrialba magadii</i>
88	d3saka	Alignment	not modelled	41.0	33	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
89	c6hmsB	Alignment	not modelled	40.6	21	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from <i>Pyrococcus abyssi</i> in complex with2 dna
90	c4phtC	Alignment	not modelled	40.4	23	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspl from the2 <i>Vibrio vulnificus</i> type ii secretion system
91	c5lp2B	Alignment	not modelled	40.1	29	PDB header: cell adhesion Chain: B: PDB Molecule: hopq; PDBTitle: adhesin domain of the type 1 hopq of <i>Helicobacter pylori</i> strain g27
92	c4ht4A	Alignment	not modelled	40.0	11	PDB header: hydrolase/dna Chain: A: PDB Molecule: nickning enzyme; PDBTitle: molecular basis of vancomycin resistance transfer in <i>Staphylococcus aureus</i>
93	d2zjrq1	Alignment	not modelled	37.8	30	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L23p
94	c3dkqB	Alignment	not modelled	37.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: pkhd-type hydroxylase sbal_3634; PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from <i>Shewanella baltica</i> os155 at 2.26 a resolution
95	c2co9A	Alignment	not modelled	37.4	24	PDB header: transcription Chain: A: PDB Molecule: thymus high mobility group box protein tox; PDBTitle: solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
96	c2ww9K	Alignment	not modelled	35.7	41	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l25; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
97	c3j21T	Alignment	not modelled	35.4	35	PDB header: ribosome Chain: T: PDB Molecule: 50s ribosomal protein l23p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
98	d1vqos1	Alignment	not modelled	34.8	29	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L23p
99	c6g6gH	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: H: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
100	c6g6gB	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: B: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
101	c6g6gD	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: D: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
102	c6g6gF	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: F: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
103	c6g6gC	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: C: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
104	c6g6gJ	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: J: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
105	c6g6gK	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: K: PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi

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106	c6g6gE_	Alignment	not modelled	34.7	26	PDB header: de novo protein Chain: E; PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
107	c5a48B_	Alignment	not modelled	34.7	50	PDB header: protein binding Chain: B; PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-240) of drosophila2 oskar in p65
108	c1wz6A_	Alignment	not modelled	34.5	31	PDB header: transcription Chain: A; PDB Molecule: hmg-box transcription factor bbx; PDBTitle: solution structure of the hmg_box domain of murine bobby2 sox homolog
109	d2o70a1	Alignment	not modelled	33.8	17	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
110	c3c4rC_	Alignment	not modelled	33.6	36	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein encoded by2 cryptic prophage
111	c6g6gL_	Alignment	not modelled	33.6	25	PDB header: de novo protein Chain: L; PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
112	c6g6gG_	Alignment	not modelled	33.6	25	PDB header: de novo protein Chain: G; PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
113	c6g6gA_	Alignment	not modelled	33.6	25	PDB header: de novo protein Chain: A; PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
114	c6g6gI_	Alignment	not modelled	33.6	25	PDB header: de novo protein Chain: I; PDB Molecule: cc-type2-fi; PDBTitle: crystal structure of a parallel six-helix coiled coil cc-type2-fi
115	c2cs1A_	Alignment	not modelled	31.9	17	PDB header: dna binding protein Chain: A; PDB Molecule: pms1 protein homolog 1; PDBTitle: solution structure of the hmg domain of human dna mismatch2 repair protein
116	c2ns6A_	Alignment	not modelled	31.4	21	PDB header: hydrolase Chain: A; PDB Molecule: mobilization protein a; PDBTitle: crystal structure of the minimal relaxase domain of moba from plasmid2 r1162
117	c4x3xA_	Alignment	not modelled	30.9	58	PDB header: signaling protein Chain: A; PDB Molecule: activity-regulated cytoskeleton-associated protein; PDBTitle: the crystal structure of arc c-lobe
118	c4b6aX_	Alignment	not modelled	29.6	41	PDB header: ribosome Chain: X; PDB Molecule: 60s ribosomal protein l25; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
119	d1cf7a_	Alignment	not modelled	29.4	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
120	c2go54_	Alignment	not modelled	29.3	35	PDB header: translation/rna Chain: 4; PDB Molecule: ribosomal protein l23; PDBTitle: structure of signal recognition particle receptor (sr) in2 complex with signal recognition particle (srp) and3 ribosome nascent chain complex