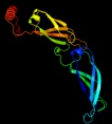
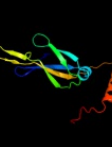
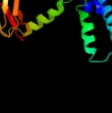


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lz8A_	 Alignment		100.0	82	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
2	c2q2gA_	 Alignment		100.0	23	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
3	c2qldA_	 Alignment		100.0	23	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 1; PDBTitle: human hsp40 hdj1
4	c1nlta_	 Alignment		100.0	22	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial protein import protein mas5; PDBTitle: the crystal structure of hsp40 ydj1
5	c2b26A_	 Alignment		100.0	22	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
6	c3i38D_	 Alignment		100.0	80	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
7	c3i38K_	 Alignment		99.9	79	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
8	c3i38G_	 Alignment		99.9	80	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
9	c3i38A_	 Alignment		99.9	80	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
10	c3i38B_	 Alignment		99.9	79	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
11	c3i38J_	 Alignment		99.9	79	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

12	c3i38F_	Alignment		99.9	80	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
13	c3apqB_	Alignment		99.9	30	PDB header: oxidoreductase Chain: B: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of j-trx1 fragment of erdj5
14	c3i38H_	Alignment		99.9	79	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
15	c3i38E_	Alignment		99.9	81	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
16	c3i38C_	Alignment		99.9	81	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
17	c3i38L_	Alignment		99.9	81	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
18	c3i38I_	Alignment		99.9	78	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
19	c2i6lA_	Alignment		99.9	21	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
20	c2kqxA_	Alignment		99.9	100	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 escherichia coli cbpa
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	d1hdja_	Alignment	not modelled	99.9	45	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
23	c1fpoA_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein hscb; PDBTitle: hsc20 (hscb), a j-type co-chaperone from e. coli
24	c2dmxA_	Alignment	not modelled	99.9	35	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
25	c3bvoA_	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
26	c2yuaA_	Alignment	not modelled	99.9	28	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
27	c3hhoA_	Alignment	not modelled	99.9	29	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb homolog; PDBTitle: chaperone hscb from vibrio cholerae
28	c2ctrA_	Alignment	not modelled	99.9	42	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

29	c2ctwA	Alignment	not modelled	99.9	33	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
30	d1c3ga2	Alignment	not modelled	99.8	26	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
31	c2lqwA	Alignment	not modelled	99.8	45	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 2; PDBTitle: solution structure of the j domain of hsj1a
32	d1xbla	Alignment	not modelled	99.8	49	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
33	c2cugA	Alignment	not modelled	99.8	39	PDB header: chaperone Chain: A: PDB Molecule: mkiaa0962 protein; PDBTitle: solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
34	c2ctpA	Alignment	not modelled	99.8	39	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
35	c2o37A	Alignment	not modelled	99.8	33	PDB header: chaperone Chain: A: PDB Molecule: protein sis1; PDBTitle: j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
36	c2qsaA	Alignment	not modelled	99.8	39	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog dnj-2; PDBTitle: crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 c.elegans.
37	c2dn9A	Alignment	not modelled	99.8	45	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
38	c1xaoA	Alignment	not modelled	99.8	18	PDB header: chaperone Chain: A: PDB Molecule: mitochondrial protein import protein mas5; PDBTitle: hsp40-ydj1 dimerization domain
39	d1gh6a	Alignment	not modelled	99.8	14	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
40	c1bq0A	Alignment	not modelled	99.8	47	PDB header: chaperone Chain: A: PDB Molecule: dnaj; PDBTitle: j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
41	c2ys8A	Alignment	not modelled	99.8	34	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
42	c2ochA	Alignment	not modelled	99.8	45	PDB header: chaperone Chain: A: PDB Molecule: hypothetical protein dnj-12; PDBTitle: j-domain of dnj-12 from caenorhabditis elegans
43	d1iura	Alignment	not modelled	99.8	26	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
44	d1wjza	Alignment	not modelled	99.8	28	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
45	c2pf4E	Alignment	not modelled	99.7	15	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
46	d1nlt2	Alignment	not modelled	99.7	24	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
47	d1fpoa1	Alignment	not modelled	99.7	31	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
48	d1fafa	Alignment	not modelled	99.7	15	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
49	c2guzO	Alignment	not modelled	99.6	22	PDB header: chaperone, protein transport Chain: O: PDB Molecule: mitochondrial import inner membrane translocase PDBTitle: structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
50	d1nz6a	Alignment	not modelled	99.5	23	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
51	d1n4ca	Alignment	not modelled	99.5	21	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
52	c2y4tA	Alignment	not modelled	99.4	50	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
53	d1c3ga1	Alignment	not modelled	99.4	21	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
54	c3apoA	Alignment	not modelled	99.4	43	PDB header: oxidoreductase Chain: A: PDB Molecule: dnaj homolog subfamily c member 10; PDBTitle: crystal structure of full-length erdj5
						PDB header: chaperone, protein transport

55	c2guzD_	Alignment	not modelled	99.3	18	Chain: D: PDB Molecule: mitochondrial import inner membrane translocase PDBTitle: structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
56	c3ag7A_	Alignment	not modelled	99.2	20	PDB header: plant protein Chain: A: PDB Molecule: putative uncharacterized protein f9e10.5; PDBTitle: an auxilin-like j-domain containing protein, jac1 j-domain
57	d1nltal	Alignment	not modelled	99.2	20	Fold: HSP40/DnaJ peptide-binding domain Superfamily: HSP40/DnaJ peptide-binding domain Family: HSP40/DnaJ peptide-binding domain
58	c3uo2A_	Alignment	not modelled	98.8	24	PDB header: chaperone Chain: A: PDB Molecule: j-type co-chaperone jac1, mitochondrial; PDBTitle: jac1 co-chaperone from saccharomyces cerevisiae
59	c3epvB_	Alignment	not modelled	60.3	18	PDB header: metal binding protein Chain: B: PDB Molecule: nickel and cobalt resistance protein cnrr; PDBTitle: x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
60	c2cttA_	Alignment	not modelled	54.0	6	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
61	d2q37a1	Alignment	not modelled	49.6	21	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
62	c2q37A_	Alignment	not modelled	49.6	21	PDB header: plant protein, lyase Chain: A: PDB Molecule: ohcu decarboxylase; PDBTitle: crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
63	d2o8ia1	Alignment	not modelled	49.1	31	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
64	d2o70a1	Alignment	not modelled	45.6	10	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
65	d1ug2a_	Alignment	not modelled	44.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
66	d1nlt3	Alignment	not modelled	40.5	9	Fold: DnaJ/Hsp40 cysteine-rich domain Superfamily: DnaJ/Hsp40 cysteine-rich domain Family: DnaJ/Hsp40 cysteine-rich domain
67	c2cs1A_	Alignment	not modelled	40.1	21	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
68	c3m1gC_	Alignment	not modelled	37.8	28	PDB header: transferase Chain: C: PDB Molecule: putative glutathione s-transferase; PDBTitle: the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
69	c2bl0B_	Alignment	not modelled	37.6	16	PDB header: muscle protein Chain: B: PDB Molecule: myosin regulatory light chain; PDBTitle: physarum polycephalum myosin ii regulatory domain
70	c2jucA_	Alignment	not modelled	37.0	12	PDB header: unknown function Chain: A: PDB Molecule: pre-mrna-splicing factor urn1; PDBTitle: urn1 ff domain yeast
71	c3orjA_	Alignment	not modelled	35.5	22	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar-binding protein; PDBTitle: crystal structure of a sugar-binding protein (bacova_04391) from2 bacteroides ovatus at 2.16 a resolution
72	d3saka_	Alignment	not modelled	35.1	42	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
73	c2crjA_	Alignment	not modelled	34.3	21	PDB header: gene regulation Chain: A: PDB Molecule: swi/snf-related matrix-associated actin- PDBTitle: solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
74	c2co9A_	Alignment	not modelled	33.6	19	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
75	c3nv4A_	Alignment	not modelled	33.5	17	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin 9 short isoform variant; PDBTitle: crystal structure of human galectin-9 c-terminal crd in complex with2 sialyllactose
76	c1wz6A_	Alignment	not modelled	33.1	24	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
77	d1lexka_	Alignment	not modelled	32.7	13	Fold: DnaJ/Hsp40 cysteine-rich domain Superfamily: DnaJ/Hsp40 cysteine-rich domain Family: DnaJ/Hsp40 cysteine-rich domain
78	c2ww9K_	Alignment	not modelled	31.9	29	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l25; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
79	c3najA_	Alignment	not modelled	31.7	11	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin-8; PDBTitle: crystal structure of a protease-resistant mutant form of human2 galectin-8
80	c1u5tA_	Alignment	not modelled	30.4	11	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
						Fold: Ribosomal proteins S24e, L23 and L15e

81	d1vqos1	Alignment	not modelled	29.1	12	Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L23p
82	d1h8ba	Alignment	not modelled	28.3	28	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
83	c2zgtB	Alignment	not modelled	28.3	7	PDB header: hydrolase Chain: B: PDB Molecule: anti-tumor lectin; PDBTitle: crystal structure of agrocybe aegerita lectin aal mutant2 f93g
84	c2e6oA	Alignment	not modelled	27.2	19	PDB header: transcription, cell cycle Chain: A: PDB Molecule: hmg box-containing protein 1; PDBTitle: solution structure of the hmg box domain from human hmg-box2 transcription factor 1
85	c3fn2A	Alignment	not modelled	26.5	25	PDB header: transferase Chain: A: PDB Molecule: putative sensor histidine kinase domain; PDBTitle: crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
86	c2go54	Alignment	not modelled	25.3	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
87	c2d6lX	Alignment	not modelled	24.5	14	PDB header: sugar binding protein Chain: X: PDB Molecule: lectin, galactose binding, soluble 9; PDBTitle: crystal structure of mouse galectin-9 n-terminal crd2 (crystal form 2)
88	d1cf7a	Alignment	not modelled	24.5	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
89	d2zjrql	Alignment	not modelled	24.4	29	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L23p
90	d1wgfa	Alignment	not modelled	24.3	21	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
91	c2zkrs	Alignment	not modelled	24.1	29	PDB header: ribosomal protein/rna Chain: S: PDB Molecule: rna expansion segment es39 part ii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
92	c3dkqB	Alignment	not modelled	23.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: pkhd-type hydroxylase sbal_3634; PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
93	c3u2bC	Alignment	not modelled	23.5	19	PDB header: transcription/dna Chain: C: PDB Molecule: transcription factor sox-4; PDBTitle: structure of the sox4 hmg domain bound to dna
94	d2gala	Alignment	not modelled	22.8	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
95	c2j11D	Alignment	not modelled	22.8	42	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant y327s t329g q331g
96	d2cqna1	Alignment	not modelled	22.5	16	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
97	c2rq5A	Alignment	not modelled	22.3	20	PDB header: transcription Chain: A: PDB Molecule: protein jumonji; PDBTitle: solution structure of the at-rich interaction domain (arid)2 of jumonji/jarid2
98	d1aiea	Alignment	not modelled	22.1	42	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
99	c4a17R	Alignment	not modelled	21.7	29	PDB header: ribosome Chain: R: PDB Molecule: rpl23a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
100	c2j10B	Alignment	not modelled	21.5	42	PDB header: transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
101	c2j10A	Alignment	not modelled	21.5	42	PDB header: transcription Chain: A: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
102	c2j10D	Alignment	not modelled	21.5	42	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
103	d1i32a2	Alignment	not modelled	20.4	14	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like