Phyre^2

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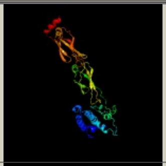
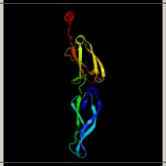
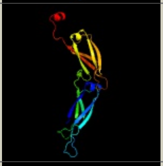
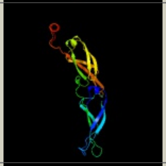
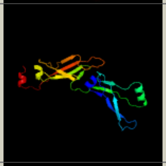
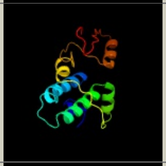
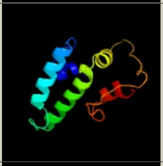
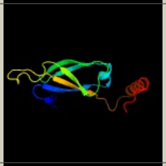
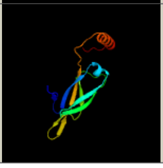
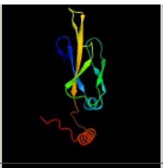
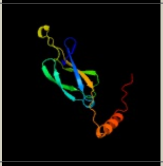
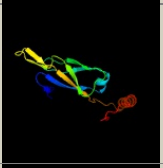
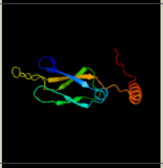
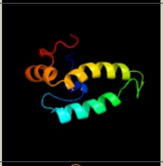
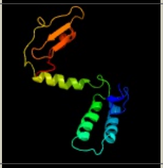
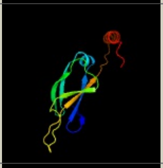
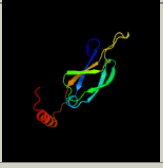
Description	RVBD2373c_(dnaJ2)_2652849_2653997
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	dc0d263a40bff06a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j80B_	Alignment		100.0	44	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein dnaj 2; **PDBTitle:** thermus thermophilus dnaj
2	c1nltA_	Alignment		100.0	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
3	c2q2gA_	Alignment		100.0	22	**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
4	c2qldA_	Alignment		100.0	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 1; **PDBTitle:** human hsp40 hdj1
5	c3lz8A_	Alignment		100.0	31	**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.
6	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
7	c3apqB_	Alignment		99.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
8	c4j7zC_	Alignment		99.9	48	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**chaperone protein dnaj 2; **PDBTitle:** thermus thermophilus dnaj j- and g/f-domains
9	c3i38D_	Alignment		99.9	29	**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
10	c3i38G_	Alignment		99.9	29	**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	29	**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	c3i38K_	Alignment		99.9	29	**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
13	c3i38F_	Alignment		99.9	29	**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	29	**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	c3i38J_	Alignment		99.9	30	**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
16	d1hdja_	Alignment		99.9	49	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
17	c2l6lA_	Alignment		99.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
18	c3i38C_	Alignment		99.9	30	**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	c3i38E_	Alignment		99.9	30	**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
20	c3i38H_	Alignment		99.9	29	**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
21	c3i38L_	Alignment	not modelled	99.9	30	**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
22	d1c3ga2	Alignment	not modelled	99.9	27	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
23	c3i38I_	Alignment	not modelled	99.8	31	**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
24	c2ctrA_	Alignment	not modelled	99.8	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 menber 9
25	c2ctqA_	Alignment	not modelled	99.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 menber 12
26	c1fpoA_	Alignment	not modelled	99.8	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hscb; **PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli
27	c2yuaA_	Alignment	not modelled	99.8	36	**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
28	c1xaoA_	Alignment	not modelled	99.8	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** hsp40-ydj1 dimerization domain

29	c2dmxA_	Alignment	not modelled	99.8	51	**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
30	c2ctwA_	Alignment	not modelled	99.8	46	**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
31	c3bvoA_	Alignment	not modelled	99.8	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
32	c3hhoA_	Alignment	not modelled	99.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog; **PDBTitle:** chaperone hscb from vibrio cholerae
33	c5vsoA_	Alignment	not modelled	99.8	54	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**yeast dnaj protein 1; **PDBTitle:** nmr structure of ydj1 j-domain, a cytosolic hsp40 from saccharomyces2 cerevisiae
34	c2kqxA_	Alignment	not modelled	99.8	44	**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
35	c2cugA_	Alignment	not modelled	99.8	51	**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	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 menber 12
37	d1xbla_	Alignment	not modelled	99.8	50	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
38	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 saccharomyces2 cerevisiae.
39	c5y88T_	Alignment	not modelled	99.8	34	**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 s.cerevisiae at 3.5 angstrom
40	c2lgwA_	Alignment	not modelled	99.8	53	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2; **PDBTitle:** solution structure of the j domain of hsj1a
41	d1gh6a_	Alignment	not modelled	99.8	26	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
42	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
43	c2qsaA_	Alignment	not modelled	99.8	31	**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.
44	c1bq0A_	Alignment	not modelled	99.8	49	**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
45	c2ys8A_	Alignment	not modelled	99.8	35	**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
46	d1iura_	Alignment	not modelled	99.8	21	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
47	c2ochA_	Alignment	not modelled	99.8	58	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
48	d1wjza_	Alignment	not modelled	99.8	32	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
49	d1nlta2	Alignment	not modelled	99.8	25	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
50	c2pf4E_	Alignment	not modelled	99.7	27	**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
51	d1fpoa1	Alignment	not modelled	99.7	26	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
52	d1fafa_	Alignment	not modelled	99.6	20	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
53	d1nz6a_	Alignment	not modelled	99.5	19	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
54	d1n4ca_	Alignment	not modelled	99.5	20	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
						PDB header:chaperone, protein transport **Chain:** O: **PDB Molecule:**mitochondrial import inner membrane

55	c2guzO_	Alignment	not modelled	99.5	19	translocase subunit **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial protein2 import motor
56	c2cttA_	Alignment	not modelled	99.4	33	**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 menber 3
57	c2y4tA_	Alignment	not modelled	99.4	53	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
58	d1c3ga1	Alignment	not modelled	99.3	18	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
59	c3apoA_	Alignment	not modelled	99.3	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
60	c3ag7A_	Alignment	not modelled	99.2	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5; **PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain
61	c2guzD_	Alignment	not modelled	99.1	12	**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
62	d1nlta1	Alignment	not modelled	99.1	19	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
63	d1exka_	Alignment	not modelled	98.8	42	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
64	c3uo2A_	Alignment	not modelled	98.7	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**j-type co-chaperone jac1, mitochondrial; **PDBTitle:** jac1 co-chaperone from saccharomyces cerevisiae
65	d1nlta3	Alignment	not modelled	98.7	25	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
66	c6ekbA_	Alignment	not modelled	97.0	33	**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	c4wb7B_	Alignment	not modelled	95.8	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)
68	c2k3vA_	Alignment	not modelled	94.1	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**tetraheme cytochrome c-type; **PDBTitle:** solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
69	c6nd1A_	Alignment	not modelled	93.9	3	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocation protein sec63; **PDBTitle:** cryoem structure of the sec complex from yeast
70	c3ld0Q_	Alignment	not modelled	87.5	44	**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	85.4	28	**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	c5z5mB_	Alignment	not modelled	77.8	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**predicted protein; **PDBTitle:** crystal structure of (s)-allantoin synthase
73	d1akha_	Alignment	not modelled	65.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	c2bx9J_	Alignment	not modelled	64.3	37	**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	c3epvB_	Alignment	not modelled	59.2	16	**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
76	d1yz8p1	Alignment	not modelled	57.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
77	c4m5dB_	Alignment	not modelled	56.6	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 saccharomyces2 cerevisiae
78	d1le8a_	Alignment	not modelled	55.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
79	c4clvB_	Alignment	not modelled	53.9	17	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel-cobalt-cadmium resistance protein nccx; **PDBTitle:** crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a

80	c2mg4B_	Alignment	not modelled	53.6	19	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**computational designed homodimer; **PDBTitle:** computational design and experimental verification of a symmetric2 protein homodimer
81	d2ecca1	Alignment	not modelled	53.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
82	d2cuea1	Alignment	not modelled	52.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
83	d1octc1	Alignment	not modelled	51.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
84	d1ug2a_	Alignment	not modelled	51.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
85	d1jgga_	Alignment	not modelled	50.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
86	d1s7ea1	Alignment	not modelled	50.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
87	c3a01A_	Alignment	not modelled	50.1	12	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
88	d2e1oa1	Alignment	not modelled	50.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
89	c3pihA_	Alignment	not modelled	50.0	25	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
90	c4qboA_	Alignment	not modelled	49.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nuclease; **PDBTitle:** vrr_nuc domain
91	d1mh3a1	Alignment	not modelled	49.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
92	c3d1nK_	Alignment	not modelled	48.9	18	**PDB header:**transcription regulator/dna **Chain:** K: **PDB Molecule:**pou domain, class 6, transcription factor 1; **PDBTitle:** structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
93	c2da7A_	Alignment	not modelled	48.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
94	c2dmuA_	Alignment	not modelled	47.8	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
95	c5z2tC_	Alignment	not modelled	47.8	20	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**double homeobox protein 4; **PDBTitle:** crystal structure of dna-bound dux4-hd2
96	c2l9rA_	Alignment	not modelled	47.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
97	d1fjlb_	Alignment	not modelled	47.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	c2da2A_	Alignment	not modelled	47.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
99	c2m34A_	Alignment	not modelled	47.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein gbx-1; **PDBTitle:** nmr structure of the homeodomain transcription factor gbx1 from homo2 sapiens
100	c2kt0A_	Alignment	not modelled	47.0	12	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** solution structure of human stem cell transcription factor nanog2 homeodomain fragment
101	d2craa1	Alignment	not modelled	46.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
102	d2hddb_	Alignment	not modelled	46.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
103	c2dmsA_	Alignment	not modelled	46.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
104	c2vi6F_	Alignment	not modelled	45.1	9	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
105	c1hf0A_	Alignment	not modelled	45.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**octamer-binding transcription factor 1; **PDBTitle:** crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
						Fold:DNA/RNA-binding 3-helical bundle

106	d1ftza_	Alignment	not modelled	44.9	16	**Superfamily:**Homeodomain-like **Family:**Homeodomain
107	d1pufa_	Alignment	not modelled	44.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
108	c2djnA_	Alignment	not modelled	44.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein dlx-5; **PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein dlx-5
109	c2ly9A_	Alignment	not modelled	44.5	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** solution nmr structure of homeobox 2 domain from human zhx1 repressor,2 northeast structural genomics consortium (nesg) target hr7907f
110	d1au7a1	Alignment	not modelled	44.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
111	c5luxK_	Alignment	not modelled	44.3	19	**PDB header:**transcription **Chain:** K: **PDB Molecule:**homeobox protein cdx-1; **PDBTitle:** homeobox transcription factor cdx1 bound to methylated dna
112	d1e3oc1	Alignment	not modelled	44.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
113	d1ig7a_	Alignment	not modelled	44.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
114	d3saka_	Alignment	not modelled	44.1	33	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
115	d1b72a_	Alignment	not modelled	43.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
116	d1nk3p_	Alignment	not modelled	43.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
117	d1bw5a_	Alignment	not modelled	43.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
118	d1ftta_	Alignment	not modelled	43.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
119	c2dmqA_	Alignment	not modelled	43.0	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**lim/homeobox protein lhx9; **PDBTitle:** solution structure of the homeobox domain of lim/homeobox2 protein lhx9
120	d9anta_	Alignment	not modelled	42.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain