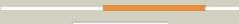




















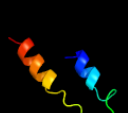


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1581c_(- )_1783913_1784308
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	a7d276a90ab9e164

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1qnta2</a>	 Alignment		89.1	30	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase domain
2	<a href="#">c2guzO</a>	 Alignment		87.6	35	<b>PDB header:</b> chaperone, protein transport <b>Chain:</b> O: <b>PDB Molecule:</b> mitochondrial import inner membrane translocase subunit <b>PDBTitle:</b> structure of the tim14-tim16 complex of the mitochondrial protein2 import motor
3	<a href="#">c3hhoA</a>	 Alignment		86.3	36	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> co-chaperone protein hscb homolog; <b>PDBTitle:</b> chaperone hscb from vibrio cholerae
4	<a href="#">c3bvoA</a>	 Alignment		81.3	24	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> co-chaperone protein hscb, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human co-chaperone protein hscb
5	<a href="#">c2ochA</a>	 Alignment		80.9	24	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dnj-12; <b>PDBTitle:</b> j-domain of dnj-12 from caenorhabditis elegans
6	<a href="#">c2o37A</a>	 Alignment		80.6	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein sis1; <b>PDBTitle:</b> j-domain of sis1 protein, hsp40 co-chaperone from saccharomyces2 cerevisiae.
7	<a href="#">c2guzD</a>	 Alignment		79.0	24	<b>PDB header:</b> chaperone, protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial import inner membrane translocase subunit <b>PDBTitle:</b> structure of the tim14-tim16 complex of the mitochondrial protein2 import motor
8	<a href="#">d1gh6a</a>	 Alignment		77.3	21	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
9	<a href="#">d1xbla</a>	 Alignment		75.3	27	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
10	<a href="#">d1hdja</a>	 Alignment		71.0	24	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
11	<a href="#">c2lqwA</a>	 Alignment		70.4	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily b member 2; <b>PDBTitle:</b> solution structure of the j domain of hsj1a

12	<a href="#">c1fpoA_</a>	Alignment		70.2	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein hscb; <b>PDBTitle:</b> hsc20 (hscb), a j-type co-chaperone from e. coli
13	<a href="#">d1fafa_</a>	Alignment		70.2	32	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
14	<a href="#">d1fpoa1</a>	Alignment		68.0	33	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
15	<a href="#">c2ctrA_</a>	Alignment		67.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily b member 9; <b>PDBTitle:</b> solution structure of j-domain from human dnaj subfamily b2 member 9
16	<a href="#">c1bq0A_</a>	Alignment		67.1	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj; <b>PDBTitle:</b> j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
17	<a href="#">c2ctqA_</a>	Alignment		66.2	30	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 12; <b>PDBTitle:</b> solution structure of j-domain from human dnaj subfamily c2 member 12
18	<a href="#">c2ctpA_</a>	Alignment		65.7	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily b member 12; <b>PDBTitle:</b> solution structure of j-domain from human dnaj subfamily b2 member 12
19	<a href="#">c2pf4E_</a>	Alignment		65.0	21	<b>PDB header:</b> hydrolase regulator/viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> small t antigen; <b>PDBTitle:</b> crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha subunit
20	<a href="#">c2yuaA_</a>	Alignment		63.7	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> williams-beuren syndrome chromosome region 18 <b>PDBTitle:</b> solution structure of the dnaj domain from human williams-2 beuren syndrome chromosome region 18 protein
21	<a href="#">c5y88T_</a>	Alignment	not modelled	63.5	37	<b>PDB header:</b> splicing <b>Chain:</b> T: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc23; <b>PDBTitle:</b> cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
22	<a href="#">c2dn9A_</a>	Alignment	not modelled	62.4	33	<b>PDB header:</b> apoptosis, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily a member 3; <b>PDBTitle:</b> solution structure of j-domain from the dnaj homolog, human2 tid1 protein
23	<a href="#">c3apqB_</a>	Alignment	not modelled	60.5	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dnaj homolog subfamily c member 10; <b>PDBTitle:</b> crystal structure of j-trx1 fragment of erdj5
24	<a href="#">c4v19N_</a>	Alignment	not modelled	59.8	23	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> mitoribosomal protein ul13m, mrp13; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
25	<a href="#">c2ys8A_</a>	Alignment	not modelled	57.8	39	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rab-related gtp-binding protein rabj; <b>PDBTitle:</b> solution structure of the dnaj-like domain from human ras-2 associated protein rap1
26	<a href="#">c2ctwA_</a>	Alignment	not modelled	56.9	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 5; <b>PDBTitle:</b> solution structure of j-domain from mouse dnaj subfamily c2 member 5
27	<a href="#">c2cugA_</a>	Alignment	not modelled	52.6	30	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> mkiaa0962 protein; <b>PDBTitle:</b> solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
28	<a href="#">c5vsoA_</a>	Alignment	not modelled	51.4	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> yeast dnaj protein 1; <b>PDBTitle:</b> nmr structure of ydj1 j-domain, a cytosolic hsp40 from saccharomyces2 cerevisiae
						<b>PDB header:</b> chaperone binding protein

29	<a href="#">c2kqxA</a>	Alignment	not modelled	49.8	24	<b>Chain:</b> A: <b>PDB Molecule:</b> curved dna-binding protein; <b>PDBTitle:</b> nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
30	<a href="#">c4j7zC</a>	Alignment	not modelled	48.6	27	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> chaperone protein dnaj 2; <b>PDBTitle:</b> thermus thermophilus dnaj j- and g/f-domains
31	<a href="#">d1wjza</a>	Alignment	not modelled	47.4	26	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
32	<a href="#">c2dmxA</a>	Alignment	not modelled	47.1	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily b member 8; <b>PDBTitle:</b> solution structure of the j domain of dnaj homolog2 subfamily b member 8
33	<a href="#">c2l6lA</a>	Alignment	not modelled	46.6	30	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog subfamily c member 24; <b>PDBTitle:</b> solution structure of human j-protein co-chaperone, dph4
34	<a href="#">c4o66A</a>	Alignment	not modelled	43.7	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> crystal structure of smarcal1 harp substrate recognition domain
35	<a href="#">c2ftcH</a>	Alignment	not modelled	42.1	26	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 39s ribosomal protein l13, mitochondrial; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
36	<a href="#">c2qsaA</a>	Alignment	not modelled	41.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnaj homolog dnj-2; <b>PDBTitle:</b> crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 c.elegans.
37	<a href="#">d1nz6a</a>	Alignment	not modelled	35.0	42	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
38	<a href="#">c1djyB</a>	Alignment	not modelled	32.7	32	<b>PDB header:</b> lipid degradation <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoinositide-specific phospholipase c, <b>PDBTitle:</b> phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
39	<a href="#">d1qasa3</a>	Alignment	not modelled	28.6	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
40	<a href="#">c3qr0A</a>	Alignment	not modelled	28.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase c-beta (plc-beta); <b>PDBTitle:</b> crystal structure of s. officinalis plc21
41	<a href="#">d1n4ca</a>	Alignment	not modelled	27.5	39	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
42	<a href="#">c5td8D</a>	Alignment	not modelled	27.2	39	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> kinetochore protein spc25; <b>PDBTitle:</b> crystal structure of an extended dwarf ndc80 complex
43	<a href="#">c2fjuB</a>	Alignment	not modelled	27.0	27	<b>PDB header:</b> signaling protein,apoptosis/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate <b>PDBTitle:</b> activated rac1 bound to its effector phospholipase c beta 2
44	<a href="#">c3ohmB</a>	Alignment	not modelled	25.2	27	<b>PDB header:</b> signaling protein / hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase <b>PDBTitle:</b> crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
45	<a href="#">d2ftxa1</a>	Alignment	not modelled	24.4	39	<b>Fold:</b> Kinetochore globular domain-like <b>Superfamily:</b> Kinetochore globular domain <b>Family:</b> Spc25-like
46	<a href="#">c3uo2A</a>	Alignment	not modelled	23.9	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> j-type co-chaperone jac1, mitochondrial; <b>PDBTitle:</b> jac1 co-chaperone from saccharomyces cerevisiae
47	<a href="#">d2zkmx4</a>	Alignment	not modelled	22.9	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
48	<a href="#">c2lywA</a>	Alignment	not modelled	14.3	42	<b>PDB header:</b> signaling protein/neuropeptide <b>Chain:</b> A: <b>PDB Molecule:</b> neurotensin receptor type 1; <b>PDBTitle:</b> intermolecular interactions between neurotensin and the third2 extracellular loop of human neurotensin 1 receptor
49	<a href="#">c6odmB</a>	Alignment	not modelled	13.8	60	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> large tegument protein deneddylase; <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
50	<a href="#">c3ag7A</a>	Alignment	not modelled	12.6	25	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein f9e10.5; <b>PDBTitle:</b> an auxilin-like j-domain containing protein, jac1 j-domain
51	<a href="#">c4j80B</a>	Alignment	not modelled	11.8	28	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone protein dnaj 2; <b>PDBTitle:</b> thermus thermophilus dnaj
52	<a href="#">c3dfuB</a>	Alignment	not modelled	10.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein from 6-phosphogluconate <b>PDBTitle:</b> crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
53	<a href="#">d1iura</a>	Alignment	not modelled	10.7	22	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Chaperone J-domain <b>Family:</b> Chaperone J-domain
54	<a href="#">c4hwmA</a>	Alignment	not modelled	10.3	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yedd; <b>PDBTitle:</b> crystal structure of a lipoprotein yedd (kpn_02420) from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 at 1.38 a

					resolution
55	<a href="#">c2qneA_</a>	Alignment	not modelled	9.0	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase (zp_00558420.1) from <i>Desulfitobacterium hafniense</i> y51 at 2.30 Å resolution
56	<a href="#">c5nfjA_</a>	Alignment	not modelled	8.9	33 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial ribonuclease p protein 1; <b>PDBTitle:</b> crystal structure of the methyltransferase subunit of human2 mitochondrial ribonuclease p (mrpp1) bound to s-adenosyl-methionine3 (sam)
57	<a href="#">c2a45H_</a>	Alignment	not modelled	8.4	40 <b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of the complex between thrombin and the central "e"2 region of fibrin
58	<a href="#">c2ctoA_</a>	Alignment	not modelled	7.7	42 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> novel protein; <b>PDBTitle:</b> solution structure of the hmg box like domain from human2 hypothetical protein flj14904
59	<a href="#">d2hg6a1</a>	Alignment	not modelled	7.5	50 <b>Fold:</b> PA1123-like <b>Superfamily:</b> PA1123-like <b>Family:</b> PA1123-like
60	<a href="#">c2kmcA_</a>	Alignment	not modelled	7.2	28 <b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fermitin family homolog 1; <b>PDBTitle:</b> solution structure of the n-terminal domain of kindlin-1
61	<a href="#">d1w7ja1</a>	Alignment	not modelled	6.5	23 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Myosin S1 fragment, N-terminal domain <b>Family:</b> Myosin S1 fragment, N-terminal domain
62	<a href="#">d1ou8a_</a>	Alignment	not modelled	6.3	36 <b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
63	<a href="#">d1edqa2</a>	Alignment	not modelled	6.1	25 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase