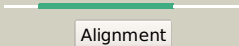

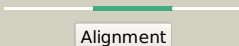

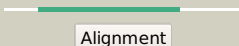

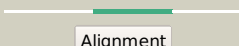
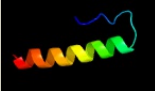
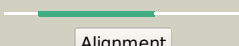

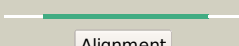

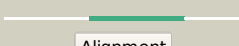
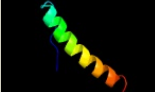
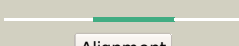


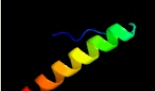



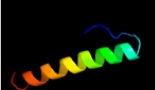







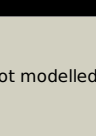
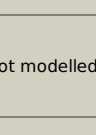


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2828A_(RVBD2828A)_3136340_3136609
 Date Wed Aug 7 12:50:49 BST 2019
 Unique Job ID 230693603fac135c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vs0A_	 Alignment		49.9	37	PDB header: chaperone Chain: A; PDB Molecule: yeast dnaj protein 1; PDBTitle: nmr structure of ydj1 j-domain, a cytosolic hsp40 from saccharomyces2 cerevisiae
2	d5pnta_	 Alignment		49.6	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
3	c2ys8A_	 Alignment		46.8	21	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
4	c4lrqC_	 Alignment		45.9	23	PDB header: hydrolase Chain: C; PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of a low molecular weight phosphotyrosine2 phosphatase from vibrio choleraeo395
5	d1hdja_	 Alignment		43.7	20	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
6	c3ol4B_	 Alignment		42.6	28	PDB header: unknown function Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
7	c2fekA_	 Alignment		41.9	19	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
8	d1dg9a_	 Alignment		40.7	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
9	c2wmyH_	 Alignment		39.2	22	PDB header: hydrolase Chain: H; PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
10	c2qsaA_	 Alignment		39.1	15	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.
11	c5z3mB_	 Alignment		38.0	15	PDB header: hydrolase Chain: B; PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of low molecular weight phosphotyrosine phosphatase2 (vclmwptp-2) from vibrio choleraeo395

12	c2l6lA_	Alignment		37.3	17	PDB header: chaperone Chain: A; PDB Molecule: dnaj homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
13	c2dn9A_	Alignment		35.1	19	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
14	c2ctrA_	Alignment		34.5	21	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
15	c2x9qA_	Alignment		34.3	18	PDB header: ligase Chain: A; PDB Molecule: cyclodipeptide synthetase; PDBTitle: structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
16	d1y1la_	Alignment		31.0	17	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
17	c2l18A_	Alignment		30.3	16	PDB header: oxidoreductase Chain: A; PDB Molecule: arsenate reductase; PDBTitle: an arsenate reductase in the phosphate binding state
18	c3f4yF_	Alignment		27.1	32	PDB header: viral protein Chain: F; PDB Molecule: mutant peptide derived from hiv gp41 chr domain; PDBTitle: hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
19	c1zggA_	Alignment		27.1	14	PDB header: hydrolase Chain: A; PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
20	c4etiA_	Alignment		27.1	14	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: crystal structure of ywle from bacillus subtilis
21	c2kvcA_	Alignment	not modelled	27.1	28	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
22	c2yy0D_	Alignment	not modelled	24.6	15	PDB header: transcription Chain: D; PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
23	c2yuaA_	Alignment	not modelled	24.4	22	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	c4d74A_	Alignment	not modelled	24.4	26	PDB header: hydrolase Chain: A; PDB Molecule: protein-tyrosine-phosphatase amsi; PDBTitle: 1.57 a crystal structure of erwinia amylovora tyrosine phosphatase2 amsi
25	c1u2pA_	Alignment	not modelled	24.1	21	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
26	c4j7zC_	Alignment	not modelled	23.5	20	PDB header: chaperone Chain: C; PDB Molecule: chaperone protein dnaj j- and g/f-domains PDBTitle: thermus thermophilus dnaj j- and g/f-domains
27	d1wjwa_	Alignment	not modelled	22.1	24	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
						Fold: Long alpha-hairpin

28	d1iura_	Alignment	not modelled	21.3	12	Superfamily: Chaperone J-domain Family: Chaperone J-domain
29	c4picA_	Alignment	not modelled	21.2	28	PDB header: hydrolase Chain: A: PDB Molecule: arginine phosphatase ywle; PDBTitle: ywle arginine phosphatase from geobacillus stearothermophilus
30	d1p8aa_	Alignment	not modelled	20.4	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
31	c4egsB_	Alignment	not modelled	18.5	15	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase rpib; PDBTitle: crystal structure analysis of low molecular weight protein tyrosine2 phosphatase from t. tengcongensis
32	d1d1qa_	Alignment	not modelled	18.3	21	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
33	c2ctpA_	Alignment	not modelled	18.2	18	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
34	c2m0nA_	Alignment	not modelled	17.7	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
35	c2cugA_	Alignment	not modelled	16.6	13	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	c5j1bB_	Alignment	not modelled	16.3	29	PDB header: signaling protein Chain: B: PDB Molecule: cell wall assembly regulator smi1; PDBTitle: structure of the core domaine of knr4, an intrinsically disordered2 protein from saccharomyces cerevisiae - wt.
37	c5xdhD_	Alignment	not modelled	15.7	17	PDB header: electron transport Chain: D: PDB Molecule: putative cytochrome c; PDBTitle: his/dopa ligated cytochrome c from an anammox organism ksu-1
38	c1x4qA_	Alignment	not modelled	15.3	27	PDB header: rna binding protein Chain: A: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
39	c2bsjB_	Alignment	not modelled	15.2	32	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein syct; PDBTitle: native crystal structure of the type iii secretion chaperone syct from2 yersinia enterocolitica
40	c2cosA_	Alignment	not modelled	14.1	43	PDB header: transferase Chain: A: PDB Molecule: serine/threonine protein kinase lats2; PDBTitle: solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
41	c2o37A_	Alignment	not modelled	14.1	21	PDB header: chaperone Chain: A: PDB Molecule: protein sis1; PDBTitle: j-domain of sis1 protein, hsp40 co-chaperone from saccharomyces2 cerevisiae.
42	c2ctqA_	Alignment	not modelled	13.3	14	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
43	c2ochA_	Alignment	not modelled	12.9	21	PDB header: chaperone Chain: A: PDB Molecule: hypothetical protein dnj-12; PDBTitle: j-domain of dnj-12 from caenorhabditis elegans
44	c2lkyA_	Alignment	not modelled	12.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
45	c2ctwA_	Alignment	not modelled	12.6	26	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
46	c5y88T_	Alignment	not modelled	11.9	18	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
47	c2lqwA_	Alignment	not modelled	11.7	20	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 2; PDBTitle: solution structure of the j domain of hsj1a
48	c6ez3C_	Alignment	not modelled	11.7	13	PDB header: rna binding protein Chain: C: PDB Molecule: cyclo(l-leucyl-l-leucyl) synthase; PDBTitle: structure of cdps from staphylococcus haemolyticus
49	c3jviA_	Alignment	not modelled	11.5	12	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase; PDBTitle: product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
50	c2mqaA_	Alignment	not modelled	10.5	26	PDB header: structural protein Chain: A: PDB Molecule: minor ampullate fibroin 1; PDBTitle: 3d structure of rp domain of misp
51	c2l2lB_	Alignment	not modelled	10.2	44	PDB header: transferase Chain: B: PDB Molecule: methyl-cpg-binding domain protein 2; PDBTitle: solution structure of the coiled-coil complex between mbd2 and2 p66alpha
52	c2lxcB_	Alignment	not modelled	9.8	22	PDB header: protein binding/protein binding Chain: B: PDB Molecule: small glutamine-rich tetratricopeptide repeat-containing PDBTitle: solution structure of the complex between the sgt2 homodimerization2 domain and the get5 ubl domain PDB header: oxidoreductase

53	c6gcsG	Alignment	not modelled	9.7	22	Chain: G: PDB Molecule: 30-kda protein (nugm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
54	c3rh0A	Alignment	not modelled	9.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
55	c2dmxA	Alignment	not modelled	9.5	25	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
56	c2kqxA	Alignment	not modelled	9.1	21	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
57	c3ci9B	Alignment	not modelled	8.8	22	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
58	d1wjza	Alignment	not modelled	8.2	8	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
59	c5lkdB	Alignment	not modelled	7.9	24	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase omega-like 2; PDBTitle: crystal structure of the xi glutathione transferase ecm4 from2 saccharomyces cerevisiae in complex with glutathione
60	d1svdm1	Alignment	not modelled	7.6	18	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
61	c1zzpA	Alignment	not modelled	6.9	12	PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase abl1; PDBTitle: solution structure of the f-actin binding domain of bcr-2 abl/c-abl
62	d1rbli	Alignment	not modelled	6.9	23	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
63	c2lkzA	Alignment	not modelled	6.7	31	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure of the second rrm domain of rbm5
64	c3hhcB	Alignment	not modelled	6.6	16	PDB header: cytokine Chain: B: PDB Molecule: interleukin-28b; PDBTitle: interferon-lambda is functionally an interferon but structurally2 related to the il-10 family
65	c2ki2A	Alignment	not modelled	6.5	17	PDB header: rna binding protein/ss-dna binding prote Chain: A: PDB Molecule: ss-dna binding protein 12rnp2; PDBTitle: solution structure of ss-dna binding protein 12rnp2 precursor, hp0827(o25501_helpy) form helicobacter pylori
66	d1ztda1	Alignment	not modelled	6.4	28	Fold: RNase III domain-like Superfamily: RNase III domain-like Family: PF0609-like
67	c5g2fB	Alignment	not modelled	6.1	55	PDB header: unknown function Chain: B: PDB Molecule: type-iv like pilin ttha1222; PDBTitle: type iv-like competence pilin ttha1222 from thermus2 thermophilus
68	c2jx0A	Alignment	not modelled	6.0	22	PDB header: cell adhesion, signaling protein Chain: A: PDB Molecule: arf gtpase-activating protein git1; PDBTitle: the paxillin-binding domain (pbd) of g protein coupled2 receptor (gpcr)-kinase (grk) interacting protein 1 (git1)
69	d2acva1	Alignment	not modelled	5.8	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
70	c1xhoB	Alignment	not modelled	5.7	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682
71	d1xhoa	Alignment	not modelled	5.7	33	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
72	c3d5pB	Alignment	not modelled	5.6	13	PDB header: gene regulation Chain: B: PDB Molecule: putative glucan synthesis regulator of smi1/knr4 family; PDBTitle: crystal structure of a putative glucan synthesis regulator of2 smi1/knr4 family (bf1740) from bacteroides fragilis nctc 9343 at 1.453 a resolution
73	d1fnja	Alignment	not modelled	5.4	27	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
74	c2ytcA	Alignment	not modelled	5.4	28	PDB header: transcription Chain: A: PDB Molecule: pre-mrna-splicing factor rbm22; PDBTitle: solution structure of rna binding domain in pre-mrna-2 splicing factor rbm22
75	c4g6uA	Alignment	not modelled	5.3	27	PDB header: toxin Chain: A: PDB Molecule: ec869 cdia-ct; PDBTitle: cdia-ct/cdii toxin and immunity complex from escherichia coli