



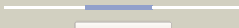
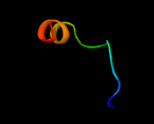



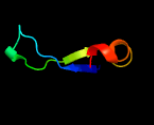
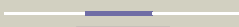
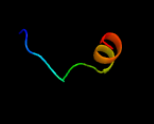



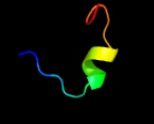

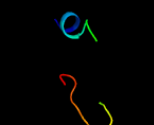



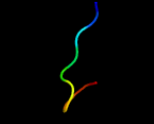


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2077Bc_(RVBD2077Bc)_2334860_2335030
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	d7eaa58cca7da0ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fnoa1	 Alignment		34.0	50	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
2	d1uw0a_	 Alignment		25.0	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: PARP-type zinc finger
3	c4oc8D_	 Alignment		23.4	29	PDB header: hydrolase Chain: D: PDB Molecule: restriction endonuclease aspbhi; PDBTitle: dna modification-dependent restriction endonuclease aspbhi
4	c2cs2A_	 Alignment		19.0	56	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase-1; PDBTitle: solution structure of the second zn-finger domain of2 poly(adp-ribose) polymerase-1
5	c2n8aA_	 Alignment		15.9	29	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: 1h, 13c and 15n chemical shift assignments and solution structure for2 parp-1 flf2 domains in complex with a dna single-strand break
6	c4oc8A_	 Alignment		14.2	29	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease aspbhi; PDBTitle: dna modification-dependent restriction endonuclease aspbhi
7	d1ok0a_	 Alignment		14.1	50	Fold: alpha-Amylase inhibitor tendamistat Superfamily: alpha-Amylase inhibitor tendamistat Family: alpha-Amylase inhibitor tendamistat
8	c1v9xA_	 Alignment		13.9	24	PDB header: transferase Chain: A: PDB Molecule: poly (adp-ribose) polymerase; PDBTitle: solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
9	c2vy2A_	 Alignment		12.8	53	PDB header: transcription Chain: A: PDB Molecule: protein leafy; PDBTitle: structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
10	c4av1C_	 Alignment		12.0	33	PDB header: transferase Chain: C: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: crystal structure of the human parp-1 dna binding domain in2 complex with dna
11	c3odeA_	 Alignment		10.6	56	PDB header: dna binding protein/dna Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: human parp-1 zinc finger 2 (zn2) bound to dna

12	c4f0qC_	Alignment		9.7	31	PDB header: hydrolase Chain: C: PDB Molecule: restriction endonuclease; PDBTitle: mspji restriction endonuclease - p21 form
13	c4f0qA_	Alignment		9.6	31	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease; PDBTitle: mspji restriction endonuclease - p21 form
14	c2kxrA_	Alignment		9.5	19	PDB header: protein binding Chain: A: PDB Molecule: tight junction protein zo-1; PDBTitle: zo1 zu5 domain mc/aa mutation
15	c2dmjA_	Alignment		8.7	40	PDB header: transferase Chain: A: PDB Molecule: poly (adp-ribose) polymerase family, member 1; PDBTitle: solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
16	c1oy5B_	Alignment		8.1	71	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a trna (m1g37) methyltransferase from aquifex2 aeolicus
17	d1oy5a_	Alignment		7.9	71	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
18	c3quvB_	Alignment		7.8	86	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
19	d1uala_	Alignment		7.7	86	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
20	c5wyrA_	Alignment		7.7	71	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure and catalytic mechanism of the essential m1g37 trna2 methyltransferase trmd from pseudomonas aeruginosa
21	c3ky7A_	Alignment	not modelled	7.4	57	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
22	c3knuD_	Alignment	not modelled	7.3	86	PDB header: transferase Chain: D: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
23	c3iefA_	Alignment	not modelled	7.0	71	PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpcs.
24	d1p9pa_	Alignment	not modelled	7.0	86	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
25	d2qxba1	Alignment	not modelled	6.9	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
26	c4h3zA_	Alignment	not modelled	6.8	71	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a symmetric dimer of a trna (guanine-(n(1)-)-2 methyltransferase from burkholderia phymatum bound to s-adenosyl3 homocystein in both half-sites
27	d1qbjc_	Alignment	not modelled	6.8	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
28	c2kxsA_	Alignment	not modelled	6.7	36	PDB header: protein binding Chain: A: PDB Molecule: tight junction protein zo-1, linker, peptide of myocardium-

						PDBTitle: zo1 zu5 domain in complex with grin1a peptide
29	c4a0tB_	Alignment	not modelled	6.6	63	PDB header: viral protein Chain: B: PDB Molecule: tail fiber protein; PDBTitle: structure of the carboxy-terminal domain of bacteriophage t7 fibre2 gp17 containing residues 371-553.
30	c5bthA_	Alignment	not modelled	6.5	57	PDB header: hydrolase Chain: A: PDB Molecule: decapping nuclease rail1; PDBTitle: crystal structure of candida albicans rail1
31	d1qgpa_	Alignment	not modelled	6.3	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
32	c6g13B_	Alignment	not modelled	6.2	22	PDB header: viral protein Chain: B: PDB Molecule: nucleoprotein; PDBTitle: c-terminal domain of mers-cov nucleocapsid
33	c5wtiZ_	Alignment	not modelled	6.2	36	PDB header: hydrolase/dna/rna Chain: Z: PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of the crispr-associated protein in complex with2 crrna and dna
34	d1qoua_	Alignment	not modelled	6.1	43	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
35	d2cjr1	Alignment	not modelled	6.1	25	Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Coronavirus nucleocapsid protein
36	c5a2gB_	Alignment	not modelled	6.0	14	PDB header: hydrolase Chain: B: PDB Molecule: carboxylic ester hydrolase; PDBTitle: an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
37	c4btpl_	Alignment	not modelled	5.9	64	PDB header: viral protein Chain: I: PDB Molecule: p1; PDBTitle: structure of the capsid protein p1 of the bacteriophage phi8
38	d2eifa1	Alignment	not modelled	5.9	57	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
39	c4xhiB_	Alignment	not modelled	5.7	33	PDB header: transcription Chain: B: PDB Molecule: rna-dependent rna polymerase; PDBTitle: crystal structure of native thosea asigna virus rna-dependent rna2 polymerase (rdrp) at 2.15 angstrom resolution
40	c4my4A_	Alignment	not modelled	5.7	56	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
41	c2e30B_	Alignment	not modelled	5.6	50	PDB header: metal binding protein/transport protein Chain: B: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: solution structure of the cytoplasmic region of na+/h+2 exchanger 1 complexed with essential cofactor calcineurin3 b homologous protein 1
42	d1tdha3	Alignment	not modelled	5.6	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
43	d2b5id2	Alignment	not modelled	5.5	50	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
44	c3j38h_	Alignment	not modelled	5.5	57	PDB header: ribosome Chain: H: PDB Molecule: 40s ribosomal protein s7; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
45	c3fqgA_	Alignment	not modelled	5.4	43	PDB header: protein binding Chain: A: PDB Molecule: protein din1; PDBTitle: crystal structure of the s. pombe rail1
46	c2xtzB_	Alignment	not modelled	5.3	44	PDB header: hydrolase Chain: B: PDB Molecule: guanine nucleotide-binding protein alpha-1 subunit; PDBTitle: crystal structure of the g alpha protein atga1 from arabidopsis2 thaliana
47	c2kdvA_	Alignment	not modelled	5.3	26	PDB header: hydrolase Chain: A: PDB Molecule: rna pyrophosphohydrolase; PDBTitle: solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
48	c5btoA_	Alignment	not modelled	5.2	50	PDB header: hydrolase Chain: A: PDB Molecule: ssrail1; PDBTitle: crystal structure of scheffersomyces stipitis rail1
49	d1iz6a1	Alignment	not modelled	5.2	57	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
50	c6dknA_	Alignment	not modelled	5.2	57	PDB header: hydrolase Chain: A: PDB Molecule: decapping nuclease dxo homolog, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana decapping nuclease dxo1
51	c5btbA_	Alignment	not modelled	5.1	57	PDB header: hydrolase Chain: A: PDB Molecule: afr263cp; PDBTitle: crystal structure of ashbya gossypii rail1
52	d1vi7a1	Alignment	not modelled	5.1	55	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: YigZ N-terminal domain-like
53	d1bkba1	Alignment	not modelled	5.1	71	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
54	d1g03a_	Alignment	not modelled	5.0	64	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain

