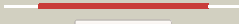
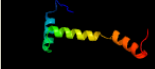

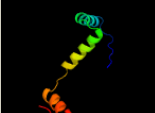
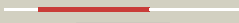




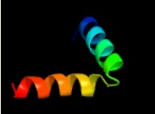

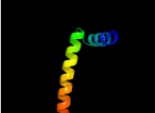

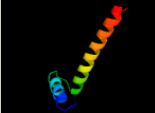
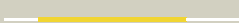
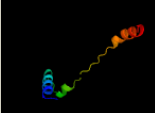








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1721c_(-)_1947423_1947650
Date	Fri Aug 2 13:30:32 BST 2019
Unique Job ID	1ece74e689376356

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bsqe1	 Alignment		97.9	26	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
2	c2h1oH	 Alignment		97.8	26	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
3	c3h87D	 Alignment		97.7	38	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
4	c2an7A	 Alignment		92.1	34	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
5	c6gtsC	 Alignment		90.1	26	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
6	d1y9ba1	 Alignment		87.0	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
7	c6ajnF	 Alignment		86.8	21	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atar bound with accoa
8	c6qeqD	 Alignment		76.3	15	PDB header: dna binding protein Chain: D: PDB Molecule: pcfj; PDBTitle: pcfj from enterococcus faecalis pcf10
9	c2k29A	 Alignment		60.9	27	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
10	c4q2uM	 Alignment		58.5	25	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
11	c4hv0B	 Alignment		46.3	27	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrivirus

12	c2k5jB_	Alignment		45.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
13	c4fxeB_	Alignment		45.1	26	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
14	d1p94a_	Alignment		42.5	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
15	c2m2jA_	Alignment		34.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: solution nmr structure of the n-terminal domain of stm1478 from2 salmonella typhimurium lt2: target str147a of the northeast3 structural genomics consortium (nesg), and apc101565 of the midwest4 center for structural genomics (mcsg).
16	c4yy2A_	Alignment		34.3	27	PDB header: de novo protein Chain: A: PDB Molecule: dtor_3x33l; PDBTitle: computationally designed left-handed alpha/alpha toroid with 3 repeats2 in space group p212121
17	d1mnta_	Alignment		33.6	31	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
18	c2zmeB_	Alignment		25.2	23	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 36; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
19	c1u9pA_	Alignment		21.7	19	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
20	d1zj8a1	Alignment		20.3	33	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
21	d1myla_	Alignment	not modelled	17.4	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
22	d2bj7a1	Alignment	not modelled	15.8	13	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
23	c2ca9B_	Alignment	not modelled	15.2	27	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
24	c3fmtF_	Alignment	not modelled	15.0	26	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
25	d1b28a_	Alignment	not modelled	14.5	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
26	c4b1yM_	Alignment	not modelled	14.5	9	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-3 bound to g-actin
27	c6f0hD_	Alignment	not modelled	14.1	21	PDB header: chaperone Chain: D: PDB Molecule: ip4; PDBTitle: crystal structure asf1-ip4
28	c6f0hB_	Alignment	not modelled	13.8	21	PDB header: chaperone Chain: B: PDB Molecule: ip4; PDBTitle: crystal structure asf1-ip4
29	c3uoeb_	Alignment	not modelled	13.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from sinorhizobium meliloti

30	c3i0pA	Alignment	not modelled	13.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from entamoeba histolytica
31	c1vbiA	Alignment	not modelled	12.7	32	PDB header: oxidoreductase Chain: A: PDB Molecule: type 2 malate/lactate dehydrogenase; PDBTitle: crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
32	c6a6xC	Alignment	not modelled	12.6	26	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
33	d1rfmA	Alignment	not modelled	11.9	16	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
34	c1v9nA	Alignment	not modelled	11.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structure of malate dehydrogenase from pyrococcus horikoshii ot3
35	d1rxrA1	Alignment	not modelled	11.5	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
36	c1rxrD	Alignment	not modelled	11.5	30	PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
37	c3zzwA	Alignment	not modelled	11.1	29	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase transmembrane receptor ror2; PDBTitle: crystal structure of the kinase domain of ror2
38	c3fdgA	Alignment	not modelled	10.4	19	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase ac. metallo peptidase. merops family m19; PDBTitle: the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
39	c2bj3D	Alignment	not modelled	10.2	13	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
40	c1q5vB	Alignment	not modelled	10.2	18	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
41	c2yjfM	Alignment	not modelled	9.8	17	PDB header: motor protein Chain: M: PDB Molecule: mkl/myocardin-like protein 1; PDBTitle: oligomeric assembly of actin bound to mrtf-a
42	c4f1oA	Alignment	not modelled	9.7	10	PDB header: transferase, signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase roco4; PDBTitle: crystal structure of the I1180t mutant roco4 kinase domain from d.2 discoideum bound to appcp
43	c3rk6A	Alignment	not modelled	9.1	21	PDB header: translation regulator Chain: A: PDB Molecule: polyadenylate-binding protein-interacting protein 1; PDBTitle: crystal structure of the middle domain of human paip1
44	c1z2iA	Alignment	not modelled	9.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
45	d2jnaa1	Alignment	not modelled	8.7	25	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
46	d1aopa2	Alignment	not modelled	8.6	17	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
47	c5abxB	Alignment	not modelled	8.3	18	PDB header: translation Chain: B: PDB Molecule: 4e-binding protein mex1li; PDBTitle: complex of c. elegans eif4e-3 with the 4e-binding protein2 mex1li and cap analog
48	c6em3J	Alignment	not modelled	8.2	31	PDB header: ribosome Chain: J: PDB Molecule: rrna-processing protein ebp2; PDBTitle: state a architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
49	c3zbeA	Alignment	not modelled	7.9	31	PDB header: toxin-antitoxin Chain: A: PDB Molecule: paaa2; PDBTitle: e. coli o157 pare2-associated antitoxin 2 (paaa2)
50	c2k9iB	Alignment	not modelled	7.9	24	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolbus2 islandicus
51	c4rqoB	Alignment	not modelled	7.7	11	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
52	c5uv4A	Alignment	not modelled	7.7	27	PDB header: transferase Chain: A: PDB Molecule: putative leucine-rich repeat protein kinase family protein; PDBTitle: crystal structure of maize sirk1 (sucrose-induced receptor kinase 1)2 kinase domain bound to amp-pnp
53	d2bcqa3	Alignment	not modelled	7.4	27	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
54	c5waiC	Alignment	not modelled	7.2	20	PDB header: transcription Chain: C: PDB Molecule: zinc finger protein aebp2; PDBTitle: crystal structure of a suz12-rbbp4-jarid2-aebp2 heterotetrameric2 complex
55	d1jqra	Alignment	not modelled	7.0	18	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like

56	d1mylb_	Alignment	not modelled	6.9	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
57	c4p4oA_	Alignment	not modelled	6.5	9	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta; ternary gap2 complex
58	d4croa_	Alignment	not modelled	6.4	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
59	c1odpA_	Alignment	not modelled	6.3	50	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
60	c1odrA_	Alignment	not modelled	6.3	50	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
61	c1odqA_	Alignment	not modelled	6.3	50	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
62	c2oidA_	Alignment	not modelled	6.2	19	PDB header: transferase Chain: A: PDB Molecule: interleukin-1 receptor-associated kinase 4; PDBTitle: crystal structure of irak4 kinase domain complexed with2 amppnp
63	d2hzab1	Alignment	not modelled	6.2	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
64	c2kl8A_	Alignment	not modelled	6.1	30	PDB header: de novo protein Chain: A: PDB Molecule: or15; PDBTitle: solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
65	d2fmpa3	Alignment	not modelled	5.9	14	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
66	d1rh5b_	Alignment	not modelled	5.7	23	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
67	d1d1la_	Alignment	not modelled	5.6	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
68	c4b1zM_	Alignment	not modelled	5.5	9	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel domain bound to g-actin
69	d1srqa_	Alignment	not modelled	5.5	17	Fold: Rap/Ran-GAP Superfamily: Rap/Ran-GAP Family: Rap/Ran-GAP
70	c5fd2B_	Alignment	not modelled	5.5	20	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: serine/threonine-protein kinase b-raf; PDBTitle: b-raf wild-type kinase domain in complex with a purinylpyridinylamino-2 based inhibitor
71	d1u9da_	Alignment	not modelled	5.5	26	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: VC0714-like
72	c3v5qB_	Alignment	not modelled	5.4	15	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: nt-3 growth factor receptor; PDBTitle: discovery of a selective trk inhibitor with efficacy in rodent cancer2 tumor models
73	c2bcuA_	Alignment	not modelled	5.3	27	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
74	d2noca1	Alignment	not modelled	5.3	12	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
75	c5xd6A_	Alignment	not modelled	5.3	20	PDB header: transferase Chain: A: PDB Molecule: protein kinase superfamily protein; PDBTitle: cark1 phosphorylates aba receptors
76	c2pijB_	Alignment	not modelled	5.2	33	PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
77	c2g8yB_	Alignment	not modelled	5.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.