

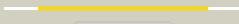
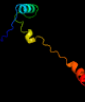
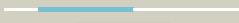







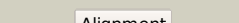
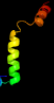





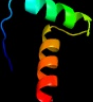




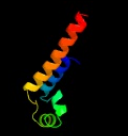

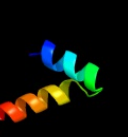
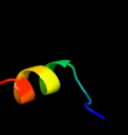

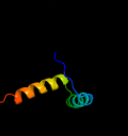
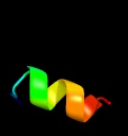


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1839c (-) _2087656_2087919
Date	Fri Aug 2 13:30:45 BST 2019
Unique Job ID	e5c0efbd30aeb9ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k9iB_	 Alignment		75.2	34	PDB header: dna binding protein Chain: B; PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
2	c6qeD_	 Alignment		74.2	14	PDB header: dna binding protein Chain: D; PDB Molecule: pcff; PDBTitle: pcff from enterococcus faecalis pcf10
3	c6gtsC_	 Alignment		34.1	17	PDB header: transcription Chain: C; PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
4	c2lseA_	 Alignment		33.4	41	PDB header: de novo protein Chain: A; PDB Molecule: four helix bundle protein; PDBTitle: solution nmr structure of de novo designed four helix bundle protein,2 northeast structural genomics consortium (nesg) target or188
5	c2h1oH_	 Alignment		23.3	16	PDB header: gene regulation/dna complex Chain: H; PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
6	d1ni8a_	 Alignment		22.1	46	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
7	d2bsqe1	 Alignment		19.3	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
8	c3kk4B_	 Alignment		17.8	29	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
9	d1dvja_	 Alignment		17.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
10	c6ajnF_	 Alignment		14.8	18	PDB header: toxin Chain: F; PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atatr bound with accoa
11	c3ldvB_	 Alignment		12.7	22	PDB header: lyase Chain: B; PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.77 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase from vibrio cholerae o1 biovar eltor str. n16961

12	dlr1a_	Alignment		12.3	44	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
13	dlrfma_	Alignment		10.6	15	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
14	dlxeaal	Alignment		10.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
15	dllov9a_	Alignment		10.0	67	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
16	c6bwqB_	Alignment		9.7	10	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
17	c4x2oB_	Alignment		9.5	31	PDB header: transport protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: sac3n peptide bound to mex67:mtr2
18	dle8ob_	Alignment		9.2	31	Fold: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Superfamily: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Family: Signal recognition particle alu RNA binding heterodimer, SRP9/14
19	c2k5jB_	Alignment		8.2	9	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
20	d2a6qb1	Alignment		8.0	38	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
21	d1j2j_b_	Alignment	not modelled	7.7	34	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
22	c3nr7A_	Alignment	not modelled	7.4	42	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein h-ns; PDBTitle: crystal structure of s. typhimurium h-ns 1-83
23	c3hs2H_	Alignment	not modelled	7.2	20	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
24	c3mfbA_	Alignment	not modelled	7.1	56	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the s-type pyocin domain of eca1669 protein from2 erwinia carotovora, northeast structural genomics consortium target3 ewr82c
25	c4chtA_	Alignment	not modelled	7.0	33	PDB header: cell cycle Chain: A: PDB Molecule: dna topoisomerase 3-alpha; PDBTitle: crystal structure of the human topoisomerase iii alpha- rmi1 complex2 with bound calcium ion
26	c6ozwA_	Alignment	not modelled	7.0	47	PDB header: isomerase,dna binding protein Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of the 65-kilodalton amino-terminal fragment of dna2 topoisomerase i from streptococcus mutans
27	d2nn6e2	Alignment	not modelled	7.0	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
28	d1mw9x_	Alignment	not modelled	7.0	27	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase

29	d1km4a_	Alignment	not modelled	6.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
30	d1rjda_	Alignment	not modelled	6.8	47	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Leucine carboxy methyltransferase Ppm1
31	c2lc0A_	Alignment	not modelled	6.3	15	PDB header: protein binding Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: rv0020c_nter structure
32	c1ceua_	Alignment	not modelled	5.7	24	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
33	c2pnzB_	Alignment	not modelled	5.7	12	PDB header: hydrolase/hydrolase Chain: B: PDB Molecule: probable exosome complex exonuclease 2; PDBTitle: crystal structure of the p. abyssi exosome rnaase ph ring2 complexed with udp and gmp
34	d1914a2	Alignment	not modelled	5.7	27	Fold: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Superfamily: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Family: Signal recognition particle alu RNA binding heterodimer, SRP9/14
35	d2bj7a1	Alignment	not modelled	5.6	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
36	c2gajA_	Alignment	not modelled	5.6	47	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase i; PDBTitle: structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
37	d1y9ba1	Alignment	not modelled	5.6	18	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
38	d1i7da_	Alignment	not modelled	5.6	33	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
39	c2l6pA_	Alignment	not modelled	5.4	23	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: phac1, phac2 and phad genes; PDBTitle: nmr solution structure of the protein np_253742.1
40	c4djdD_	Alignment	not modelled	5.3	14	PDB header: transferase/vitamin-binding protein Chain: D: PDB Molecule: corrinoid/iron-sulfur protein small subunit; PDBTitle: crystal structure of folate-free corrinoid iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
41	c3hefB_	Alignment	not modelled	5.3	32	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
42	c3c19A_	Alignment	not modelled	5.3	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
43	c3ieiD_	Alignment	not modelled	5.2	32	PDB header: transferase Chain: D: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
44	c5gveA_	Alignment	not modelled	5.1	33	PDB header: isomerase/protein binding Chain: A: PDB Molecule: dna topoisomerase 3-beta-1; PDBTitle: human top3b-tdrd3 complex