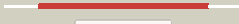



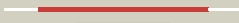








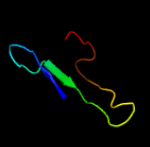

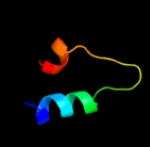

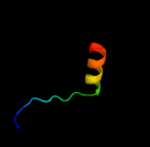

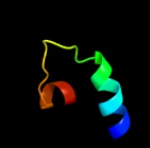


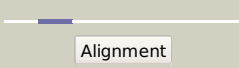
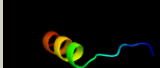

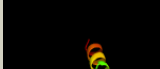
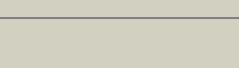



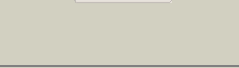

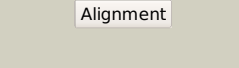
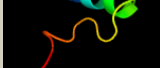
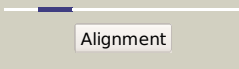

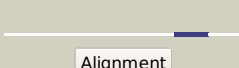

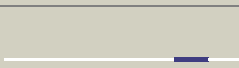


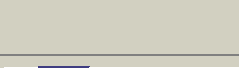
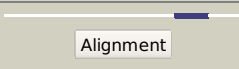
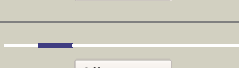
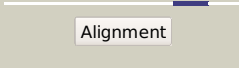
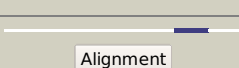
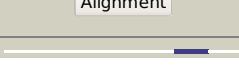



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0289 (-)_352149_353036
Date	Tue Jul 23 14:50:35 BST 2019
Unique Job ID	36211bfda9156a3d

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4w4iA_	 Alignment		100.0	100	PDB header: protein transport Chain: A: PDB Molecule: esx-3 secretion-associated protein esp33; PDBTitle: crystal structure of esp33 from the esx-3 type vii secretion system of2 m. tuberculosis
2	c4l4wB_	 Alignment		100.0	60	PDB header: protein transport Chain: B: PDB Molecule: esp33; PDBTitle: structure of esp33 chaperone from the type vii (esx-3) secretion2 system
3	c4kxrC_	 Alignment		100.0	20	PDB header: protein transport Chain: C: PDB Molecule: esp35; PDBTitle: structure of the mycobacterium tuberculosis type vii secretion system2 chaperone esp35 in complex with pe25-ppe41 dimer
4	c4rc1B_	 Alignment		100.0	62	PDB header: chaperone Chain: B: PDB Molecule: esp33; PDBTitle: structure of esp33 chaperone from the type vii (esx-3) secretion2 system, space group p43212
5	c5vbaA_	 Alignment		100.0	30	PDB header: chaperone, hydrolase Chain: A: PDB Molecule: lysozyme, esx-1 secretion-associated protein esp1 chimera; PDBTitle: structure of esp1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
6	d1qnta1	 Alignment		27.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
7	c4rdkB_	 Alignment		17.6	27	PDB header: viral protein Chain: B: PDB Molecule: capsid; PDBTitle: crystal structure of norovirus boxer p domain in complex with lewis b2 tetrasaccharide
8	c2kimA_	 Alignment		15.2	16	PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.
9	c2l3aA_	 Alignment		13.9	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
10	d1mgtA1	 Alignment		13.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
11	c3ilkB_	 Alignment		13.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized trna/rrna methyltransferase hi0380; PDBTitle: the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20

12	c3pm7A_			12.3	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ef_3132 protein from enterococcus faecalis at the 2 resolution 2a, northeast structural genomics consortium target efr184
13	c2ltdA_			11.1	9	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ydbc; PDBTitle: solution nmr structure of apo ydbc from lactococcus lactis, northeast2 structural genomics consortium (nesg) target kr150
14	c4zyeA_			10.6	11	PDB header: transferase Chain: A; PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
15	c3gx4X_			10.3	12	PDB header: dna binding protein/dna Chain: X; PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
16	c3u5gK_			9.4	17	PDB header: ribosome Chain: K; PDB Molecule: 40s ribosomal protein s10-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
17	c3jcmK_			8.5	17	PDB header: transcription Chain: K; PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: cryo-em structure of the spliceosomal u4/u6.u5 tri-snrrp
18	d1sfea1			8.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
19	c2ly2A_			7.3	23	PDB header: rna binding protein Chain: A; PDB Molecule: tudor domain-containing protein 7; PDBTitle: nmr structure of the second and third lotus domains of tudor domain-2 containing protein 7 (nmr ensemble overlay for lotus #3)
20	c2v4oB_			7.0	20	PDB header: hydrolase Chain: B; PDB Molecule: multifunctional protein sur e; PDBTitle: crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
21	c5w4zA_		not modelled	6.9	17	PDB header: flavoprotein Chain: A; PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
22	c4u5pA_		not modelled	6.9	26	PDB header: isomerase Chain: A; PDB Molecule: rhcc; PDBTitle: crystal structure of native rhcc (yp_702633.1) from rhodococcus jostii2 rha1 at 1.78 angstrom
23	c5cukA_		not modelled	6.6	29	PDB header: cell invasion Chain: A; PDB Molecule: ruler protein; PDBTitle: crystal structure of the pscp ss domain
24	c3obhA_		not modelled	6.6	5	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
25	c3erpA_		not modelled	6.6	11	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
26	c4r7kA_		not modelled	6.2	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein jhp0584; PDBTitle: 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori.
27	c1fwxB_		not modelled	6.1	13	PDB header: oxidoreductase Chain: B; PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
28	d1g26a_		not modelled	5.7	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Granulin repeat Family: Granulin repeat PDB header: transferase

29	c1wrjA_	Alignment	not modelled	5.6	8	Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
30	d2hs5a1	Alignment	not modelled	5.5	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators