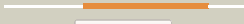
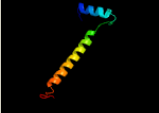
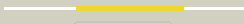
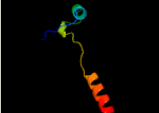
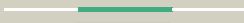
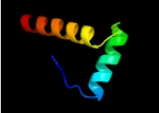
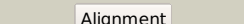








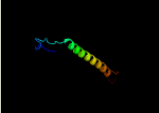


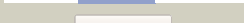


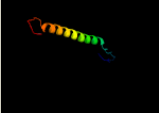


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1103c_(-)_1230976_1231296
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	adb3ed5df5d4dbc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kxeD_	 Alignment		82.0	34	PDB header: protein binding Chain: D; PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
2	c5cegC_	 Alignment		75.9	12	PDB header: toxin Chain: C; PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
3	d2hzaa1	 Alignment		47.7	12	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	d2bj7a1	 Alignment		47.1	8	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
5	d1cxa2	 Alignment		38.2	46	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
6	c2ca9B_	 Alignment		30.6	17	PDB header: transcription Chain: B; PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
7	c1cxC_	 Alignment		27.2	46	PDB header: oxidoreductase Chain: C; PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: crystal structure of pseudomonas fluorescens hppd
8	c2izpB_	 Alignment		24.6	30	PDB header: toxin Chain: B; PDB Molecule: putative membrane antigen; PDBTitle: bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
9	c3sohB_	 Alignment		23.9	24	PDB header: motor protein Chain: B; PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
10	c2bj3D_	 Alignment		22.8	9	PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
11	d2izpa1	 Alignment		22.0	30	Fold: !paD-like Superfamily: !paD-like Family: !paD-like

12	c1q5vB_	Alignment		20.0	14	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
13	c4rgwB_	Alignment		18.8	31	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of a taf1-taf7 complex in human transcription factor2 iid
14	d1v4aa2	Alignment		18.4	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GlnE-like domain
15	d2hzab1	Alignment		16.8	15	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
16	c2k5jB_	Alignment		13.1	23	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
17	c4me7E_	Alignment		11.5	28	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
18	c3hqxA_	Alignment		10.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0345 protein aciad0356; PDBTitle: crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
19	c3mkyP_	Alignment		10.3	16	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
20	c2wl2B_	Alignment		10.1	28	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
21	c2rqoA_	Alignment	not modelled	9.6	48	PDB header: toxin Chain: A: PDB Molecule: polytheonamide b; PDBTitle: solution structure of polytheonamide b
22	c4f9kA_	Alignment	not modelled	9.4	42	PDB header: transferase regulator Chain: A: PDB Molecule: camp-dependent protein kinase type i-beta regulatory PDBTitle: crystal structure of human camp-dependent protein kinase type i-beta2 regulatory subunit (fragment 11-73), northeast structural genomics3 consortium (nesg) target hr8613a
23	c2nr1A_	Alignment	not modelled	9.3	50	PDB header: receptor Chain: A: PDB Molecule: nr1 m2; PDBTitle: transmembrane segment 2 of nmda receptor nr1, nmr, 102 structures
24	c4imyH_	Alignment	not modelled	9.2	67	PDB header: transferase Chain: H: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
25	c3mkzU_	Alignment	not modelled	8.0	18	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
26	c6g1nB_	Alignment	not modelled	8.0	29	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
27	c6nklD_	Alignment	not modelled	7.7	47	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vapb1; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
28	c5xonV_	Alignment	not modelled	7.2	50	PDB header: transcription/rna Chain: V: PDB Molecule: transcription elongation factor spt4; PDBTitle: rna polymerase ii elongation complex bound with spt4/5

						and tfiis
29	c3ifzA_	Alignment	not modelled	6.8	31	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
30	c4z2cA_	Alignment	not modelled	6.3	31	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
31	c3ilwA_	Alignment	not modelled	6.3	31	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: structure of dna gyrase subunit a n-terminal domain
32	d1ab4a_	Alignment	not modelled	6.2	28	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase Family: Type II DNA topoisomerase
33	c4f6cA_	Alignment	not modelled	5.9	50	PDB header: oxidoreductase Chain: A: PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain
34	c4o5pB_	Alignment	not modelled	5.8	26	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from pseudomonas2 aeruginosa
35	c3rafA_	Alignment	not modelled	5.7	31	PDB header: isomerase/dna/antibiotic Chain: A: PDB Molecule: dna topoisomerase 4 subunit a; PDBTitle: quinazolidione-dna cleavage complex of type iv topoisomerase from s.2 pneumoniae
36	c3h7hA_	Alignment	not modelled	5.7	45	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)