

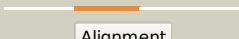
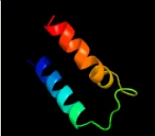
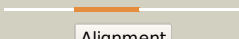
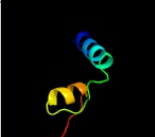

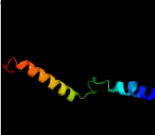
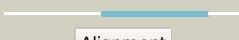

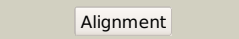

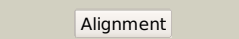

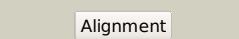

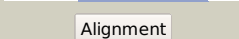
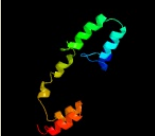


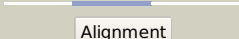
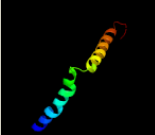


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1578c_(-)_1782765_1783235
Date	Fri Aug 2 13:30:16 BST 2019
Unique Job ID	6f5569e887584dba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o35A_	 Alignment		83.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf1244; PDBTitle: protein of unknown function (duf1244) from sinorhizobium meliloti
2	d2o35a1	 Alignment		83.4	20	Fold: SMc04008-like Superfamily: SMc04008-like Family: SMc04008-like
3	c3fybA_	 Alignment		83.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function (duf1244); PDBTitle: crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
4	c5d6aA_	 Alignment		44.4	19	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase of the abc class; PDBTitle: 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
5	c3neuA_	 Alignment		33.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
6	c4o2xA_	 Alignment		33.0	21	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, atp-dependent clp PDBTitle: structure of a malarial protein
7	c4xjnM_	 Alignment		25.2	39	PDB header: viral protein/rna Chain: M: PDB Molecule: nucleocapsid; PDBTitle: structure of the parainfluenza virus 5 nucleocapsid-rna complex: an2 insight into paramyxovirus polymerase activity
8	c2k29A_	 Alignment		24.0	15	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
9	c2gf5A_	 Alignment		23.9	12	PDB header: apoptosis Chain: A: PDB Molecule: fadd protein; PDBTitle: structure of intact fadd (mort1)
10	d1z0xa2	 Alignment		23.5	21	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
11	c4yiyA_	 Alignment		22.5	8	PDB header: rna binding protein Chain: A: PDB Molecule: krna editing a6 specific protein; PDBTitle: structure of mrb1590 bound to amp-pnp

12	c4fxeB_	Alignment		19.3	15	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
13	c5kkoD_	Alignment		18.9	28	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterised protein; PDBTitle: a 1.55a x-ray structure from vibrio cholerae o1 biovar el tor of a2 hypothetical protein
14	c4r1hA_	Alignment		16.4	13	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0741 protein; PDBTitle: gntr family transcriptional regulator from listeria monocytogenes
15	c2vcbA_	Alignment		16.3	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
16	c4xwhA_	Alignment		15.4	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: crystal structure of the human n-acetyl-alpha-glucosaminidase
17	d2hs5a1	Alignment		14.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
18	c5e4vA_	Alignment		13.9	29	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein,phosphoprotein; PDBTitle: crystal structure of measles n0-p complex
19	d1chka_	Alignment		12.2	16	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Chitosanase
20	d16vpa_	Alignment		12.1	20	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
21	d2a1jb1	Alignment	not modelled	11.1	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
22	c3zplE_	Alignment	not modelled	10.9	22	PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
23	c2jrbA_	Alignment	not modelled	10.6	28	PDB header: rna binding protein Chain: A: PDB Molecule: orf 1 protein; PDBTitle: c-terminal domain of orf1p from mouse line-1
24	c2rkkA_	Alignment	not modelled	10.0	11	PDB header: lipid transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein vta1; PDBTitle: crystal structure of s.cerevisiae vta1 n-terminal domain
25	c2x2iB_	Alignment	not modelled	9.6	25	PDB header: lyase Chain: B: PDB Molecule: alpha-1,4-glucan lyase isozyme 1; PDBTitle: crystal structure of the gracilariopsis lemaneiformis alpha-1,4-2 glucan lyase with acarbose
26	d1w7pd1	Alignment	not modelled	9.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
27	c2kngA_	Alignment	not modelled	9.4	13	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
28	d2fqma1	Alignment	not modelled	9.2	18	Fold: Phosphoprotein oligomerization domain-like Superfamily: Phosphoprotein oligomerization domain-like Family: Phosphoprotein oligomerization domain-like

29	c2marA	Alignment	not modelled	9.1	16	PDB header: unknown function Chain: A: PDB Molecule: sxp/ral-2 family protein; PDBTitle: solution structure of ani s 5 anisakis simplex allergen
30	c4q2uM	Alignment	not modelled	8.7	21	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
31	c1xi4D	Alignment	not modelled	8.6	22	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
32	c2cazB	Alignment	not modelled	7.9	11	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein vps28; PDBTitle: escrt-i core
33	d2cazb1	Alignment	not modelled	7.9	11	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
34	c3by6C	Alignment	not modelled	7.8	16	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
35	d2e9xb1	Alignment	not modelled	7.7	50	Fold: GINS helical bundle-like Superfamily: GINS helical bundle-like Family: PSF2 C-terminal domain-like
36	c3enoC	Alignment	not modelled	7.2	19	PDB header: hydrolase/unknown function Chain: C: PDB Molecule: uncharacterized protein pf2011; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
37	d1eija	Alignment	not modelled	6.9	70	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
38	c5kvrA	Alignment	not modelled	6.7	24	PDB header: translation Chain: A: PDB Molecule: pyruvate dehydrogenase complex repressor; PDBTitle: x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
39	d3bwga1	Alignment	not modelled	6.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
40	d1biaa1	Alignment	not modelled	6.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
41	c5oeiA	Alignment	not modelled	6.4	11	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein family upf0065:tat pathway signal; PDBTitle: r. palustris rpa4515 with oxoadipate
42	c6jx3B	Alignment	not modelled	6.4	13	PDB header: peptide binding protein Chain: B: PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
43	c2fh0A	Alignment	not modelled	6.3	50	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 16.0 kda protein in abf2-ch12 PDBTitle: nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
44	d1iq0a1	Alignment	not modelled	6.2	15	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
45	d1zj8a1	Alignment	not modelled	6.1	9	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
46	d2f6mb1	Alignment	not modelled	6.0	13	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
47	c2du9A	Alignment	not modelled	5.9	16	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
48	c4p96B	Alignment	not modelled	5.9	15	PDB header: transcription Chain: B: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from vibrio cholerae
49	c2g3nA	Alignment	not modelled	5.7	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of the sulfolobus solfataricus alpha-2 glucosidase mala in complex with beta-octyl-glucopyranoside
50	c3ic7A	Alignment	not modelled	5.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator of gntR family2 from bacteroides thetaiotaomicron
51	c3we3B	Alignment	not modelled	5.6	16	PDB header: dna binding protein Chain: B: PDB Molecule: bloom syndrome protein; PDBTitle: structure of blm rqc domain bound to an arsenate ion
52	d1efea	Alignment	not modelled	5.5	30	Fold: Insulin-like Superfamily: Insulin-like Family: Insulin-like
53	d1p4wa	Alignment	not modelled	5.4	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
54	d1fjlb	Alignment	not modelled	5.2	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain