







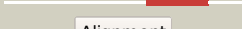

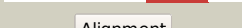

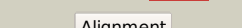


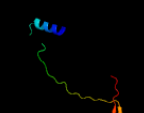


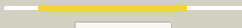

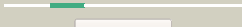
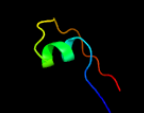


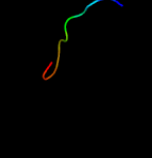
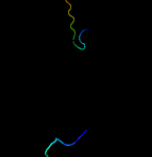
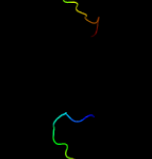
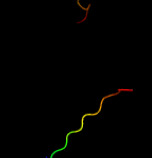

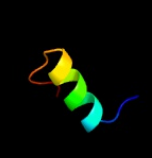
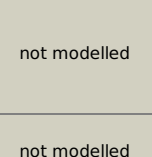


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1482c_(-) _1672463_1673305
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	7d777ea18572e006

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r3pB_	 Alignment		99.5	14	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
2	c3hrIA_	 Alignment		99.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endonuclease-like protein; PDBTitle: crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
3	d1cw0a_	 Alignment		99.0	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
4	d1vsra_	 Alignment		97.5	23	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
5	c4oq2A_	 Alignment		96.9	18	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease pvurts1 i; PDBTitle: 5hmc specific restriction endonuclease pvurts1i
6	c4parC_	 Alignment		96.0	26	PDB header: dna binding protein/dna Chain: C: PDB Molecule: uncharacterized protein abasi; PDBTitle: the 5-hydroxymethylcytosine-specific restriction enzyme abasi in a2 complex with product-like dna
7	c6rdu2_	 Alignment		94.8	17	PDB header: proton transport Chain: 2: PDB Molecule: asa-2: polytomella f-atp synthase associated subunit 2; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
8	d1m0da_	 Alignment		88.8	14	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
9	d1zela2	 Alignment		83.0	19	Fold: Rv2827c C-terminal domain-like Superfamily: Rv2827c C-terminal domain-like Family: Rv2827c C-terminal domain-like
10	c1zela_	 Alignment		76.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2827c; PDBTitle: crystal structure of rv2827c protein from mycobacterium tuberculosis
11	d2fcla1	 Alignment		47.6	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: TM1012-like

12	d2ieaa2	Alignment		35.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
13	c4gqzB_	Alignment		31.5	16	PDB header: metal binding protein Chain: B: PDB Molecule: putative periplasmic or exported protein; PDBTitle: crystal structure of s.cuep
14	c4ytkA_	Alignment		21.5	27	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow1-linker1 domain of transcription elongation2 factor spt5
15	c3wbzD_	Alignment		16.1	16	PDB header: transferase Chain: D: PDB Molecule: likely histidyl trna-specific guanylyltransferase; PDBTitle: crystal structure of c. albicans trna(his) guanylyltransferase (thg1)2 with atp
16	c5xoxD_	Alignment		15.9	16	PDB header: transferase Chain: D: PDB Molecule: trna(his) guanylyltransferase; PDBTitle: crystal structure of trna(his) guanylyltransferase from saccharomyces2 cerevisiae
17	c3otbB_	Alignment		15.0	21	PDB header: transferase Chain: B: PDB Molecule: trna(his) guanylyltransferase; PDBTitle: crystal structure of human trnahis guanylyltransferase (thg1) - dgt2 complex
18	c4kgkB_	Alignment		12.1	24	PDB header: transferase Chain: B: PDB Molecule: thg1-like uncharacterized protein; PDBTitle: bacterial trna(his) guanylyltransferase (thg1)-like protein in complex2 with gtp
19	d2fuka1	Alignment		7.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
20	c5n35A_	Alignment		7.0	30	PDB header: polymerase binding protein Chain: A: PDB Molecule: polb1 binding protein 2 (pbp2); PDBTitle: gadolinium phased pbp2 (sso6202) at 2.2 ang
21	c2kvcA_	Alignment	not modelled	7.0	28	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
22	d1dj0a_	Alignment	not modelled	6.9	31	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase I TruA
23	d1ccwa_	Alignment	not modelled	6.4	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
24	d2csba2	Alignment	not modelled	6.2	42	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
25	d3bula2	Alignment	not modelled	6.0	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
26	c1qmoG_	Alignment	not modelled	6.0	67	PDB header: lectin Chain: G: PDB Molecule: mannose binding lectin, fril; PDBTitle: structure of fril, a legume lectin that delays hematopoietic2 progenitor maturation
27	d1xi8a3	Alignment	not modelled	5.9	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
28	c3bd0D_	Alignment	not modelled	5.7	9	PDB header: peptide binding protein Chain: D: PDB Molecule: protein memo1; PDBTitle: crystal structure of memo, form ii

29	d1fmfa_	Alignment	not modelled	5.7	21	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
30	c2xxsA_	Alignment	not modelled	5.6	44	PDB header: protein binding Chain: A: PDB Molecule: protein mxig; PDBTitle: solution structure of the n-terminal domain of the shigella2 type iii secretion protein mxig
31	d2hja1_	Alignment	not modelled	5.5	40	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: Ykff-like
32	c2hja_	Alignment	not modelled	5.5	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ykff; PDBTitle: solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
33	c4qoyC_	Alignment	not modelled	5.5	15	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydropolpyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
34	d1y88a2_	Alignment	not modelled	5.5	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: MRR-like
35	c5axlB_	Alignment	not modelled	5.5	27	PDB header: transferase Chain: B: PDB Molecule: trna(his)-5'-guanylyltransferase (thg1) like protein; PDBTitle: crystal structure of thg1 like protein (tip) with gtp
36	c3ahhA_	Alignment	not modelled	5.4	18	PDB header: lyase Chain: A: PDB Molecule: xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; PDBTitle: h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
37	c2mn4A_	Alignment	not modelled	5.4	17	PDB header: de novo protein Chain: A: PDB Molecule: computational designed protein based on structure template PDBTitle: nmr solution structure of a computational designed protein based on2 structure template 1cy5
38	c4mp4B_	Alignment	not modelled	5.3	17	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a glutathione transferase family member from2 acinetobacter baumannii, target efi-501785, apo structure
39	d7reqa2_	Alignment	not modelled	5.2	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
40	c1y80A_	Alignment	not modelled	5.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica