
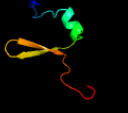



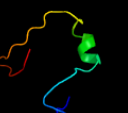

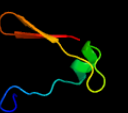





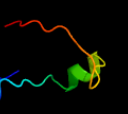

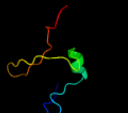



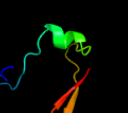

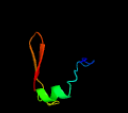
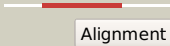
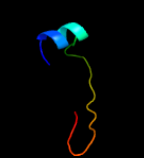
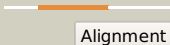
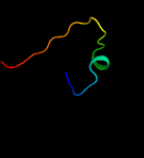
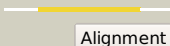
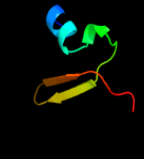
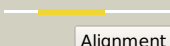
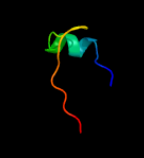
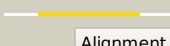
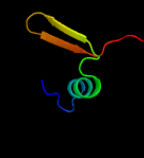
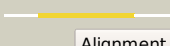

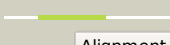
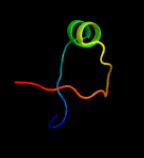



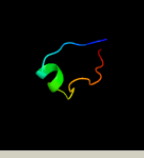
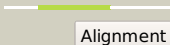
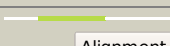
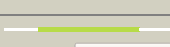
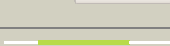
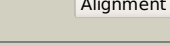
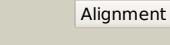

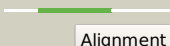


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2595_(-)_2925502_2925747
Date	Wed Aug 7 12:50:23 BST 2019
Unique Job ID	395396f4dfc20b1e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w1tB_	 Alignment		98.7	33	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of b. subtilis spovt
2	d1yfa1	 Alignment		98.4	38	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
3	c2l66B_	 Alignment		98.3	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrb family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
4	d2fy9a1	 Alignment		98.3	26	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
5	c2ro5B_	 Alignment		98.0	41	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: rdc-refined solution structure of the n-terminal dna recognition2 domain of the bacillus subtilis transition-state regulator spovt
6	c2mrnB_	 Alignment		98.0	28	PDB header: dna binding protein Chain: B: PDB Molecule: antitoxin maze; PDBTitle: structure of truncated ecmaze
7	c2glwA_	 Alignment		97.6	21	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
8	d1ub4c_	 Alignment		97.5	27	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addiction antidote
9	d1mvfd_	 Alignment		97.3	36	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addiction antidote
10	c1n0ff_	 Alignment		93.8	23	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mraz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
11	d1n0ea_	 Alignment		92.9	23	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ

12	c3o27B_	 Alignment		91.7	36	PDB header: dna binding protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of c68 from the hybrid virus-plasmid pssvx
13	d2vbua1	 Alignment		86.5	24	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
14	c3zvkg_	 Alignment		79.5	23	PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
15	d2d9ra1	 Alignment		78.8	29	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: PG0164-like
16	c5l6lD_	 Alignment		71.8	19	PDB header: hydrolase Chain: D: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 bound to operator dna
17	c5udfb_	 Alignment		71.4	25	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein-releasing system transmembrane protein lole; PDBTitle: structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lole from acinetobacter baumannii
18	c2pjhb_	 Alignment		69.4	19	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
19	d1ylea1	 Alignment		68.7	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
20	c1cz5A_	 Alignment		66.5	28	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
21	c1zc1A_	 Alignment	not modelled	65.9	26	PDB header: protein turnover Chain: A: PDB Molecule: ubiquitin fusion degradation protein 1; PDBTitle: ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
22	d1cz5a1	 Alignment	not modelled	64.8	28	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
23	c2c45F_	 Alignment	not modelled	64.3	18	PDB header: lyase Chain: F: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: native precursor of pyruvoyl dependent aspartate decarboxylase
24	c1pt1B_	 Alignment	not modelled	61.4	15	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
25	d1ppya_	 Alignment	not modelled	61.0	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
26	c6nk1D_	 Alignment	not modelled	60.2	23	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vapb1; PDBTitle: 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
27	c2yuja_	 Alignment	not modelled	52.2	18	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
28	c2oqkA_	 Alignment	not modelled	47.4	19	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a PDB header: ribosome

29	c4bpp0_	Alignment	not modelled	40.7	19	Chain: 0: PDB Molecule: translation initiation factor eif-1a family protein; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
30	c1uheA_	Alignment	not modelled	39.3	19	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase alpha chain; PDBTitle: crystal structure of aspartate decarboxylase, isoasparagine complex
31	d2jioa1	Alignment	not modelled	39.3	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1d7qa_	Alignment	not modelled	38.7	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
33	d1g8ka1	Alignment	not modelled	36.9	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
34	c5naaB_	Alignment	not modelled	36.5	13	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein-releasing system transmembrane protein lolc; PDBTitle: lipoprotein-releasing system transmembrane protein lolc
35	c2k4vA_	Alignment	not modelled	35.2	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1076; PDBTitle: solution structure of uncharacterized protein pa1076 from pseudomonas2 aeruginosa. northeast structural genomics consortium (nesg) target3 pat3, ontario center for structural proteomics target pa1076 .
36	c1h9mB_	Alignment	not modelled	34.3	14	PDB header: binding protein Chain: B: PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. peg-grown form with4 molybdate bound
37	c3plxB_	Alignment	not modelled	34.3	13	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
38	c3ougA_	Alignment	not modelled	34.2	16	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
39	c1vc3B_	Alignment	not modelled	33.4	13	PDB header: lyase Chain: B: PDB Molecule: l-aspartate-alpha-decarboxylase heavy chain; PDBTitle: crystal structure of l-aspartate-alpha-decarboxylase
40	c3pijB_	Alignment	not modelled	31.8	29	PDB header: transcription regulator Chain: B: PDB Molecule: hypothetical signal peptide protein; PDBTitle: crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
41	c3m7aA_	Alignment	not modelled	31.7	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sar0_0823 (yp_496102.1) a protein of unknown2 function from novosphingobium aromaticivorans dsm 12444 at 1.22 a3 resolution
42	c4zsiA_	Alignment	not modelled	30.7	18	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor dasr; PDBTitle: crystal structure of the effector-binding domain of dasr (dasr-ebd) in2 complex with glucosamine-6-phosphate
43	c3j81i	Alignment	not modelled	30.4	13	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
44	d1h9ma1	Alignment	not modelled	30.4	14	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
45	d1jt8a_	Alignment	not modelled	28.6	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
46	c5lxyH_	Alignment	not modelled	28.5	25	PDB header: rna binding protein Chain: H: PDB Molecule: zinc finger cchc domain-containing protein 8; PDBTitle: structure of the minimal rbm7 - zcchc8 complex
47	d1hr0w_	Alignment	not modelled	28.0	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
48	d2iv2x1	Alignment	not modelled	27.8	26	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
49	c5l6mA_	Alignment	not modelled	27.8	18	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
50	d1qvpa_	Alignment	not modelled	27.7	38	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
51	d1h0ha1	Alignment	not modelled	27.7	13	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
52	d1h9ra1	Alignment	not modelled	27.2	21	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
53	c2kl0A_	Alignment	not modelled	27.1	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target

					rpr325	
54	d3dl3a1	Alignment	not modelled	27.0	10	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: TehB-like
55	d2eifa2	Alignment	not modelled	27.0	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
56	d1vpka1	Alignment	not modelled	26.9	18	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase III, beta subunit
57	c4trtB_	Alignment	not modelled	25.7	13	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit beta; PDBTitle: deinococcus radiodurans dna polymerase iii subunit beta
58	c1uebB_	Alignment	not modelled	25.6	18	PDB header: rna binding protein Chain: B: PDB Molecule: elongation factor p; PDBTitle: crystal structure of translation elongation factor p from2 thermus thermophilus hb8
59	c1zeqX_	Alignment	not modelled	25.4	10	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
60	d1ogyal	Alignment	not modelled	24.9	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
61	d1h9ma2	Alignment	not modelled	24.8	14	Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
62	d2fala1	Alignment	not modelled	24.2	9	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
63	d1kqfa1	Alignment	not modelled	23.9	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
64	c2ra5A_	Alignment	not modelled	23.9	24	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator2 from streptomyces coelicolor
65	d2ra5a1	Alignment	not modelled	23.9	24	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
66	c3ll7A_	Alignment	not modelled	23.9	10	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
67	c6c00A_	Alignment	not modelled	22.4	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: solution structure of translation initiation factor 1 from clostridium2 difficile
68	c3nnqA_	Alignment	not modelled	22.3	29	PDB header: viral protein Chain: A: PDB Molecule: n-terminal domain of moloney murine leukemia virus PDBTitle: crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
69	d1zq1a1	Alignment	not modelled	21.7	15	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
70	c4ql5A_	Alignment	not modelled	20.8	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4
71	d1vlfm1	Alignment	not modelled	20.1	13	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
72	d2pkha1	Alignment	not modelled	20.1	12	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
73	c5ccbA_	Alignment	not modelled	19.9	21	PDB header: transferase/rna Chain: A: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase catalytic subunit PDBTitle: crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
74	d2zjda1	Alignment	not modelled	19.8	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
75	c5t5il_	Alignment	not modelled	19.6	16	PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdd; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
76	c3tndF_	Alignment	not modelled	19.6	23	PDB header: translation, toxin Chain: F: PDB Molecule: antitoxin vapb; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
77	c1ybyB_	Alignment	not modelled	19.6	20	PDB header: translation Chain: B: PDB Molecule: translation elongation factor p; PDBTitle: conserved hypothetical protein cth-95 from clostridium thermocellum
78	c3i4oA_	Alignment	not modelled	19.5	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
						PDB header: unknown function

79	c5ly5A_	Alignment	not modelled	19.4	32	Chain: A: PDB Molecule: arcadin-1; PDBTitle: arcadin-1 from pyrobaculum calidifontis
80	c3mhxB_	Alignment	not modelled	19.2	13	PDB header: metal transport Chain: B: PDB Molecule: putative ferrous iron transport protein a; PDBTitle: crystal structure of stentrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
81	d2p19a1	Alignment	not modelled	19.2	27	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
82	c1qw1A_	Alignment	not modelled	19.0	28	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: solution structure of the c-terminal domain of dtxr2 residues 110-226
83	c2ki8A_	Alignment	not modelled	18.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
84	d1fr3a_	Alignment	not modelled	18.7	21	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
85	d3bwga2	Alignment	not modelled	18.6	9	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
86	d3cnva1	Alignment	not modelled	18.5	30	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
87	d1tmoa1	Alignment	not modelled	18.5	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
88	d3d31a1	Alignment	not modelled	18.4	16	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
89	d1eu1a1	Alignment	not modelled	18.0	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
90	c4esnB_	Alignment	not modelled	17.7	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1312 family protein (rumgna_02503) from2 ruminococcus gnavus atcc 29149 at 2.20 a resolution
91	d1guta_	Alignment	not modelled	17.2	17	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
92	c4mnoA_	Alignment	not modelled	17.1	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
93	d1e32a1	Alignment	not modelled	17.0	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
94	c4cjdA_	Alignment	not modelled	16.8	16	PDB header: cell adhesion Chain: A: PDB Molecule: nada; PDBTitle: crystal structure of neisseria meningitidis trimeric2 autotransporter and vaccine antigen nada
95	d1dmra1	Alignment	not modelled	16.5	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
96	c3wwwvA_	Alignment	not modelled	16.0	4	PDB header: unknown function Chain: A: PDB Molecule: stomatatin operon partner protein; PDBTitle: c-terminal domain of stomatatin operon partner protein 1510-c from2 pyrococcus horikoshii
97	d1zud21	Alignment	not modelled	15.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
98	c5azhA_	Alignment	not modelled	15.5	16	PDB header: protein binding Chain: A: PDB Molecule: eeeweel peptide,protein lgg-2; PDBTitle: crystal structure of lgg-2 fused with an eeeweel peptide
99	c3treA_	Alignment	not modelled	15.1	13	PDB header: translation Chain: A: PDB Molecule: elongation factor p; PDBTitle: structure of a translation elongation factor p (efp) from coxiella2 burnetii