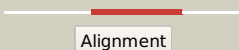
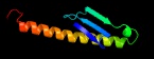
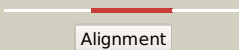

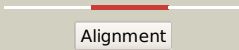

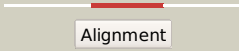

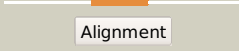

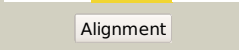

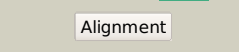

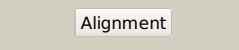

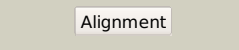



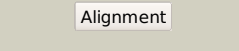




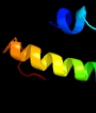
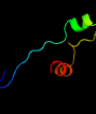
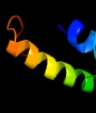
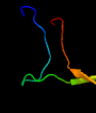
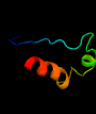
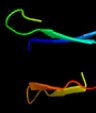


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3867_(-)_4342948_4343499
Date	Sat Aug 10 22:05:05 BST 2019
Unique Job ID	853f0776804b5240

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1puga_	 Alignment		97.5	15	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
2	d1j8ba_	 Alignment		96.9	14	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
3	c1ybxA_	 Alignment		96.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: conserved hypothetical protein cth-383 from clostridium thermocellum
4	d1pugb_	 Alignment		93.5	18	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
5	c5yrxA_	 Alignment		87.1	18	PDB header: dna binding protein Chain: A: PDB Molecule: nucleoid-associated protein rv3716c; PDBTitle: crystal structure of a hypothetical protein rv3716c from mycobacterium2 tuberculosis
6	c3f42A_	 Alignment		72.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
7	c4oiyA_	 Alignment		48.3	22	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec7; PDBTitle: crystal structure of sec7p catalytic domain
8	c1ls4A_	 Alignment		42.1	33	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein-iii; PDBTitle: nmr structure of apolipoprotein-iii from locusta migratoria
9	c6bbqA_	 Alignment		40.2	27	PDB header: lipid binding protein Chain: A: PDB Molecule: cytohesin-3, adp-ribosylation factor 6; PDBTitle: model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
10	d1aepa_	 Alignment		38.8	35	Fold: Apolipoprotein-III Superfamily: Apolipoprotein-III Family: Apolipoprotein-III
11	d2r09a1	 Alignment		38.6	26	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain

12	c3rhiB	Alignment		38.5	14	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein hu; PDBTitle: dna-binding protein hu from bacillus anthracis
13	c2r09A	Alignment		37.7	27	PDB header: signaling protein Chain: A: PDB Molecule: cytohesin-3; PDBTitle: crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor
14	c3l8nA	Alignment		37.7	31	PDB header: nucleotide-binding protein, metal-bindin Chain: A: PDB Molecule: brefeldin a-inhibited guanine nucleotide-exchange PDBTitle: crystal structure of a domain of brefeldin a-inhibited2 guanine nucleotide-exchange protein 2 (brefeldina-inhibited3 gep 2) from homo sapiens (human). northeast structural4 genomics consortium target id hr5562a
15	d1r8se	Alignment		36.1	27	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
16	d1seza2	Alignment		31.4	15	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
17	d1re0b	Alignment		30.8	23	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
18	c4e6zA	Alignment		29.9	15	PDB header: transport protein Chain: A: PDB Molecule: apicoplast tic22, putative; PDBTitle: tic22 from plasmodium falciparum
19	d2ivda2	Alignment		26.5	19	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
20	c5n76C	Alignment		25.8	35	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
21	d1pbva	Alignment	not modelled	25.7	20	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
22	c3dinB	Alignment	not modelled	24.8	26	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
23	c3juxA	Alignment	not modelled	24.2	26	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the translocation atpase seca from thermotoga2 maritima
24	c3no0B	Alignment	not modelled	23.4	43	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit a; PDBTitle: aquifex aeolicus type iia topoisomerase c-terminal domain
25	d1ofcx1	Alignment	not modelled	22.1	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
26	c4u3qA	Alignment	not modelled	21.5	37	PDB header: lipid binding protein Chain: A: PDB Molecule: 17 kda lipoprotein; PDBTitle: crystal structure of recombinant tp0435 from treponema pallidum
27	d1sf9a	Alignment	not modelled	21.2	30	Fold: SH3-like barrel Superfamily: Hypothetical protein YfhH Family: Hypothetical protein YfhH
28	c1xsza	Alignment	not modelled	20.9	15	PDB header: signaling protein Chain: A: PDB Molecule: guanine nucleotide exchange protein; PDBTitle: the structure of raf
						PDB header: structural genomics, unknown function

29	c2xyxA	Alignment	not modelled	20.8	30	Chain: A: PDB Molecule: hypothetical conserved protein, gk0453; PDBTitle: crystal structure of hypothetical conserved protein, gk0453
30	d1bc9a	Alignment	not modelled	20.6	27	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
31	d1xsza1	Alignment	not modelled	18.6	15	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
32	d1ku1a	Alignment	not modelled	18.6	16	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
33	d1v54e	Alignment	not modelled	18.3	24	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
34	d2a9da1	Alignment	not modelled	16.7	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Molybdenum-containing oxidoreductases-like dimerisation domain
35	c3d18B	Alignment	not modelled	16.5	26	PDB header: protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca
36	d1huua	Alignment	not modelled	15.2	15	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
37	c6n21A	Alignment	not modelled	14.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein dna-binding protein; PDBTitle: crystal structure of a histone family protein dna-binding protein from2 burkholderia ambifaria
38	c2y69R	Alignment	not modelled	14.8	24	PDB header: electron transport Chain: R: PDB Molecule: cytochrome c oxidase subunit 5a; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
39	c1tf2A	Alignment	not modelled	14.6	26	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of seca:adp in an open conformation from2 bacillus subtilis
40	c3i71B	Alignment	not modelled	14.1	22	PDB header: unknown function Chain: B: PDB Molecule: ethanolamine utilization protein eutk; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
41	d1owfa	Alignment	not modelled	14.1	17	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
42	d1xrsb2	Alignment	not modelled	13.8	32	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
43	c5fmfV	Alignment	not modelled	13.0	9	PDB header: transcription Chain: V: PDB Molecule: transcription initiation factor iif subunit beta, tfg2; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
44	d1ogpa1	Alignment	not modelled	12.8	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Molybdenum-containing oxidoreductases-like dimerisation domain
45	c2vdaA	Alignment	not modelled	12.5	30	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
46	d2ifta1	Alignment	not modelled	11.9	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
47	d1b33n	Alignment	not modelled	11.9	46	Fold: Allophycocyanin linker chain (domain) Superfamily: Allophycocyanin linker chain (domain) Family: Allophycocyanin linker chain (domain)
48	c5mq9A	Alignment	not modelled	11.9	21	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
49	c6hu9r	Alignment	not modelled	11.8	29	PDB header: oxidoreductase/electron transport Chain: R: PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
50	c3bovA	Alignment	not modelled	11.1	35	PDB header: immune system Chain: A: PDB Molecule: programmed cell death 1 ligand 2; PDBTitle: crystal structure of the receptor binding domain of mouse pd-l2
51	d1ea0a2	Alignment	not modelled	11.0	63	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
52	c1nl3B	Alignment	not modelled	10.9	27	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase seca 1 subunit; PDBTitle: crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
53	c1junB	Alignment	not modelled	10.7	24	PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
54	c2ndpA	Alignment	not modelled	10.6	20	PDB header: dna binding protein Chain: A: PDB Molecule: histone-like dna-binding superfamily protein; PDBTitle: structure of dna-binding hu protein from micoplasma mycoplasma2 gallisepticum
						PDB header: dna binding protein

55	c5ekaA_	Alignment	not modelled	10.6	14	Chain: A: PDB Molecule: dna-binding protein hu; PDBTitle: hu dna-binding protein from thermus thermophilus
56	c3k2kA_	Alignment	not modelled	10.6	18	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxypeptidase; PDBTitle: crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
57	d1ofda2	Alignment	not modelled	10.3	63	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
58	c2ipcB_	Alignment	not modelled	10.3	38	PDB header: transport protein Chain: B: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
59	c4ph8B_	Alignment	not modelled	10.3	26	PDB header: cell adhesion Chain: B: PDB Molecule: aggregative adherence fimbrial subunit agga; PDBTitle: crystal structure of agga, the major subunit of aggregative adherence2 fimbriae type i (aaf/i) from the escherichia coli o4h104
60	c3c4iA_	Alignment	not modelled	10.2	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu homolog; PDBTitle: crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
61	c4ev1A_	Alignment	not modelled	10.0	21	PDB header: chaperone Chain: A: PDB Molecule: anabena tic22; PDBTitle: anabaena tic22 (protein transport)
62	d1cz5a2	Alignment	not modelled	9.8	21	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
63	c3blcB_	Alignment	not modelled	9.6	18	PDB header: chaperone, protein transport Chain: B: PDB Molecule: inner membrane protein oxaa; PDBTitle: crystal structure of the periplasmic domain of the escherichia coli2 yidc
64	c3v8vB_	Alignment	not modelled	9.4	23	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase l; PDBTitle: crystal structure of bifunctional methyltransferase ycby (rlmlk) from2 escherichia coli, sam binding
65	c6gzbD_	Alignment	not modelled	9.4	7	PDB header: structural protein Chain: D: PDB Molecule: spore germination protein germ; PDBTitle: tandem germn domains of the sporulation protein germ from bacillus2 subtilis
66	c3bs6B_	Alignment	not modelled	9.3	18	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: inner membrane protein oxaa; PDBTitle: 1.8 angstrom crystal structure of the periplasmic domain of2 the membrane insertase yidc
67	d1exea_	Alignment	not modelled	9.2	15	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
68	c4qjuB_	Alignment	not modelled	9.1	18	PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna-binding protein hu; PDBTitle: crystal structure of dna-bound nucleoid associated protein, sav1473
69	c4c0aA_	Alignment	not modelled	9.1	18	PDB header: protein transport Chain: A: PDB Molecule: iq motif and sec7 domain-containing protein 1; PDBTitle: arf1(delta1-17)in complex with brag2 sec7-ph domain
70	d1h0ha1	Alignment	not modelled	9.0	12	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
71	c5hqhA_	Alignment	not modelled	8.7	17	PDB header: unknown function Chain: A: PDB Molecule: lmo2119 protein; PDBTitle: 1.32 angstrom crystal structure of ybbr like domain of lmo2119 protein2 from listeria monocytogenes.
72	c4uaqA_	Alignment	not modelled	8.6	38	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca 2; PDBTitle: crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis
73	c5bncB_	Alignment	not modelled	8.6	25	PDB header: heme binding protein Chain: B: PDB Molecule: heme binding protein msmeq_6519; PDBTitle: structure of heme binding protein msmeq_6519 from mycobacterium2 smegmatis
74	d1jmta_	Alignment	not modelled	8.5	31	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Splicing factor U2AF subunits
75	c3t7yB_	Alignment	not modelled	8.4	19	PDB header: protein transport Chain: B: PDB Molecule: yop proteins translocation protein u; PDBTitle: structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
76	d1hn0a3	Alignment	not modelled	8.3	12	Fold: Hyaluronate lyase-like, C-terminal domain Superfamily: Hyaluronate lyase-like, C-terminal domain Family: Hyaluronate lyase-like, C-terminal domain
77	c2jlhA_	Alignment	not modelled	8.2	14	PDB header: protein transport Chain: A: PDB Molecule: yop proteins translocation protein u; PDBTitle: crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
78	d1b8za_	Alignment	not modelled	8.1	15	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
79	c3b1sB_	Alignment	not modelled	8.1	19	PDB header: protein transport Chain: B: PDB Molecule: flagellar biosynthetic protein flhb; PDBTitle: crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus

80	c5lvC_	Alignment	not modelled	8.1	12	PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding protein hu; PDBTitle: structure of hu protein from lactococcus lactis
81	c3b0zB_	Alignment	not modelled	8.1	19	PDB header: protein transport Chain: B: PDB Molecule: flagellar biosynthetic protein flhb; PDBTitle: crystal structure of cytoplasmic domain of flhb from salmonella2 typhimurium
82	c4bpyA_	Alignment	not modelled	8.0	24	PDB header: chaperone Chain: A: PDB Molecule: sco protein; PDBTitle: crystal structure of the c90a mutant of the sco copper chaperone2 protein from streptomyces lividans
83	c2vt1B_	Alignment	not modelled	7.8	14	PDB header: membrane protein Chain: B: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structure of the cytoplasmic domain of spa40, the specificity2 switch for the shigella flexneri type iii secretion system
84	d1py9a_	Alignment	not modelled	7.7	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
85	c2lf6A_	Alignment	not modelled	7.6	18	PDB header: signaling protein Chain: A: PDB Molecule: effector protein hopab1; PDBTitle: solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a
86	d1nsza_	Alignment	not modelled	7.5	28	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Aldose 1-epimerase (mutarotase)
87	d1kqfa1	Alignment	not modelled	7.3	15	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
88	d3bzra1	Alignment	not modelled	7.2	14	Fold: EscU C-terminal domain-like Superfamily: EscU C-terminal domain-like Family: EscU C-terminal domain-like
89	c3bzrA_	Alignment	not modelled	7.2	14	PDB header: membrane protein, protein transport Chain: A: PDB Molecule: escu; PDBTitle: crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
90	d2as0a2	Alignment	not modelled	7.2	9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: hypothetical RNA methyltransferase
91	c6gf8B_	Alignment	not modelled	7.1	19	PDB header: cell adhesion Chain: B: PDB Molecule: zona pellucida sperm-binding protein 1, zona pellucida PDBTitle: molecular basis of egg coat filament cross-linking: structure of the2 glycosylated zp1 zp-n1 domain homodimer
92	c1rrqA_	Alignment	not modelled	7.0	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
93	c2n51A_	Alignment	not modelled	6.9	38	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 c-terminal domain
94	d2hu7a1	Alignment	not modelled	6.8	21	Fold: 7-bladed beta-propeller Superfamily: Peptidase/esterase 'gauge' domain Family: Acylamino-acid-releasing enzyme, N-terminal donain
95	c2vdcF_	Alignment	not modelled	6.8	63	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
96	c1lm1A_	Alignment	not modelled	6.6	63	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
97	c6iibB_	Alignment	not modelled	6.5	25	PDB header: toxin/protein binding Chain: B: PDB Molecule: putative rtx-toxin; PDBTitle: crystal structure of the makes caterpillars floppy (mcf)-like effector2 of vibrio vulnificus mo6-24/o in complex with a human adp-3 ribosylation factor 3 (arf3)
98	c2wb7B_	Alignment	not modelled	6.4	30	PDB header: unknown function Chain: B: PDB Molecule: pt26-6p; PDBTitle: pt26-6p
99	c3c01H_	Alignment	not modelled	6.4	14	PDB header: membrane protein, protein transport Chain: H: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structural of native spas c-terminal domain