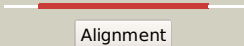

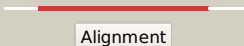

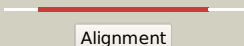







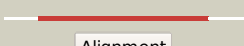






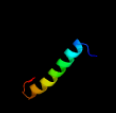

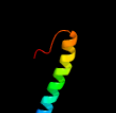

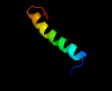


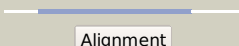

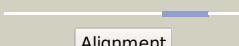
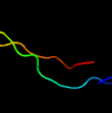
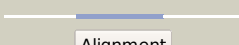

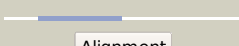

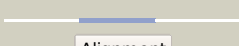



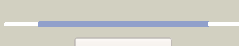


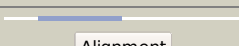
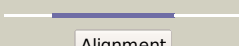
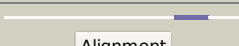

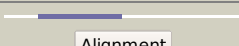

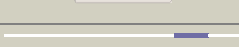


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1848_(ureA)_2097355_2097657
Date	Fri Aug 2 13:30:46 BST 2019
Unique Job ID	e1906be5c720fe91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d4ubpa_	 Alignment		100.0	65	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
2	c4furD_	 Alignment		100.0	50	PDB header: hydrolase Chain: D: PDB Molecule: urease subunit gamma 2; PDBTitle: crystal structure of urease subunit gamma 2 from brucella melitensis2 biovar abortus 2308
3	d1ejxa_	 Alignment		100.0	65	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
4	d1e9ya2	 Alignment		100.0	58	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
5	c1e9zA_	 Alignment		100.0	58	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
6	c4z42A_	 Alignment		100.0	51	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit gamma; PDBTitle: crystal structure of urease from yersinia enterocolitica
7	c2fvhB_	 Alignment		100.0	100	PDB header: hydrolase Chain: B: PDB Molecule: urease gamma subunit; PDBTitle: crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
8	c3qgaD_	 Alignment		100.0	57	PDB header: hydrolase Chain: D: PDB Molecule: fusion of urease beta and gamma subunits; PDBTitle: 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
9	c3la4A_	 Alignment		100.0	55	PDB header: hydrolase Chain: A: PDB Molecule: urease; PDBTitle: crystal structure of the first plant urease from jack bean (canavalia2 ensiformis)
10	d2dfaa1	 Alignment		53.8	34	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
11	c2x5eA_	 Alignment		49.0	16	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa

12	d1v6ta_	 Alignment		43.5	38	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
13	c4chmB_	 Alignment		33.6	35	PDB header: cell cycle Chain: B: PDB Molecule: imc sub-compartment protein isp1; PDBTitle: structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from toxoplasma gondii
14	c5zq2C_	 Alignment		29.1	14	PDB header: cell invasion Chain: C: PDB Molecule: side; PDBTitle: side apo form
15	c4chjA_	 Alignment		27.7	29	PDB header: cell cycle Chain: A: PDB Molecule: imc sub-compartment protein isp3; PDBTitle: structure of inner membrane complex (imc) sub-compartment2 protein 3 (isp3) from toxoplasma gondii
16	c6fddC_	 Alignment		25.1	14	PDB header: structural protein Chain: C: PDB Molecule: whirlin; PDBTitle: crystal structure of the hhd2 domain of whirlin
17	d2ffha2	 Alignment		23.7	24	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
18	c2v75A_	 Alignment		23.1	24	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
19	d1hq1a_	 Alignment		21.9	16	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
20	c4d2qC_	 Alignment		21.4	14	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)
21	c6ch2E_	 Alignment	not modelled	21.0	30	PDB header: structural protein Chain: E: PDB Molecule: flagellar hook-associated protein 2,flagellar protein flit; PDBTitle: crystal structure of the cytoplasmic domain of flha and flit-flid2 complex
22	d1dula_	 Alignment	not modelled	21.0	16	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
23	d1brwa1	 Alignment	not modelled	19.9	15	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
24	c4uerb_	 Alignment	not modelled	19.6	50	PDB header: translation Chain: B: PDB Molecule: us2; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
25	c2jqeA_	 Alignment	not modelled	19.6	18	PDB header: signaling protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: soution structure of af54 m-domain
26	c4ue4C_	 Alignment	not modelled	19.5	24	PDB header: translation Chain: C: PDB Molecule: signal recognition particle protein; PDBTitle: structural basis for targeting and elongation arrest of bacillus2 signal recognition particle
27	d1fskc1	 Alignment	not modelled	18.4	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
28	c6hiuA_	 Alignment	not modelled	18.3	45	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from methylococcus capsulatus (bath)

29	c5o9zE_	Alignment	not modelled	18.3	45	PDB header: splicing Chain: E: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
30	c3ml6D_	Alignment	not modelled	18.0	15	PDB header: protein transport Chain: D: PDB Molecule: chimeric complex between protein dishevelled2 homolog dvl-2 PDBTitle: a complex between dishevelled2 and clathrin adaptor ap-2
31	c6hihB_	Alignment	not modelled	17.4	36	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: cytochrome c prime beta from methylococcus capsulatus (bath)
32	c2c5qE_	Alignment	not modelled	17.2	16	PDB header: structural genomics,unknown function Chain: E: PDB Molecule: rraa-like protein yer010c; PDBTitle: crystal structure of yeast yer010cp
33	d1j6wa_	Alignment	not modelled	16.6	35	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
34	c4cdgC_	Alignment	not modelled	16.4	27	PDB header: hydrolase Chain: C: PDB Molecule: nanobody; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
35	d1ucbh1	Alignment	not modelled	16.3	42	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: V set domains (antibody variable domain-like)
36	d2tpta1	Alignment	not modelled	16.1	18	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
37	d1qb2a_	Alignment	not modelled	16.0	13	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
38	c5m30B_	Alignment	not modelled	16.0	42	PDB header: secretion system Chain: B: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
39	c3h3mB_	Alignment	not modelled	15.9	17	PDB header: structural genomics Chain: B: PDB Molecule: flagellar protein flit; PDBTitle: crystal structure of flagellar protein flit from bordetella2 bronchiseptica
40	d2ddha2	Alignment	not modelled	15.8	30	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: acyl-CoA oxidase C-terminal domains
41	c2w1oA_	Alignment	not modelled	15.5	24	PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
42	c2je2A_	Alignment	not modelled	15.4	45	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form
43	c2rlwA_	Alignment	not modelled	15.2	39	PDB header: toxin Chain: A: PDB Molecule: plnf; PDBTitle: three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaricin ef
44	c5kp0A_	Alignment	not modelled	14.6	30	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein flit,flagellum-specific atp synthase; PDBTitle: recognition and targeting mechanisms by chaperones in flagella2 assembly and operation
45	d2rhea_	Alignment	not modelled	14.2	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: V set domains (antibody variable domain-like)
46	d1qzxa2	Alignment	not modelled	14.2	24	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
47	c4xcoC_	Alignment	not modelled	13.9	26	PDB header: rna binding protein Chain: C: PDB Molecule: signal recognition particle 54 kda protein,signal sequence; PDBTitle: signal-sequence induced conformational changes in the signal2 recognition particle
48	c5m30C_	Alignment	not modelled	13.2	42	PDB header: secretion system Chain: C: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
49	c4f55A_	Alignment	not modelled	13.1	26	PDB header: hydrolase Chain: A: PDB Molecule: spore cortex-lytic enzyme; PDBTitle: crystal structure of the catalytic domain of the bacillus cereus sleb2 protein
50	c5m30A_	Alignment	not modelled	13.0	42	PDB header: secretion system Chain: A: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
51	c6amgA_	Alignment	not modelled	12.5	26	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cyt p460 of nitrosomonas sp. al212
52	d1jk0b_	Alignment	not modelled	12.1	13	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
53	c6et8B_	Alignment	not modelled	12.0	16	PDB header: protein binding Chain: B: PDB Molecule: albicidin resistance protein; PDBTitle: crystal structure of alba in complex with albicidin
						PDB header: immune system

54	c3iy1B_	Alignment	not modelled	11.6	30	Chain: B: PDB Molecule: fab b, heavy chain; PDBTitle: variable domains of the wam of fab b fitted into the cryoem2 reconstruction of the virus-fab b complex
55	c4d0uD_	Alignment	not modelled	11.5	50	PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of the fiber head domain of the atadenovirus snake2 adenovirus 1, selenomethionine-derivative
56	d1v8ga1	Alignment	not modelled	10.9	29	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
57	d1kj2b_	Alignment	not modelled	10.9	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
58	d1fvcb_	Alignment	not modelled	10.9	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
59	c5fvcF_	Alignment	not modelled	10.8	25	PDB header: viral protein Chain: F: PDB Molecule: hmpv nucleoprotein; PDBTitle: structure of rna-bound decameric hmpv nucleoprotein
60	d1n10l1	Alignment	not modelled	10.8	46	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
61	c1r6bX_	Alignment	not modelled	10.6	19	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
62	d1dpua_	Alignment	not modelled	10.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
63	c1dpuA_	Alignment	not modelled	10.2	15	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
64	c3hefB_	Alignment	not modelled	10.2	22	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
65	c4behB_	Alignment	not modelled	10.2	18	PDB header: translation Chain: B: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: solution structure of human ribosomal protein p1.p2 heterodimer
66	c5gafi_	Alignment	not modelled	10.1	16	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
67	c2e0cA_	Alignment	not modelled	10.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 409aa long hypothetical nadp-dependent isocitrate PDBTitle: crystal structure of isocitrate dehydrogenase from sulfobolus tokodaii2 strain7 at 2.0 a resolution
68	c6qrzA_	Alignment	not modelled	9.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: crystal structure of r2-like ligand-binding oxidase from sulfobolus2 acidocaldarius solved by 3d micro-crystal electron diffraction
69	d1lk3h1	Alignment	not modelled	9.8	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
70	c3iz5w_	Alignment	not modelled	9.7	46	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein I22 (I22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
71	d1eiJa_	Alignment	not modelled	9.7	37	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
72	c2dsjA_	Alignment	not modelled	9.7	13	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
73	c6q8jA_	Alignment	not modelled	9.6	22	PDB header: splicing Chain: A: PDB Molecule: wd40 repeat-containing protein smu1; PDBTitle: nterminal domain of human smu1 in complex with lsp641
74	c5gapG_	Alignment	not modelled	9.6	55	PDB header: transcription Chain: G: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: body region of the u4/u6.u5 tri-snrnp
75	c6f0gC_	Alignment	not modelled	9.4	73	PDB header: chaperone Chain: C: PDB Molecule: ip3; PDBTitle: crystal structure asf1-ip3
76	c6f0gD_	Alignment	not modelled	9.4	73	PDB header: chaperone Chain: D: PDB Molecule: ip3; PDBTitle: crystal structure asf1-ip3
77	d1n4xl_	Alignment	not modelled	9.3	60	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
78	c2yk5A_	Alignment	not modelled	9.2	83	PDB header: transferase Chain: A: PDB Molecule: cmp-n-acetylneuraminate-beta-galactosamide-alpha-2,3- PDBTitle: structure of neisseria los-specific sialyltransferase (nst), in2 complex with cmp.
						PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein;

79	c3dm5A_	Alignment	not modelled	9.2	16	PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
80	c5vm4B_	Alignment	not modelled	9.2	31	PDB header: unknown function Chain: B: PDB Molecule: single domain camelid nanobody vhh t10; PDBTitle: the apo form of the triclocarban-binding single domain camelid2 nanobody vhh t10
81	d1u3hb1	Alignment	not modelled	9.1	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
82	c2cfuA_	Alignment	not modelled	9.1	18	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
83	c4v0bA_	Alignment	not modelled	9.1	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: escherichia coli ftsh hexameric n-domain
84	c3pl5A_	Alignment	not modelled	8.9	16	PDB header: lipid binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: fatty acid binding protein
85	c2q6oB_	Alignment	not modelled	8.8	31	PDB header: biosynthetic protein Chain: B: PDB Molecule: hypothetical protein; PDBTitle: sall-y70t with sam and cl
86	d2jb5h1	Alignment	not modelled	8.8	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
87	c2fh0A_	Alignment	not modelled	8.7	16	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 16.0 kda protein in abf2-chl12 PDBTitle: nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
88	c5dhxA_	Alignment	not modelled	8.7	31	PDB header: immune system Chain: A: PDB Molecule: PDBTitle: hiv-1 rev ntd dimers with variable crossing angles
89	d2atpb1	Alignment	not modelled	8.6	55	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
90	c3jcmK_	Alignment	not modelled	8.5	55	PDB header: transcription Chain: K: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp
91	c5gs0D_	Alignment	not modelled	8.5	30	PDB header: immune system Chain: D: PDB Molecule: heavy chain (anti-tlr3); PDBTitle: crystal structure of the complex of tlr3 and bi-specific diabody
92	c4bmtB_	Alignment	not modelled	8.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleoside-diphosphate reductase subunit beta; PDBTitle: crystal structure of ribonucleotide reductase di-iron nrdf2 from bacillus cereus
93	d1o17a1	Alignment	not modelled	8.4	15	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
94	c3izcw_	Alignment	not modelled	8.4	38	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpl22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
95	d2pp6a1	Alignment	not modelled	8.3	28	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
96	d2cqqa1	Alignment	not modelled	8.2	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
97	d2o4ta1	Alignment	not modelled	8.1	32	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
98	d43c9b_	Alignment	not modelled	8.1	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
99	d1nakl1	Alignment	not modelled	8.0	60	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)