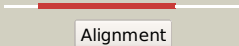
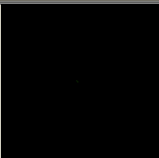


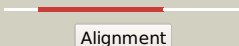

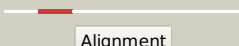

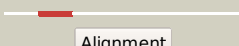
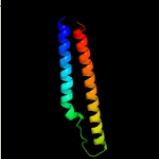
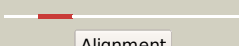
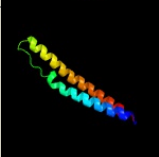
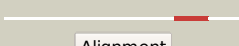

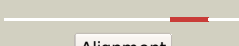




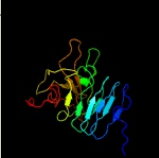


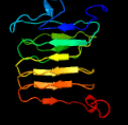










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2490c_(PE_PGRS43)_2801264_2806246
Date	Wed Aug 7 12:50:12 BST 2019
Unique Job ID	d674b45713b82c63

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		100.0	28	PDB header: structural protein/contractile protein Chain: A: PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule: rigid refinement
2	c1y0fB_	 Alignment		100.0	27	PDB header: structural protein/contractile protein Chain: B: PDB Molecule: collagen i alpha 2; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
3	c3hqvB_	 Alignment		100.0	26	PDB header: structural protein, contractile protein Chain: B: PDB Molecule: collagen alpha-2(i) chain; PDBTitle: low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
4	c2g38A_	 Alignment		99.9	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
5	d2g38a1	 Alignment		99.9	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
6	c5xfA_	 Alignment		99.9	49	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-pep15 in complex with esp95 from m.2 tuberculosis
7	c2qubG_	 Alignment		99.1	15	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
8	c2zj6A_	 Alignment		98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
9	c1k7qA_	 Alignment		98.6	13	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
10	c2ml3A_	 Alignment		98.2	22	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
11	c1satA_	 Alignment		98.0	15	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens

12	d1kapp1	Alignment		97.9	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
13	c1om8A_	Alignment		97.7	20	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
14	c2ml2A_	Alignment		97.7	23	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
15	d1k7ia1	Alignment		97.7	26	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
16	c3p4gD_	Alignment		97.6	14	PDB header: antifreeze protein Chain: D: PDB Molecule: antifreeze protein; PDBTitle: x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
17	c1jiwP_	Alignment		97.5	22	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
18	c2agmA_	Alignment		97.5	21	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
19	d1sata1	Alignment		97.4	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
20	c3bogB_	Alignment		97.4	41	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
21	c3bogA_	Alignment	not modelled	97.4	41	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
22	c2pneA_	Alignment	not modelled	97.2	40	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
23	c3boiB_	Alignment	not modelled	97.2	40	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
24	c3boiA_	Alignment	not modelled	97.2	40	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
25	d1g9ka1	Alignment	not modelled	97.1	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
26	c5cxlA_	Alignment	not modelled	96.4	29	PDB header: toxin Chain: A: PDB Molecule: bifunctional hemolysin/adenylate cyclase; PDBTitle: crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
27	c1nayC_	Alignment	not modelled	91.4	26	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
28	c5ctdB_	Alignment	not modelled	91.1	33	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain,collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen

29	c5ctiC	Alignment	not modelled	91.0	33	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
30	c5ctdA	Alignment	not modelled	90.6	33	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
31	c4q1qA	Alignment	not modelled	82.6	14	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tiba autotransporter; PDBTitle: crystal structure of tibi-catalyzed hyper-glycosylated tiba55-3502 fragment
32	c2klwA	Alignment	not modelled	73.8	30	PDB header: de novo protein Chain: A: PDB Molecule: (pkg)10; PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
33	c3mbfA	Alignment	not modelled	72.9	14	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from2 encephalitozoon cuniculi, bound to fructose 1,6-bisphosphate
34	c5juhA	Alignment	not modelled	72.6	19	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
35	c4wj2A	Alignment	not modelled	58.3	14	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
36	d1r31a2	Alignment	not modelled	52.2	23	Fold: Substrate-binding domain of HMG-CoA reductase Superfamily: Substrate-binding domain of HMG-CoA reductase Family: Substrate-binding domain of HMG-CoA reductase
37	d1lghb	Alignment	not modelled	47.3	53	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
38	c3cz6A	Alignment	not modelled	37.6	26	PDB header: protein binding Chain: A: PDB Molecule: dna-binding protein rap1; PDBTitle: crystal structure of the rap1 c-terminus
39	d1fbaa	Alignment	not modelled	37.2	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	c4jn6B	Alignment	not modelled	36.8	32	PDB header: lyase/oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
41	d2pv7a1	Alignment	not modelled	36.8	15	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
42	c1k6fA	Alignment	not modelled	36.4	31	PDB header: structural protein Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
43	c1k6fB	Alignment	not modelled	36.4	31	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
44	c1k6fD	Alignment	not modelled	36.4	31	PDB header: structural protein Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
45	c1k6fC	Alignment	not modelled	36.4	31	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
46	c1k6fF	Alignment	not modelled	36.4	31	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
47	c1k6fE	Alignment	not modelled	36.4	31	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
48	d1tg6a1	Alignment	not modelled	36.1	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
49	d1uaya	Alignment	not modelled	35.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
50	c1wrgA	Alignment	not modelled	34.1	27	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
51	c6et5u	Alignment	not modelled	30.8	33	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
52	c3h6pB	Alignment	not modelled	30.2	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
53	c4xgnD	Alignment	not modelled	30.2	25	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase in complex with2 nad from burkholderia thailandensis
		Alignment				Fold: Ferritin-like

54	d1mtyd_	Alignment	not modelled	27.8	14	Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
55	c2marA_	Alignment	not modelled	27.7	26	PDB header: unknown function Chain: A: PDB Molecule: sxp/ral-2 family protein; PDBTitle: solution structure of ani s 5 anisakis simplex allergen
56	c4o5oA_	Alignment	not modelled	26.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: x-ray crystal structure of a 3-hydroxyacyl-coa dehydrogenase from2 brucella suis
57	d1nvmb2	Alignment	not modelled	25.8	22	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
58	d1n7ka_	Alignment	not modelled	25.7	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
59	c3a0mF_	Alignment	not modelled	25.7	31	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
60	c5ff9C_	Alignment	not modelled	25.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcraugsodine reductase; PDBTitle: noroxomaritidine/norcraugsodine reductase in complex with nadp+ and2 tyramine
61	c5muul_	Alignment	not modelled	25.2	42	PDB header: virus Chain: I: PDB Molecule: major outer capsid protein; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
62	c3jclC_	Alignment	not modelled	24.4	20	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
63	d1l1na_	Alignment	not modelled	24.2	20	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Plant cytotoxins
64	c5ggfC_	Alignment	not modelled	23.0	15	PDB header: transferase, sugar binding protein Chain: C: PDB Molecule: protein o-linked-mannose beta-1,2-n- PDBTitle: crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
65	c1zorB_	Alignment	not modelled	22.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
66	c3ce9A_	Alignment	not modelled	22.6	6	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
67	c2cuoF_	Alignment	not modelled	22.6	33	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
68	c2cuoC_	Alignment	not modelled	22.6	33	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
69	c3onjA_	Alignment	not modelled	22.3	17	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
70	c3kthD_	Alignment	not modelled	21.8	12	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of clpp from bacillus subtilis in orthorhombic crystal form
71	c3w5mA_	Alignment	not modelled	21.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative rhamnosidase; PDBTitle: crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
72	d1xfba1	Alignment	not modelled	20.8	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
73	d2o70a1	Alignment	not modelled	20.0	8	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
74	c6cmxA_	Alignment	not modelled	19.5	24	PDB header: membrane protein Chain: A: PDB Molecule: teneurin-2; PDBTitle: human teneurin 2 extra-cellular region
75	c5xlrC_	Alignment	not modelled	19.0	23	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
76	c5ulmB_	Alignment	not modelled	18.6	18	PDB header: transferase Chain: B: PDB Molecule: mitogen-activated protein kinase kinase kinase 5; PDBTitle: structure of the ask1 central regulatory region
77	c6cv0C_	Alignment	not modelled	18.5	23	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
78	c4pcvB_	Alignment	not modelled	18.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: bdca (yjgi); PDBTitle: the structure of bdca (yjgi) from e. coli
79	c3bezC_	Alignment	not modelled	18.1	19	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
						PDB header: ribosome Chain: E: PDB Molecule: rpl6;

80	c4a1dE_	Alignment	not modelled	17.8	9	PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
81	c6nzkB_	Alignment	not modelled	17.6	18	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
82	c3l7vA_	Alignment	not modelled	17.6	18	PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1377c; PDBTitle: crystal structure of a hypothetical protein smu.1377c from2 streptococcus mutans ua159
83	d2g84a1	Alignment	not modelled	17.5	25	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
84	c6cs2A_	Alignment	not modelled	16.9	23	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrinin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
85	c6a2uA_	Alignment	not modelled	16.4	18	PDB header: signaling protein/oxidoreductase Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
86	c4rglA_	Alignment	not modelled	16.4	23	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
87	c1kmiZ_	Alignment	not modelled	16.3	18	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
88	c2oyyF_	Alignment	not modelled	16.3	29	PDB header: unknown function Chain: F: PDB Molecule: hexameric cytochrome; PDBTitle: htp: a hexameric tyrosine-coordinated heme protein
89	d1yg6a1	Alignment	not modelled	15.9	11	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
90	c5z5mB_	Alignment	not modelled	15.7	20	PDB header: lyase Chain: B: PDB Molecule: predicted protein; PDBTitle: crystal structure of (s)-allantoin synthase
91	d2ew8a1	Alignment	not modelled	15.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c5mgzA_	Alignment	not modelled	15.6	30	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobioc acid c(8)-methyltransferase; PDBTitle: streptomycetes spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah
93	c6nvvC_	Alignment	not modelled	15.1	14	PDB header: hydrolase Chain: C: PDB Molecule: penicillin g acylase; PDBTitle: crystal structure of penicillin g acylase from bacillus thermotolerans
94	c3p4iA_	Alignment	not modelled	15.0	26	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
95	c5i08A_	Alignment	not modelled	14.8	20	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
96	c6f0kB_	Alignment	not modelled	14.6	18	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
97	c3q7hM_	Alignment	not modelled	14.2	10	PDB header: hydrolase Chain: M: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of the clpp subunit of the atp-dependent clp protease from2 coxiella burnetii
98	d1qaxa2	Alignment	not modelled	14.1	28	Fold: Substrate-binding domain of HMG-CoA reductase Superfamily: Substrate-binding domain of HMG-CoA reductase Family: Substrate-binding domain of HMG-CoA reductase
99	c6b7nC_	Alignment	not modelled	13.8	19	PDB header: viral protein Chain: C: PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state