

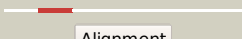

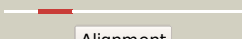








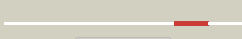


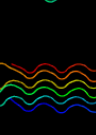



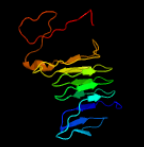



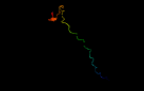
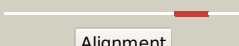
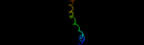


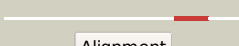
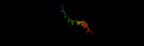
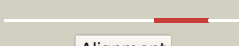
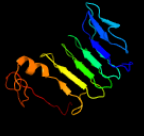






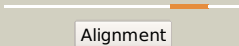
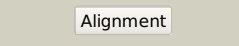

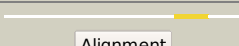

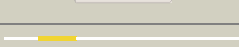


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1243c_(PE_PGRS23)_1384995_1386683
 Date Wed Jul 31 22:05:33 BST 2019
 Unique Job ID 7d8fa691a5e49fde

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfA_	 Alignment		100.0	49	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38A_	 Alignment		100.0	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppa protein complex from mycobacterium tuberculosis
3	d2g38a1	 Alignment		100.0	26	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c1ygvA_	 Alignment		99.6	25	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
5	c3hqvB_	 Alignment		99.6	30	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
6	c1y0fB_	 Alignment		99.1	28	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
7	c3bogB_	 Alignment		97.7	35	PDB header: antifreeze protein Chain: B; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
8	c3bogA_	 Alignment		97.7	35	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
9	c2pneA_	 Alignment		97.7	36	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
10	c3boiB_	 Alignment		97.7	36	PDB header: antifreeze protein Chain: B; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
11	c3boiA_	 Alignment		97.7	36	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate

12	c1k7qA_	 Alignment		95.0	14	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
13	c5ctdA_	 Alignment		94.1	37	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
14	c1nayC_	 Alignment		94.0	28	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
15	c5ctiC_	 Alignment		93.9	37	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)
16	c2qubG_	 Alignment		93.7	16	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
17	c5ctdB_	 Alignment		93.6	31	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
18	c1satA_	 Alignment		92.8	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
19	d1kapp1	 Alignment		92.2	15	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
20	c2zj6A_	 Alignment		91.5	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
21	c2ml3A_	 Alignment	not modelled	89.1	19	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
22	c2ml2A_	 Alignment	not modelled	86.8	16	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
23	c1jiwP_	 Alignment	not modelled	83.7	19	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
24	d1k7ia1	 Alignment	not modelled	79.2	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
25	c5szsC_	 Alignment	not modelled	78.8	22	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
26	c2agmA_	 Alignment	not modelled	78.4	22	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
27	d1g9ka1	 Alignment	not modelled	77.2	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
28	c3gvmA_	 Alignment	not modelled	74.6	11	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein

						from streptococcus2 agalactiae
29	c1om8A_	Alignment	not modelled	74.0	19	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
30	d1sata1	Alignment	not modelled	66.5	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
31	d1wa8a1	Alignment	not modelled	66.2	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
32	c5cx1A_	Alignment	not modelled	65.2	27	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
33	c6nb3B_	Alignment	not modelled	64.2	26	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
34	c5x5fC_	Alignment	not modelled	64.0	27	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
35	c4lwsA_	Alignment	not modelled	58.6	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
36	c4iogD_	Alignment	not modelled	52.9	16	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
37	c5x5bB_	Alignment	not modelled	48.3	28	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
38	c5i08A_	Alignment	not modelled	48.3	21	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
39	c4wj2A_	Alignment	not modelled	45.9	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
40	c6b7nC_	Alignment	not modelled	45.6	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
41	c6nzkB_	Alignment	not modelled	45.3	18	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
42	c5x1rC_	Alignment	not modelled	45.3	27	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
43	c6cs2A_	Alignment	not modelled	42.8	25	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
44	c2klwA_	Alignment	not modelled	42.6	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
45	c3j1cC_	Alignment	not modelled	40.4	21	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
46	c3p4gD_	Alignment	not modelled	34.1	18	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
47	c6cv0C_	Alignment	not modelled	32.3	18	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
48	c3zbhC_	Alignment	not modelled	31.5	12	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
49	d1lghb_	Alignment	not modelled	29.0	43	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
50	c2vs0B_	Alignment	not modelled	27.0	9	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
51	c2kg7B_	Alignment	not modelled	26.3	14	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
52	c3a0mF_	Alignment	not modelled	25.8	46	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
53	c1wrgA_	Alignment	not modelled	22.6	29	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
54	c2cuoF_	Alignment	not modelled	22.3	41	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9

55	c2cuoC_	Alignment	not modelled	22.3	41	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
56	c6et5u_	Alignment	not modelled	21.6	36	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
57	c2w0cR_	Alignment	not modelled	21.6	29	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
58	c3ah9F_	Alignment	not modelled	20.7	46	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
59	c3ah9A_	Alignment	not modelled	20.3	48	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
60	c3onjA_	Alignment	not modelled	19.1	22	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
61	c3ah9B_	Alignment	not modelled	17.3	46	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
62	c3ah9E_	Alignment	not modelled	17.3	46	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
63	c3ah9C_	Alignment	not modelled	17.3	46	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
64	c3ah9D_	Alignment	not modelled	16.8	45	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
65	c5wrgB_	Alignment	not modelled	15.3	30	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
66	c2cuoE_	Alignment	not modelled	14.5	46	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
67	c2cuoA_	Alignment	not modelled	14.5	46	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
68	c2cuoD_	Alignment	not modelled	14.5	46	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
69	c2cuoB_	Alignment	not modelled	14.5	46	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
70	c4krrA_	Alignment	not modelled	14.2	29	PDB header: signaling protein Chain: A: PDB Molecule: wnt inhibitor of dorsal protein; PDBTitle: crystal structure of drosophila wntd n-terminal domain-linker2 (residues 31-240)
71	c3w5mA_	Alignment	not modelled	12.7	22	PDB header: hydrolase Chain: A: PDB Molecule: putative rhamnosidase; PDBTitle: crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
72	c5mgzA_	Alignment	not modelled	12.1	27	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobiocic acid2 methyltransferase) with sah
73	c6ahyD_	Alignment	not modelled	11.4	35	PDB header: signaling protein Chain: D: PDB Molecule: proto-oncogene wnt-3; PDBTitle: wnt signaling complex
74	c6bjcP_	Alignment	not modelled	10.3	38	PDB header: cell cycle Chain: P: PDB Molecule: targeting protein for xklp2; PDBTitle: tpx2_mini decorated gmppcp-microtubule
75	c6bjcT_	Alignment	not modelled	10.3	38	PDB header: cell cycle Chain: T: PDB Molecule: targeting protein for xklp2; PDBTitle: tpx2_mini decorated gmppcp-microtubule
76	c4f0aB_	Alignment	not modelled	9.7	41	PDB header: signaling protein Chain: B: PDB Molecule: protein wnt-8; PDBTitle: crystal structure of xwnt8 in complex with the cysteine-rich domain of2 frizzled 8
77	c4rglA_	Alignment	not modelled	9.6	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
78	d1cvra2	Alignment	not modelled	9.1	4	Fold: Caspase-like Superfamily: Caspase-like Family: Gingipain R (RgpB), N-terminal domain
79	c4f9iA_	Alignment	not modelled	9.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase/delta-1-pyrroline-5-carboxylate PDBTitle: crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
80	c2v8sV_	Alignment	not modelled	6.9	22	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
81	c3g9kD_	Alignment	not modelled	6.3	25	PDB header: hydrolase Chain: D: PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase

						enzyme capd
82	c1k6fD_	Alignment	not modelled	6.0	38	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
83	c1k6fC_	Alignment	not modelled	6.0	38	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
84	c1k6fE_	Alignment	not modelled	6.0	38	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
85	c1k6fA_	Alignment	not modelled	6.0	38	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
86	c1k6fF_	Alignment	not modelled	6.0	38	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
87	c1k6fB_	Alignment	not modelled	6.0	38	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
88	c1cvrA_	Alignment	not modelled	5.4	4	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: gingipain r; PDBTitle: crystal structure of the arg specific cysteine proteinase gingipain r2 (rgpb)
89	c2qapC_	Alignment	not modelled	5.4	29	PDB header: lyase Chain: C: PDB Molecule: fructose-1,6-bisphosphate aldolase; PDBTitle: fructose-1,6-bisphosphate aldolase from leishmania mexicana
90	c2z8jA_	Alignment	not modelled	5.3	25	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark
91	c5yqgE_	Alignment	not modelled	5.2	29	PDB header: peptide binding protein Chain: E: PDB Molecule: peptide from protein numb homolog; PDBTitle: the structure of 14-3-3 and pnumb peptide
92	c4gdxA_	Alignment	not modelled	5.1	34	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase 1 heavy chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex