
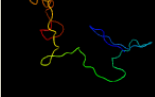





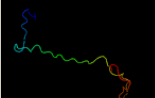
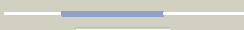




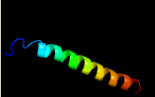

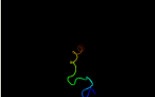

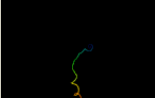

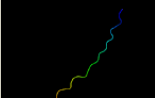

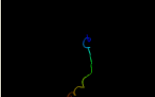
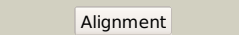
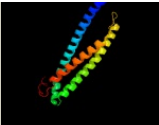
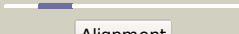
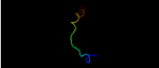




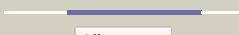
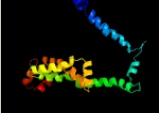




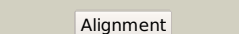
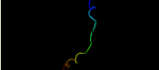
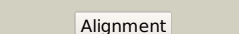


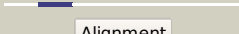

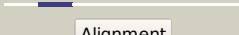
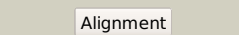
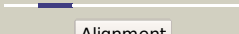
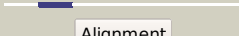


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2560_(-)_2880085_2881062
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	35a75670462662f7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4nl6C_</a>	 Alignment		95.3	21	<b>PDB header:</b> splicing <b>Chain:</b> C; <b>PDB Molecule:</b> survival motor neuron protein; <b>PDBTitle:</b> structure of the full-length form of the protein smn found in healthy2 patients
2	<a href="#">c6d79A_</a>	 Alignment		56.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> sulfate transporter cysz; <b>PDBTitle:</b> structure of cysz, a sulfate permease from pseudomonas fragi
3	<a href="#">c4djiA_</a>	 Alignment		46.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
4	<a href="#">c2kpyA_</a>	 Alignment		41.2	25	<b>PDB header:</b> allergen <b>Chain:</b> A; <b>PDB Molecule:</b> major pollen allergen art v 1; <b>PDBTitle:</b> solution structure of the major allergen of artemisia vulgaris (art v2 1)
5	<a href="#">c6hwhb_</a>	 Alignment		26.3	16	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
6	<a href="#">c5ndaA_</a>	 Alignment		13.4	21	<b>PDB header:</b> protein <b>Chain:</b> A; <b>PDB Molecule:</b> rsp-c33leu -recombinant pulmonary surfactant-associated <b>PDBTitle:</b> nmr structural characterisation of pharmaceutically relevant proteins2 obtained through a novel recombinant production: the case of the3 pulmonary surfactant polypeptide c analogue rsp-c33leu.
7	<a href="#">c3ixzB_</a>	 Alignment		13.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
8	<a href="#">c3admE_</a>	 Alignment		12.9	62	<b>PDB header:</b> structural protein <b>Chain:</b> E; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
9	<a href="#">c3admF_</a>	 Alignment		12.9	62	<b>PDB header:</b> structural protein <b>Chain:</b> F; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
10	<a href="#">c3admB_</a>	 Alignment		12.9	62	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
11	<a href="#">c3admA_</a>	 Alignment		12.9	62	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4

12	<a href="#">c5lj7B_</a>	 Alignment		12.3	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
13	<a href="#">c3abnA_</a>	 Alignment		10.9	62	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
14	<a href="#">c3admC_</a>	 Alignment		10.8	60	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
15	<a href="#">c3j8eG_</a>	 Alignment		10.5	6	<b>PDB header:</b> transport protein/isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> cryo-em structure of ryanodine receptor/calstabin-2 complex
16	<a href="#">c4tqvl_</a>	 Alignment		10.4	9	<b>PDB header:</b> transport protein <b>Chain:</b> I: <b>PDB Molecule:</b> algm1; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
17	<a href="#">c2jlnA_</a>	 Alignment		10.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
18	<a href="#">c5ws4A_</a>	 Alignment		10.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
19	<a href="#">c3admD_</a>	 Alignment		9.9	64	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
20	<a href="#">c2d3fE_</a>	 Alignment		9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
21	<a href="#">c1x1kD_</a>	 Alignment	not modelled	9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
22	<a href="#">c1x1kC_</a>	 Alignment	not modelled	9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
23	<a href="#">c1x1kB_</a>	 Alignment	not modelled	9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
24	<a href="#">c1x1kA_</a>	 Alignment	not modelled	9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
25	<a href="#">c2d3fF_</a>	 Alignment	not modelled	9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
26	<a href="#">c2d3fD_</a>	 Alignment	not modelled	9.6	62	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
27	<a href="#">c2cuoF_</a>	 Alignment	not modelled	9.4	52	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9

28	<a href="#">c2cuoC_</a>	Alignment	not modelled	9.4	52	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
29	<a href="#">d2bcgg2</a>	Alignment	not modelled	8.2	25	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
30	<a href="#">c2nq2A_</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical abc transporter permease protein <b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.
31	<a href="#">c2d3fB_</a>	Alignment	not modelled	7.2	64	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
32	<a href="#">c2d3fA_</a>	Alignment	not modelled	7.2	64	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
33	<a href="#">c1x1kE_</a>	Alignment	not modelled	7.2	64	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
34	<a href="#">c2d3fC_</a>	Alignment	not modelled	7.2	64	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
35	<a href="#">c3aqpB_</a>	Alignment	not modelled	6.9	9	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
36	<a href="#">c3abnB_</a>	Alignment	not modelled	6.8	63	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
37	<a href="#">c3k07A_</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
38	<a href="#">c4fzIB_</a>	Alignment	not modelled	6.3	16	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacteriocin; <b>PDBTitle:</b> high resolution structure of truncated bacteriocin syringacin m from2 pseudomonas syringae pv. tomato dc3000
39	<a href="#">c2cuoA_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
40	<a href="#">c2cuoE_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
41	<a href="#">c2cuoB_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
42	<a href="#">c2cuoD_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
43	<a href="#">c4yzfA_</a>	Alignment	not modelled	6.1	11	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> band 3 anion transport protein; <b>PDBTitle:</b> crystal structure of the anion exchanger domain of human erythrocyte2 band 3
44	<a href="#">d2cvba1</a>	Alignment	not modelled	6.0	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
45	<a href="#">c2xzbB_</a>	Alignment	not modelled	5.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> pig gastric h,k-atpase with bound bef and sch28080
46	<a href="#">c3abnC_</a>	Alignment	not modelled	5.8	59	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
47	<a href="#">c5h7yB_</a>	Alignment	not modelled	5.8	25	<b>PDB header:</b> hydrolase inhibitor/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of immunity protein tplei of t6ss from pseudomonas2 aeruginosa complexed with "I" peptide
48	<a href="#">c5tj6A_</a>	Alignment	not modelled	5.8	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> high conductance calcium-activated potassium channel; <b>PDBTitle:</b> ca2+ bound aplysia slo1
49	<a href="#">c4clqB_</a>	Alignment	not modelled	5.6	13	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome biogenesis protein bms1; <b>PDBTitle:</b> structure of rcl1p - bms1p complex
50	<a href="#">c5mg3D_</a>	Alignment	not modelled	5.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
51	<a href="#">c3a0aC_</a>	Alignment	not modelled	5.5	59	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
52	<a href="#">c3a0aB_</a>	Alignment	not modelled	5.5	62	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal

53	<a href="#">c3ah9A_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
54	<a href="#">d1rh5b_</a>	Alignment	not modelled	5.4	15	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Preprotein translocase SecE subunit <b>Family:</b> Preprotein translocase SecE subunit
55	<a href="#">c1x1kF_</a>	Alignment	not modelled	5.4	41	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
56	<a href="#">c3ah9C_</a>	Alignment	not modelled	5.3	48	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
57	<a href="#">c3ah9B_</a>	Alignment	not modelled	5.3	48	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
58	<a href="#">c3ah9E_</a>	Alignment	not modelled	5.3	48	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
59	<a href="#">c3a0aF_</a>	Alignment	not modelled	5.2	62	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
60	<a href="#">c4fzmA_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin; <b>PDBTitle:</b> crystal structure of the bacteriocin syringacin m from pseudomonas2 syringae pv. tomato dc3000
61	<a href="#">c3a1hF_</a>	Alignment	not modelled	5.1	59	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
62	<a href="#">c3a0mA_</a>	Alignment	not modelled	5.1	64	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal