


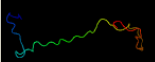

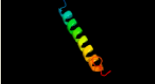

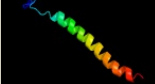


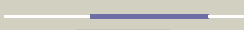
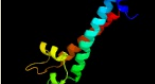



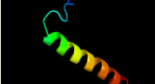

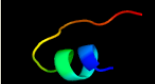

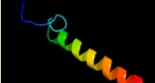




# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1078\_(pra)\_1203318\_1204040  
 Date Wed Jul 31 22:05:15 BST 2019  
 Unique Job ID 3270c813e480a9c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4nl6C_</a>	 Alignment		95.3	32	<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="#">c2kpyA_</a>	 Alignment		47.1	33	<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)
3	<a href="#">c2k1aA_</a>	 Alignment		36.6	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iib) transmembrane segment
4	<a href="#">c2kncA_</a>	 Alignment		34.8	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
5	<a href="#">c2kncB_</a>	 Alignment		21.6	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
6	<a href="#">c2axtc_</a>	 Alignment		17.8	12	<b>PDB header:</b> electron transport <b>Chain:</b> C; <b>PDB Molecule:</b> photosystem ii cp43 protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
7	<a href="#">d2axtc1</a>	 Alignment		17.8	12	<b>Fold:</b> Photosystem II antenna protein-like <b>Superfamily:</b> Photosystem II antenna protein-like <b>Family:</b> Photosystem II antenna protein-like
8	<a href="#">d1v54j_</a>	 Alignment		16.0	20	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIa <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIa
9	<a href="#">d1hywa_</a>	 Alignment		16.0	19	<b>Fold:</b> gpW/XkdW-like <b>Superfamily:</b> Head-to-tail joining protein W, gpW <b>Family:</b> Head-to-tail joining protein W, gpW
10	<a href="#">c5z62j_</a>	 Alignment		14.0	17	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> cytochrome c oxidase subunit 7a2, mitochondrial; <b>PDBTitle:</b> structure of human cytochrome c oxidase
11	<a href="#">c2y69W_</a>	 Alignment		14.0	20	<b>PDB header:</b> electron transport <b>Chain:</b> W; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 7a1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen

12	<a href="#">d1u9da_</a>	Alignment		13.9	24	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> VC0714-like
13	<a href="#">c6m97A_</a>	Alignment		13.7	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1 <b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1
14	<a href="#">c5zazA_</a>	Alignment		13.4	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
15	<a href="#">c2voyB_</a>	Alignment		12.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium atpase 1; <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
16	<a href="#">d2qlza1</a>	Alignment		12.3	19	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> FwdE-like <b>Family:</b> FwdE-like
17	<a href="#">c3b8eB_</a>	Alignment		12.2	10	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
18	<a href="#">c3d00A_</a>	Alignment		11.5	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit e; <b>PDBTitle:</b> crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
19	<a href="#">c4y7jE_</a>	Alignment		10.8	16	<b>PDB header:</b> membrane protein,transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> large conductance mechanosensitive channel protein, <b>PDBTitle:</b> structure of an archaeal mechanosensitive channel in expanded state
20	<a href="#">c5ireA_</a>	Alignment		9.7	22	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
21	<a href="#">c2l8sA_</a>	Alignment	not modelled	9.6	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
22	<a href="#">c5o6vC_</a>	Alignment	not modelled	9.3	27	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
23	<a href="#">c2clbP_</a>	Alignment	not modelled	9.2	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> P: <b>PDB Molecule:</b> dps-like protein; <b>PDBTitle:</b> the structure of the dps-like protein from sulfolobus2 solfataricus reveals a bacterioferritin-like di-meta13 binding site within a dps-like dodecameric assembly
24	<a href="#">c5xvjB_</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> phd finger protein alfin-like 7; <b>PDBTitle:</b> crystal structure of al7 pal domain
25	<a href="#">c4m1aB_</a>	Alignment	not modelled	8.8	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a domain of unknown function (duf1904) from2 sebaldeella termitidis atcc 33386
26	<a href="#">d1k28d2</a>	Alignment	not modelled	8.7	19	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
27	<a href="#">c2l6wA_</a>	Alignment	not modelled	8.5	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-type platelet-derived growth factor receptor; <b>PDBTitle:</b> pdgfr beta-tm
28	<a href="#">c2l6wB_</a>	Alignment	not modelled	8.5	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> beta-type platelet-derived growth factor receptor; <b>PDBTitle:</b> pdgfr beta-tm

29	<a href="#">c2xq2A_</a>	Alignment	not modelled	8.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsgl
30	<a href="#">c4jcbD_</a>	Alignment	not modelled	8.4	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> light-harvesting protein b-875 alpha chain; <b>PDBTitle:</b> rc-lh1-pufx dimer complex from rhodobacter sphaeroides
31	<a href="#">c3iz6S_</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 40s ribosomal protein s19 (s19e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
32	<a href="#">c4xw5B_</a>	Alignment	not modelled	7.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase inhibitor alpha; <b>PDBTitle:</b> x-ray structure of pkac with atp, cp20, calcium ions
33	<a href="#">c4xw6B_</a>	Alignment	not modelled	7.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase inhibitor alpha; <b>PDBTitle:</b> x-ray structure of pkac with adp, free phosphate ion, cp20, magnesium2 ions
34	<a href="#">c3kdpD_</a>	Alignment	not modelled	7.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit beta-1; <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
35	<a href="#">c4qmdB_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> envoplakin; <b>PDBTitle:</b> crystal structure of human envoplakin plakin repeat domain
36	<a href="#">c4q28B_</a>	Alignment	not modelled	7.2	17	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplakin; <b>PDBTitle:</b> crystal structure of the plectin 1 and 2 repeats of the human2 periplakin. northeast structural genomics consortium (nesg) target3 hr9083a
37	<a href="#">c2n03A_</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> solution nmr structure plectin repeat domain 6 (4403-4606) of plectin2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr6354e
38	<a href="#">d1ymga1</a>	Alignment	not modelled	6.7	18	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
39	<a href="#">c1ymgA_</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> the channel architecture of aquaporin o at 2.2 angstrom resolution
40	<a href="#">c5kzoA_</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> notch1 transmembrane and associated juxtamembrane segment
41	<a href="#">c1xrdA_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> light-harvesting protein b-880, alpha chain; <b>PDBTitle:</b> light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
42	<a href="#">d1xrda1</a>	Alignment	not modelled	6.6	22	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
43	<a href="#">c5dzzaA_</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> desmoplakin; <b>PDBTitle:</b> structural characterization of intermediate filaments binding domain2 of desmoplakin
44	<a href="#">d1lm5a_</a>	Alignment	not modelled	6.1	10	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Plakin repeat <b>Family:</b> Plakin repeat
45	<a href="#">c3admD_</a>	Alignment	not modelled	5.8	52	<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
46	<a href="#">c3a19E_</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
47	<a href="#">c3a19C_</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
48	<a href="#">c3wmmY_</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> lh1 alpha polypeptide; <b>PDBTitle:</b> crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
49	<a href="#">c6c6lO_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> membrane protein <b>Chain:</b> O: <b>PDB Molecule:</b> v-type proton atpase subunit f; <b>PDBTitle:</b> yeast vacuolar atpase vo in lipid nanodisc
50	<a href="#">d2gvia1</a>	Alignment	not modelled	5.6	24	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> FwdE-like <b>Family:</b> FwdE-like
51	<a href="#">c5yq72_</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> beta subunit of light-harvesting 1; <b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
52	<a href="#">c2yevB_</a>	Alignment	not modelled	5.5	5	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase
53	<a href="#">c2n28A_</a>	Alignment	not modelled	5.4	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein vpu; <b>PDBTitle:</b> solid-state nmr structure of vpu
54	<a href="#">c2n09E_</a>	Alignment	not modelled	5.4	57	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide;

54	<a href="#">c3advl_</a>	Alignment	not modelled	5.4	57	<b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal <b>PDB header:</b> structural protein
55	<a href="#">c3admA_</a>	Alignment	not modelled	5.4	52	<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
56	<a href="#">c3admB_</a>	Alignment	not modelled	5.4	52	<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
57	<a href="#">c3admF_</a>	Alignment	not modelled	5.4	52	<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
58	<a href="#">c3admE_</a>	Alignment	not modelled	5.4	52	<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
59	<a href="#">c2qviA_</a>	Alignment	not modelled	5.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
60	<a href="#">c3ixzB_</a>	Alignment	not modelled	5.4	13	<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
61	<a href="#">c2cuoF_</a>	Alignment	not modelled	5.4	48	<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
62	<a href="#">c2cuoC_</a>	Alignment	not modelled	5.4	48	<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
63	<a href="#">c2lu2A_</a>	Alignment	not modelled	5.3	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> microneme tgmic5 protein; <b>PDBTitle:</b> mic5 regulates the activity of toxoplasma subtilisin 1 by mimicking a2 subtilisin prodomain
64	<a href="#">d1lm7a_</a>	Alignment	not modelled	5.3	19	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Plakin repeat <b>Family:</b> Plakin repeat
65	<a href="#">c3a19A_</a>	Alignment	not modelled	5.3	48	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
66	<a href="#">c2d3hC_</a>	Alignment	not modelled	5.3	48	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-hyp-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
67	<a href="#">c2lx0A_</a>	Alignment	not modelled	5.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> membrane fusion protein p14; <b>PDBTitle:</b> arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
68	<a href="#">c3a19D_</a>	Alignment	not modelled	5.2	54	<b>PDB header:</b> structural protein <b>Chain:</b> D; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
69	<a href="#">c4aq5C_</a>	Alignment	not modelled	5.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> acetylcholine receptor delta subunit; <b>PDBTitle:</b> gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
70	<a href="#">c2bg9C_</a>	Alignment	not modelled	5.2	10	<b>PDB header:</b> ion channel/receptor <b>Chain:</b> C; <b>PDB Molecule:</b> acetylcholine receptor protein, delta chain; <b>PDBTitle:</b> refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
71	<a href="#">c3a19B_</a>	Alignment	not modelled	5.1	55	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
72	<a href="#">c2d3hB_</a>	Alignment	not modelled	5.1	55	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-hyp-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
73	<a href="#">c2d3hA_</a>	Alignment	not modelled	5.1	55	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-hyp-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
74	<a href="#">c3a19F_</a>	Alignment	not modelled	5.1	57	<b>PDB header:</b> structural protein <b>Chain:</b> F; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
75	<a href="#">c3a08D_</a>	Alignment	not modelled	5.1	57	<b>PDB header:</b> structural protein <b>Chain:</b> D; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
76	<a href="#">c2d3hD_</a>	Alignment	not modelled	5.1	57	<b>PDB header:</b> structural protein <b>Chain:</b> D; <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-hyp-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4