















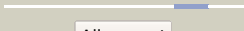




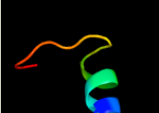
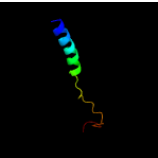

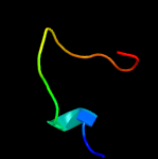
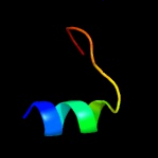
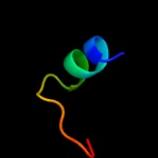


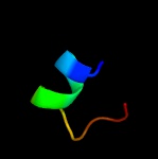



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3605c (-) _4047884_4048360
Date	Fri Aug 9 18:20:29 BST 2019
Unique Job ID	cf53fa7cfa7c92a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2o3ga1</a>	 Alignment		29.0	24	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
2	<a href="#">c3rvdM_</a>	 Alignment		26.0	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> M: <b>PDB Molecule:</b> photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4) <b>PDBTitle:</b> crystal structure of the binary complex, obtained by soaking, of2 photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh)3 with cp12-2, both from arabidopsis thaliana.
3	<a href="#">c3rvdJ_</a>	 Alignment		24.5	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> J: <b>PDB Molecule:</b> photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4) <b>PDBTitle:</b> crystal structure of the binary complex, obtained by soaking, of2 photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh)3 with cp12-2, both from arabidopsis thaliana.
4	<a href="#">c3qv1G_</a>	 Alignment		24.5	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> cp12 protein; <b>PDBTitle:</b> crystal structure of the binary complex of photosynthetic a42 glyceraldehyde 3-phosphate dehydrogenase (gapdh) with cp12-2, both3 from arabidopsis thaliana.
5	<a href="#">c3rvdK_</a>	 Alignment		24.5	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4) <b>PDBTitle:</b> crystal structure of the binary complex, obtained by soaking, of2 photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh)3 with cp12-2, both from arabidopsis thaliana.
6	<a href="#">d3deda1</a>	 Alignment		22.9	18	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
7	<a href="#">c2lj9A_</a>	 Alignment		22.6	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cp12 domain-containing protein 2; <b>PDBTitle:</b> partial 3d structure of the c-terminal part of the free arabidopsis2 thaliana cp12-2 in its oxidized form
8	<a href="#">c3rvdI_</a>	 Alignment		22.3	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> I: <b>PDB Molecule:</b> photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4) <b>PDBTitle:</b> crystal structure of the binary complex, obtained by soaking, of2 photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh)3 with cp12-2, both from arabidopsis thaliana.
9	<a href="#">d2oaia1</a>	 Alignment		22.0	12	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
10	<a href="#">d2r2za1</a>	 Alignment		21.6	12	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
11	<a href="#">c3dedB_</a>	 Alignment		20.9	18	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable hemolysin; <b>PDBTitle:</b> c-terminal domain of probable hemolysin from chromobacterium violaceum

12	<a href="#">c2kncA_</a>	Alignment		20.2	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
13	<a href="#">c2kv5A_</a>	Alignment		18.8	14	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rna1; <b>PDBTitle:</b> solution structure of the par toxin fst in dpc micelles
14	<a href="#">d2plsA1</a>	Alignment		18.4	12	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
15	<a href="#">c3llbA_</a>	Alignment		18.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
16	<a href="#">d2p3ha1</a>	Alignment		18.1	12	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
17	<a href="#">d2rk5a1</a>	Alignment		17.9	18	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
18	<a href="#">c3rvdN_</a>	Alignment		17.0	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> N: <b>PDB Molecule:</b> photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4) <b>PDBTitle:</b> crystal structure of the binary complex, obtained by soaking, of2 photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh)3 with cp12-2, both from arabidopsis thaliana.
19	<a href="#">c3qv1_</a>	Alignment		17.0	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> I: <b>PDB Molecule:</b> cp12 protein; <b>PDBTitle:</b> crystal structure of the binary complex of photosynthetic a42 glyceraldehyde 3-phosphate dehydrogenase (gapdh) with cp12-2, both3 from arabidopsis thaliana.
20	<a href="#">c3qv1H_</a>	Alignment		16.9	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> H: <b>PDB Molecule:</b> cp12 protein; <b>PDBTitle:</b> crystal structure of the binary complex of photosynthetic a42 glyceraldehyde 3-phosphate dehydrogenase (gapdh) with cp12-2, both3 from arabidopsis thaliana.
21	<a href="#">d2o1ra1</a>	Alignment	not modelled	14.7	29	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
22	<a href="#">c6a2uA_</a>	Alignment	not modelled	14.6	18	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal; <b>PDBTitle:</b> crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
23	<a href="#">d2p13a1</a>	Alignment	not modelled	12.2	12	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
24	<a href="#">c2l5bA_</a>	Alignment	not modelled	10.1	43	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> activator of apoptosis harakiri; <b>PDBTitle:</b> solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
25	<a href="#">d2plia1</a>	Alignment	not modelled	9.8	18	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
26	<a href="#">c1jcaC_</a>	Alignment	not modelled	8.2	43	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> C: <b>PDB Molecule:</b> insulin a; <b>PDBTitle:</b> non-standard design of unstable insulin analogues with enhanced2 activity
27	<a href="#">c1jcaA_</a>	Alignment	not modelled	8.2	43	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> insulin a; <b>PDBTitle:</b> non-standard design of unstable insulin analogues with enhanced2 activity
28	<a href="#">c4hkrA_</a>	Alignment	not modelled	8.1	46	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium release-activated calcium channel protein 1; <b>PDBTitle:</b> calcium release-activated calcium (crac) channel orai
						<b>Fold:</b> FAD-binding/transporter-associated domain-like

29	<a href="#">d2nqwa1</a>	Alignment	not modelled	8.0	18	<b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
30	<a href="#">c2uurA</a>	Alignment	not modelled	7.6	29	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> collagen alpha-1(ix) chain; <b>PDBTitle:</b> n-terminal nc4 domain of collagen ix
31	<a href="#">d1ppjw</a>	Alignment	not modelled	6.7	20	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
32	<a href="#">c6ghrF</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> F; <b>PDB Molecule:</b> cp12 polypeptide; <b>PDBTitle:</b> cyanobacterial gapdh with full-length cp12
33	<a href="#">d1ufaa1</a>	Alignment	not modelled	6.6	33	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> AmyC C-terminal domain-like
34	<a href="#">c1xw7C</a>	Alignment	not modelled	6.6	43	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> C; <b>PDB Molecule:</b> insulin; <b>PDBTitle:</b> diabetes-associated mutations in human insulin: crystal structure and2 photo-cross-linking studies of a-chain variant insulin wakayama
35	<a href="#">c6btmA</a>	Alignment	not modelled	6.5	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> alternative complex iii subunit a; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
36	<a href="#">c4i0oA</a>	Alignment	not modelled	6.5	9	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein elys; <b>PDBTitle:</b> nucleoporin elys (aa1-494), mus musculus
37	<a href="#">c3rvdL</a>	Alignment	not modelled	6.4	31	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> L; <b>PDB Molecule:</b> photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4) <b>PDBTitle:</b> crystal structure of the binary complex, obtained by soaking, of2 photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh)3 with cp12-2, both from arabidopsis thaliana.
38	<a href="#">c1xw7A</a>	Alignment	not modelled	6.4	43	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A; <b>PDB Molecule:</b> insulin; <b>PDBTitle:</b> diabetes-associated mutations in human insulin: crystal structure and2 photo-cross-linking studies of a-chain variant insulin wakayama
39	<a href="#">c2n2sA</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> pheromone ep-1; <b>PDBTitle:</b> nmr solution structure of the pheromone ep-1 from euplotes petzi
40	<a href="#">c2l6sA</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> antiviral protein <b>Chain:</b> A; <b>PDB Molecule:</b> vir-576; <b>PDBTitle:</b> efficacy of an hiv-1 entry inhibitor targeting the gp41 fusion peptide
41	<a href="#">c2l6tA</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> antiviral protein <b>Chain:</b> A; <b>PDB Molecule:</b> vir-576; <b>PDBTitle:</b> efficacy of an hiv-1 entry inhibitor targeting the gp41 fusion peptide
42	<a href="#">c2mtpB</a>	Alignment	not modelled	6.0	20	<b>PDB header:</b> protein binding/cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> the structure of filamin repeat 21 bound to integrin
43	<a href="#">d3cx5i1</a>	Alignment	not modelled	6.0	17	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
44	<a href="#">c1j73A</a>	Alignment	not modelled	5.9	25	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A; <b>PDB Molecule:</b> insulin a; <b>PDBTitle:</b> crystal structure of an unstable insulin analog with native activity.
45	<a href="#">c1j73C</a>	Alignment	not modelled	5.9	25	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> C; <b>PDB Molecule:</b> insulin a; <b>PDBTitle:</b> crystal structure of an unstable insulin analog with native activity.
46	<a href="#">c1m8oA</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> platelet integrin alfaiib subunit: cytoplasmic <b>PDBTitle:</b> platelet integrin alfaiib-beta3 cytoplasmic domain
47	<a href="#">c1s4wA</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> nmr structure of the cytoplasmic domain of integrin aiib in2 dpc micelles
48	<a href="#">c1dpkA</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iib subunit; <b>PDBTitle:</b> solution structure of the cytoplasmic domain of the2 integrin alpha-iib subunit
49	<a href="#">c2mn8A</a>	Alignment	not modelled	5.5	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> maculatin g15; <b>PDBTitle:</b> nmr structure of a peptoid analogue of maculatin g15 containing cis-2 nleu at position 13
50	<a href="#">c2mn9A</a>	Alignment	not modelled	5.5	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> maculatin g15; <b>PDBTitle:</b> peptoid analogue of maculatin g15 - peptoid trans-nleu at position 13
51	<a href="#">d2p4pa1</a>	Alignment	not modelled	5.3	12	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
52	<a href="#">c2z9fC</a>	Alignment	not modelled	5.2	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C; <b>PDB Molecule:</b> cellulose synthase operon protein d; <b>PDBTitle:</b> crystal structure of axcesd protein from acetobacter xylinum