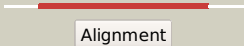

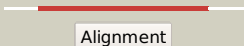

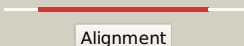


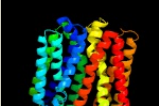




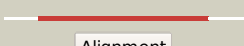








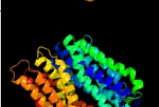


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1250_(- )_1394185_1395924
Date	Wed Jul 31 22:05:34 BST 2019
Unique Job ID	54780a5ad6166559

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pw4a_</a>	 Alignment		100.0	14	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
2	<a href="#">c6e9oA_</a>	 Alignment		100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactonate transport; <b>PDBTitle:</b> e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
3	<a href="#">c3wdoA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
4	<a href="#">c4zp0A_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
5	<a href="#">c4ldsB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcb; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
6	<a href="#">c6gs7A_</a>	 Alignment		100.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide and tripeptide permease a; <b>PDBTitle:</b> crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
7	<a href="#">c4cl5B_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate transporter 1.1; <b>PDBTitle:</b> crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
8	<a href="#">c6h7dA_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transport protein 10; <b>PDBTitle:</b> crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
9	<a href="#">c4j05A_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatase transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
10	<a href="#">c6g9xB_</a>	 Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> major facilitator superfamily mfs_1; <b>PDBTitle:</b> crystal structure of a mfs transporter at 2.54 angstrom resolution
11	<a href="#">c4ikyA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide abc transporter (permease); <b>PDBTitle:</b> crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate

12	<a href="#">c6exsA_</a>	Alignment		100.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter permease; <b>PDBTitle:</b> crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
13	<a href="#">c4gbzA_</a>	Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-proton symporter; <b>PDBTitle:</b> the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
14	<a href="#">c4apsB_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> di- or tripeptide h+ symporter; <b>PDBTitle:</b> crystal structure of a pot family peptide transporter in an inward2 open conformation.
15	<a href="#">c2gfpA_</a>	Alignment		100.0	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
16	<a href="#">c4w6vA_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-/tripeptide transporter; <b>PDBTitle:</b> crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
17	<a href="#">c6ei3A_</a>	Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
18	<a href="#">c5c65A_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> structure of the human glucose transporter glut3 / slc2a3
19	<a href="#">c2xutC_</a>	Alignment		100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
20	<a href="#">c3o7pA_</a>	Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
21	<a href="#">c4ybgB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> rat glut5 with fv in the outward-open form
22	<a href="#">c4pypA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> crystal structure of the human glucose transporter glut1
23	<a href="#">d1pv7a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
24	<a href="#">c1pv7B_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lactose permease; <b>PDBTitle:</b> crystal structure of lactose permease with tdg
25	<a href="#">c4lepB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton:oligopeptide symporter pot family; <b>PDBTitle:</b> structural insights into substrate recognition in proton dependent2 oligopeptide transporters
26	<a href="#">c4q65A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide permease d; <b>PDBTitle:</b> structure of the e. coli peptide transporter ybgh
27	<a href="#">c4iu8A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
28	<a href="#">c4iu9A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter
						<b>PDB header:</b> transport protein

29	<a href="#">c5aynA_</a>	Alignment	not modelled	100.0	11	<b>Chain:</b> A; <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
30	<a href="#">c5aymA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
31	<a href="#">c4m64D_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> melibiose carrier protein; <b>PDBTitle:</b> 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
32	<a href="#">c6ob7A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> equilibrative nucleoside transporter 1; <b>PDBTitle:</b> human equilibrative nucleoside transporter-1, dilazep bound
33	<a href="#">c3b9yA_</a>	Alignment	not modelled	92.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> ammonium transporter family rh-like protein; <b>PDBTitle:</b> crystal structure of the nitrosomonas europaea rh protein
34	<a href="#">c5aezA_</a>	Alignment	not modelled	58.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> mep2; <b>PDBTitle:</b> crystal structure of candida albicans mep2
35	<a href="#">c5xpda_</a>	Alignment	not modelled	57.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> sugar transporter; <b>PDBTitle:</b> sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
36	<a href="#">c6nbxG_</a>	Alignment	not modelled	31.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
37	<a href="#">c6e1kA_</a>	Alignment	not modelled	26.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> two pore calcium channel protein 1; <b>PDBTitle:</b> structure of attpc1(dde) reconstituted in saposin a with cat06 fab
38	<a href="#">c2b6pA_</a>	Alignment	not modelled	18.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
39	<a href="#">c2g9pA_</a>	Alignment	not modelled	17.4	36	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> antimicrobial peptide latarcin 2a; <b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
40	<a href="#">c3a08C_</a>	Alignment	not modelled	17.1	32	<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, monoclinic, twinned crystal
41	<a href="#">c6hwhX_</a>	Alignment	not modelled	15.4	16	<b>PDB header:</b> electron transport <b>Chain:</b> X; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
42	<a href="#">c2d3hC_</a>	Alignment	not modelled	13.0	33	<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
43	<a href="#">c3a19A_</a>	Alignment	not modelled	13.0	33	<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
44	<a href="#">c2d3hB_</a>	Alignment	not modelled	12.9	33	<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
45	<a href="#">c2d3hA_</a>	Alignment	not modelled	12.9	33	<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
46	<a href="#">c3a19B_</a>	Alignment	not modelled	12.9	33	<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
47	<a href="#">c5klbB_</a>	Alignment	not modelled	12.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> ion transport protein; <b>PDBTitle:</b> crystal structure of the cavab voltage-gated calcium channel(wild-2 type, 2.7a)
48	<a href="#">c3qngD_</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
49	<a href="#">c3a08E_</a>	Alignment	not modelled	12.3	38	<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, monoclinic, twinned crystal
50	<a href="#">c2d3hE_</a>	Alignment	not modelled	12.1	36	<b>PDB header:</b> structural protein <b>Chain:</b> E; <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
51	<a href="#">c3a19F_</a>	Alignment	not modelled	11.2	38	<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
52	<a href="#">c3a08D_</a>	Alignment	not modelled	11.2	38	<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
						<b>PDB header:</b> structural protein

53	<a href="#">c2d3hD_</a>	Alignment	not modelled	11.2	38	<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
54	<a href="#">c3a19D_</a>	Alignment	not modelled	11.1	36	<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
55	<a href="#">c3a08F_</a>	Alignment	not modelled	10.8	33	<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, monoclinic, twinned crystal
56	<a href="#">c3a19E_</a>	Alignment	not modelled	10.0	36	<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
57	<a href="#">c3a19C_</a>	Alignment	not modelled	10.0	36	<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
58	<a href="#">c4dveA_</a>	Alignment	not modelled	10.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biotin transporter bio; <b>PDBTitle:</b> crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter
59	<a href="#">c4djiA_</a>	Alignment	not modelled	9.2	13	<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
60	<a href="#">c2d3hF_</a>	Alignment	not modelled	8.8	35	<b>PDB header:</b> structural protein <b>Chain:</b> F: <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
61	<a href="#">c2miiA_</a>	Alignment	not modelled	8.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein activator lpob; <b>PDBTitle:</b> nmr structure of e. coli lpob
62	<a href="#">c6btmC_</a>	Alignment	not modelled	8.0	8	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> alternative complex iii subunit c; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
63	<a href="#">d3cx5c2</a>	Alignment	not modelled	7.6	11	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
64	<a href="#">c1x1kF_</a>	Alignment	not modelled	7.3	36	<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
65	<a href="#">c4qxIA_</a>	Alignment	not modelled	7.2	21	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flhe; <b>PDBTitle:</b> crystal structure of flhe
66	<a href="#">d2e45a1</a>	Alignment	not modelled	7.2	13	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
67	<a href="#">c5khnB_</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
68	<a href="#">c3abnC_</a>	Alignment	not modelled	6.7	67	<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
69	<a href="#">c4r0cB_</a>	Alignment	not modelled	6.7	4	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> abgt putative transporter family; <b>PDBTitle:</b> crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology
70	<a href="#">c4r1iB_</a>	Alignment	not modelled	6.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aminobenzoyl-glutamate transporter; <b>PDBTitle:</b> structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
71	<a href="#">c5u1dA_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> antigen peptide transporter 1; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
72	<a href="#">c1wa7B_</a>	Alignment	not modelled	6.1	40	<b>PDB header:</b> sh3 domain <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical 28.7 kda protein in dhfr 3'region <b>PDBTitle:</b> sh3 domain of human lyn tyrosine kinase in complex with a2 herpesviral ligand
73	<a href="#">c3abnB_</a>	Alignment	not modelled	6.1	67	<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
74	<a href="#">c3a1hF_</a>	Alignment	not modelled	6.0	67	<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
75	<a href="#">c5aexB_</a>	Alignment	not modelled	5.8	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> ammonium transporter mep2; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2
76	<a href="#">c3a08B_</a>	Alignment	not modelled	5.8	35	<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, monoclinic, twinned crystal
77	<a href="#">c3a08A_</a>	Alignment	not modelled	5.8	35	<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, monoclinic, twinned crystal
						<b>PDB header:</b> transcription

78	<a href="#">c2rmsB_</a>	Alignment	not modelled	5.7	28	<b>Chain:</b> B: <b>PDB Molecule:</b> msin3a-binding protein; <b>PDBTitle:</b> solution structure of the msin3a pah1-sap25 sid complex
79	<a href="#">c3a0mF_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
80	<a href="#">c6oh2A_</a>	Alignment	not modelled	5.6	6	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cmp-sialic acid transporter; <b>PDBTitle:</b> x-ray crystal structure of the mouse cmp-sialic acid transporter in2 complex with cmp, by lipidic cubic phase
81	<a href="#">c1wrgA_</a>	Alignment	not modelled	5.4	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> light-harvesting protein b-880, beta chain; <b>PDBTitle:</b> light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
82	<a href="#">c3a1hE_</a>	Alignment	not modelled	5.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
83	<a href="#">c3a1hC_</a>	Alignment	not modelled	5.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
84	<a href="#">c3a1hD_</a>	Alignment	not modelled	5.4	67	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
85	<a href="#">c3abnA_</a>	Alignment	not modelled	5.3	67	<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
86	<a href="#">c3a0aB_</a>	Alignment	not modelled	5.3	67	<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
87	<a href="#">c3a0aE_</a>	Alignment	not modelled	5.3	67	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
88	<a href="#">c3v5uA_</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized membrane protein mj0091; <b>PDBTitle:</b> structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
89	<a href="#">c3a0aD_</a>	Alignment	not modelled	5.2	46	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal