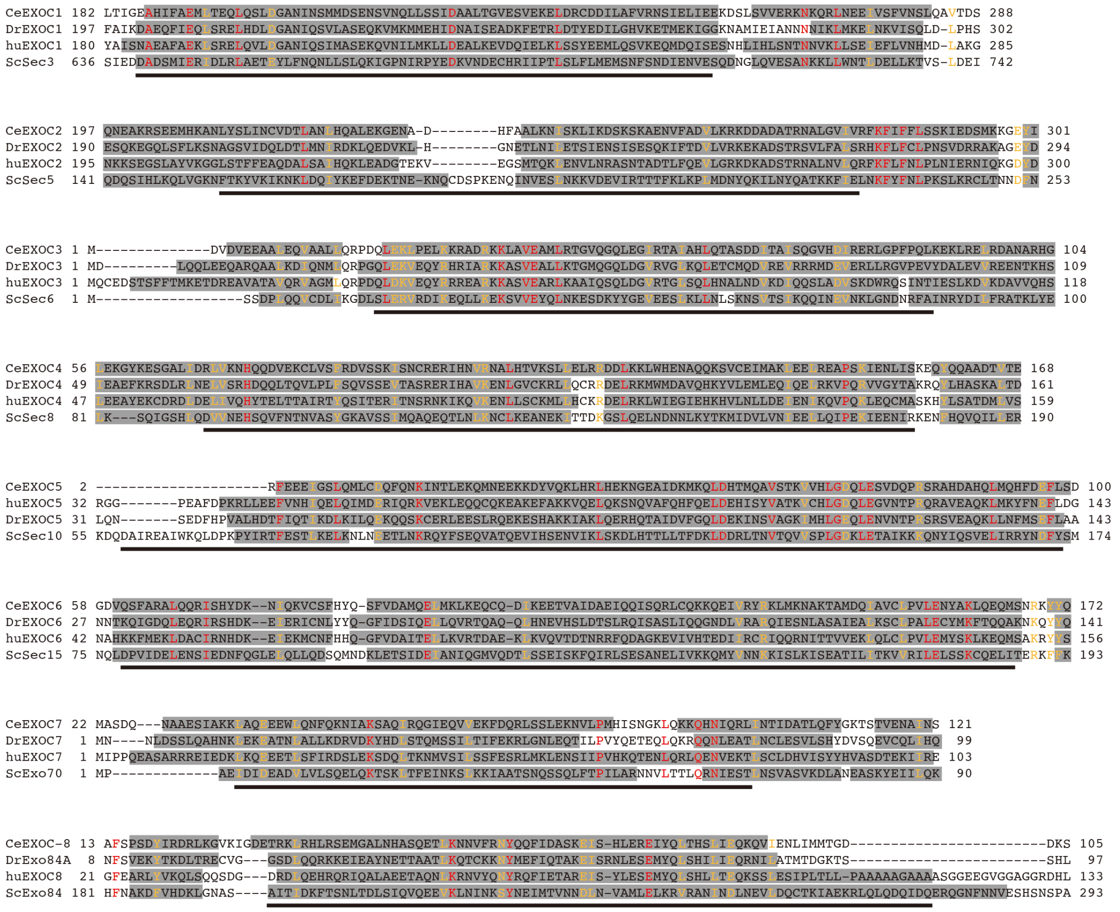
Supplementary Table 1. Summary of model building for the yeast exocyst complex

Subunit	Length	Built region	Domain	PDB code	Modeling
Sec3	1336	611-1332	CorEx motif (640-710)	-	De novo building
			CAT-A (740-881)	-	De novo building
			CAT-B (920-1035)	-	De novo building
			CAT-C (1040-1208)	-	De novo building
			CAT-D (1213-1332)	-	De novo building
Sec5	971	1-971	CorEx motif (155-231)	-	De novo building
			CAT-A (238-331)	-	De novo building
			CAT-B (350-619)	-	De novo building
			CAT-C (623-812)	-	De novo building
			CAT-D (813-936)	-	De novo building
Sec6	805	1-805	CorEx motif (18-85)	-	De novo building
			CAT-A (92-253)	-	De novo building
			CAT-B (297-396)	-	De novo building
			CAT-C (414-609)	2FJI	Rigid docking
			CAT-D (619-725)	2FJI	Rigid docking
Sec8	1065	23-1065	CorEx motif (91-177)	-	De novo building
			CAT-A (180-335)	-	De novo building
			CAT-B (338-570)	-	De novo building
			CAT-C (588-858)	-	De novo building
			CAT-D (874-968)	-	De novo building
Sec10	871	3-867	CorEx motif (58-172)	-	De novo building
			CAT-A (191-279)	5H11	Homology modeling
			CAT-B (317-428)	5H11	Homology modeling
			CAT-C (432-696)	5H11	Homology modeling
			CAT-D (697-825)	5H11	Homology modeling
Sec15	910	42-890	CorEx motif (78-186)	-	De novo building
			CAT-A (190-445)	-	De novo building
			CAT-B (453-667)	2A2F	Homology modeling
			CAT-C (668-830)	2A2F	Homology modeling
			CAT-D (838-890)	2A2F	Homology modeling
Exo70	623	1-623	CorEx motif (5-67)	-	De novo building
			CAT-A (74-190)	2B1E	Rigid docking
			CAT-B (194-340)	2B1E	Rigid docking
			CAT-C (341-513)	2B1E	Rigid docking
			CAT-D (514-623)	2B1E	Rigid docking
Exo84	753	170-753	CorEx motif (197-276)	-	De novo building
			PH domain (346-452)	1ZC4	Homology modeling
			CAT-A (527-622)	2D2S	Rigid docking
			CAT-B (625-753)	2D2S	Rigid docking

Supplementary Table 2. Plasmids and yeast strains used in this study

Name	**Description**
pGV373	*p415TEF-TOM20-mCherry*
pG1831	*pRS416-Cit1-GFP*
pG1872	*p415TEF-TOM20-mCherry-sec3(1-1336)*
pG1976	*p415TEF-TOM20-mCherry-sec3(1-620)*
pG1977	*p415TEF-TOM20-mCherry-sec3(1-740)*
pG1978	*p415TEF-TOM20-mCherry-sec3(601-1336)*
pG1979	*p415TEF-TOM20-mCherry-sec3(710-1336)*
pG215	*Prs304(TRP)-SEC3-GFP*
pG1980	*Prs304(TRP)-sec3(Δ621-710)-GFP*
GY1132	*MAT a trp1, leu2, his3, ura3, lys2*
GY1143	*MAT a trp1, leu2, his3, ura3, lys2, Sec5-GFP::URA3*
GY2624	*Mat α leu2-3, 112, ura3-52, trp1, his3Δ200, L-A-+, GAL+, sec3::Kan*
GY3485	*MAT a his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 SEC3-TAP::HIS3*
GY3486	*MAT a his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 SEC5-TAP::HIS3*
GY3487	*MAT a his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 SEC6-TAP::HIS3*
GY3489	*MAT a his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 SEC15-TAP::HIS3*
GY3924	*Mat a ura3-52, leu2-3, 112, his3D200, trp1 Gal+, LA+, SEC6-Protein A-HIS3::SEC6*
GY3933	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 EXO70-TAP::HIS3, SEC8-GFP::LEU2*
GY3937	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 Exo70-TAP::HIS3, Exo84-GFP::LEU2*
GY3948	*Mat α leu2-3, 112, ura3-52, trp1::SEC3-GFP-TRP1, his3Δ200, L-A-+, GAL+, sec3::Kan*
GY3949	*Mat α leu2-3, 112, ura3-52, trp1::sec3(Δ621-710)-GFP-TRP1, his3Δ200, L-A-+, GAL+, sec3::Kan*

Supplementary Note 1. Evolutionary conversation of the CorEx motif in the exocyst subunits.



Sequences of full-length exocyst subunits from *Saccharomyces cerevisiae* (“Sc”), *C. elegans* (“Ce”), *Human* (“Hu”) and *Drosophila* (“Dr”) are aligned based on their secondary structures using PROMALS3D[1]. The CorEx motifs are indicated by black lines under each alignment. Same residues in the alignment are colored in red and the conserved ones in orange. The gray background in each sequence shows predicted α-helices in the alignment.

Reference

1. Pei, J., Kim, B.H. & Grishin, N.V. PROMALS3D: a tool for multiple protein sequence and structure alignments. *Nucleic Acids Res.* **36,** 2295–2300 (2008).