

General functional category	Human gene (unless only yeast gene known)	<i>D. melanogaster</i> gene name and/or CG #	E-value for relatedness	Fold change in CrebA null	Requires CrebA based on in situ
Signal recognition particle - SRP	Srp9	Srp9/CG8268	2.250e-13	-2.00	Yes
	Srp68	Srp68/CG5064	1.19e-128	-2.04	Yes
	Srp72	Srp72/CG5434	3.97e-124	-1.81	Yes
	Srp54	Srp54k/CG4659	0	-1.44	Yes
	Srp14	Srp14/CG5417	3.705e-13	-1.59	Yes
	Srp19	Srp19/CG4457	4.836e-29	-1.89	Yes
	SRP-RNA	CG9272	2.468e-40	No change	n.d.
SRP Receptor - SR	SrpR α	Gtp-bp/CG2522	1.99e-177	Not on array	Yes
	SrpR β	SrpR /CG3316 2	1.859e-37	-3.31	Yes
Sec61 translocon complex	Sec61 α	Sec61 α	0	-1.78	Yes
	Sec61 β	Sec61 β	2.531e-27	-1.99	Yes
	Sec61 γ	Sec61	2.530e-29	-2.08	Yes
Cytosolic Hsp70 proteins that maintain unfolded state	Ssa1 (yeast) Ssa2 (yeast) Ssa3 (yeast) Ssa4 (yeast)	Hsc70-1/ CG8937/ CG4264	0	Goes up	n.d.
Cytosolic Hsp40	Ydj1 (yeast)	Droj2/CG8863	5.811e-80	Goes up	n.d.
Sec63 complex: post-translational translocation	Sec62	Trp1	1.049e-55	-1.62	n.d.
	Sec63	Sec63	1.02e-176	-2.03	n.d.
	Sec71 (yeast)	Sec71		-1.24	n.d.
	TRAM	TR	2.429e-65	-5.21	Yes
	TRAP δ	TAP δ	1.798e-21	-2.12	Yes
ER luminal Hsp70s	BiP	CG4147	0	-1.32*	Yes
	Scj1 (yeast)	CG2887	1.345e-11	No Change	Yes
	Jem1	CG9356	1.119e-16	-1.50	Yes
	Si1	CG10420	4.567e-31	-1.87	n.d.
	Lhs1 (yeast)	CG2918	1.226e-44	-1.45	n.d.
Get pathway for insertion of tail-anchored proteins	WRB	CG32022	4.642e-06	-1.24	n.d.
	TRC40	CG1598	1.01e-127	No Change	n.d.
	TRC35	CG9853	2.037e-60	No Change	n.d.
	Ubl4A	CG7215	8.288e-12	No Change	n.d.
	SGTA	Sgt/CG5094	2.389e-29	Not on array	n.d.
	Bag6	CG7546	4.665e-17	No change	n.d.
	ER morphology proteins	Spastin	spas/CG5977	3.19e-138	-1.41
Atlastin		atl/CG6668	3.38e-178	-1.23*	n.d.
Reep3		CG8331	1.978e-20	-1.84	n.d.
Rtn1/Rtn2		Rtnl1/CG33113	4.606e-58	-1.33	n.d.
Coupling of ER to PM	STIM1	Stim/CG9126	2.3889e-93	No Change	n.d.
Secretory mRNA ER tethering	CD109 = p180	Tep2/CG7052	4.32e-179	Not on array	n.d.
Signal peptidase complex	Spase 22-23	Spase 22-23	1.138e-56	-1.81*	Yes
	Spase 12	Spase12	1.755e-16	-2.5	Yes
	Spase 18-21	twr/CG2358	2.639e-77	-2.3	Yes
	Spase 25	Spase25	2.074e-40	-2.2	Yes
N-linked glycosylation	Ribophorin I	CG33303	5.65e-116	Not on array	n.d.
	Dad1	CG13393	7.147e-41	No Change	n.d.
	MagT1	Osty/CG7830	6.43e-101	-1.43	Yes
	Ost4	CG33774	2.177e-07	Not on array	n.d.
	Wbp1 (yeast)	Ost48/CG9022	1.621e-24	No Change	n.d.
	Rpn2	Ost δ /CG6370	1.294e-82	-1.26	n.d.
	Stt3 (yeast)	OstStt3/CG7748	0	-1.72	n.d.
Disulfide bond formation	Ero1	Ero1L/CG1333	2.22e-112	Not on array	n.d.
	Pdi1 (yeast)	Pdi/CG6988	3.701e-52	-1.40	n.d.
	Mpd1 (yeast)	CaBP1/CG5809	2.393e-18	-1.52*	n.d.
	Mpd2 (yeast)	ERp60/CG8983	3.340e-06	-1.30	n.d.
	Eps1 (yeast)	prtp/CG1837	3.572e-08	-1.29*	n.d.
GPI-anchor addition	GPI8p (yeast)/	CG4406	1.08e-100	No change	n.d.
	GPAA1	GAA1/CG3033	4.738e-71	-1.57	n.d.
Glycosidase, mannosidase trimming and protein folding	Cwh41	CG1597	2.89e-168	No change	n.d.
	Gls2 (yeast)	CG14476	1.04e-152	No change	n.d.
	UGGT	Ugt/CG6850	0	-1.54	n.d.
	Calreticulin	Crc	0	-1.42	n.d.
	Cnel (yeast)	Cnx99A/ CG11958	4.233e-51	No change	n.d.
ERAD	Mns1 (yeast)	CG11874	1.103e-71	No change	n.d.
	Htm1 (yeast)	Edem2/CG5682	5.271e-79	No change	n.d.
	HSPC039	CG32069	6.102e-20	-1.72*	n.d.

ER cargo receptors	CHOp24	CHOp24	2.648e-68	-2.2	Yes
	TMED7	P24-1/CG1967	1.951e-51	-1.60	Yes
	TMED4	P24-2/CG33105	3.647e-77	-1.9	Yes
CopII components	Sar1	Sar1/CG7073	2.606e-79	-1.28	Yes
	Sec23	Sec23/CG1250	0	-1.73*	Yes
	Sec24B	Sec24/CG1472	0	-1.18*	Yes
	Sec13	Sec13/CG6773	1.10e-100	-2.44	Yes
	Sec31	Sec31/CG8266	0	-1.8	Yes
ER export of TM proteins	TEX261	CG3500	1.713e-46	-1.34*	n.d.
	Erv14 (yeast)	cni/CG5855	2.961e-18	No change	n.d.
CopII regulators	Sec12 (yeast)	Smu1/CG5451	2.178e-04	-1.21	n.d.
	PREB	CG9175	4.163e-54	-1.49	n.d.
	Sec16A	Sec16/CG32654	8.358e-60	-1.54	n.d.
Tethering of CopII vesicles to Golgi	RAB1A	CG3320	5.731e-98	No change	n.d.
	Uso1	p115/CG1422	0	-1.24*	n.d.
	TRAPPC3	Bet3/CG3911	3.683e-62	Not in array	n.d.
	TRAPPC1	Bet5/CG1359	4.479e-44	Not in array	n.d.
	TRAPPC2	Trs20/CG5161	3.259e-46	-1.34*	n.d.
	TRAPPC4	Trs23/CG9298	4.291e-75	Not in array	n.d.
	Trs31	Trs31/CG10153	6.704e-69	Goes up	n.d.
	Trs33	Trs33/CG6196	2.968e-36	No change	n.d.
CopII vesicle-Golgi membrane fusion	Stx5	Syx5/CG4214	3.570e-87	No change	n.d.
	Bos1	eya/CG9554	1.28e-122	-1.50	n.d.
	Bet1	Bet1/CG14084	1.788e-13	Not in array	n.d.
	Sec22 (yeast)	Sec22/CG7359	6.877e-28	Not in array	n.d.
	SCFD1	Slh/CG3539	0	-1.46	n.d.
Golgi structural proteins	Grasp65	Grasp65	5.305e-61	-2.38	n.d.
	GCC185	GCC185	1.687e-15	Goes up	n.d.
	GCC88	GCC88	1.048e-58	-1.20	n.d.
	Golgin-97	cbs/CG4840	1.174e-27	No change	n.d.
	Golgin245	Golgin245	1.785e-10	No change	n.d.
	GMAP210	Gmap/CG33206	5.113e-21	No change	n.d.
	Giantin	Iva/CG6450	0.0488955	No change	n.d.
	Golgin-84	Golgin84	1.177e-25	-1.35	n.d.
O-linked glycosylation	Pmt1,2,3,5,6 (yeast)	tw/CG12311	1.757e-88	-1.76	n.d.
	Pmt4,7 (yeast)	rt/CG6097	5.727e-89	-1.31	n.d.
General membrane fusion	Sec17 (yeast)	α Snap/CG6625	2.966e-38	No change	n.d.
	Sec18 (yeast)	comt/CG1618	2.87e-175	Goes up	n.d.
CopI vesicle components (Golgi – ER)	α -Cop	α -Cop/CG7961	0	-2.11	n.d.
	β -Cop	β -Cop/CG6223	0	-1.9	n.d.
	β' -Cop	β' -Cop/CG6699	0	-1.9	n.d.
	γ -Cop	γ -Cop/CG1528	0	-1.74	Yes
	δ -Cop	δ -Cop/CG14813	1.70e-168	-1.68*	n.d.
	ϵ -Cop	ϵ -Cop/CG9543	1.470e-50	-1.77*	Yes
	ζ -Cop	ζ -Cop/CG3948	1.878e-62	-2.7/-1.95	Yes
	Arf1	ARF79F	8.49e-101	-1.2*	Yes
Recruitment of Arf1 (Arf1-GEF)	Gea1 (yeast)	garz/CG8487	1.083e-51	No change	n.d.
	Gea2 (yeast)	garz/CG8487	1.490e-34	No change	n.d.
Arf-1 GAPs	Gcs1 (yeast)	ArfGAP1	2.380e-36	-1.95	n.d.
	Glo3 (yeast)	ArfGAP3	4.538e-29	-1.58	n.d.
ER retrieval from Golgi	KDEL-R	KdelR/CG5183	1.303e-93	-1.68	n.d.
	Rer1	CG11857	8.289e-37	-1.43	n.d.
CopI tethering and fusion to ER	Tip20	cg/CG8367	1.341e-38	No change	n.d.
	Use1	Bruce/CG6303	5.627e-29	Goes up	n.d.
Retrograde fusion of CopI vesicles with cis-Golgi	Gos1 (yeast)	Gos28/CG7700	6.256e-10	-1.24*	n.d.
	Ykt6	Ykt6/CG1515	1.968e-69	Goes up	n.d.
	Sec14 (yeast)	retm/CG9528	5.881e-23	No change	n.d.
	Pik1 (yeast)	fwd/CG7004	4.324e-76	Goes up	n.d.
	Vps74 (yeast)	rti/CG7085	1.339e-48	No change	n.d.
Early Golgi retrograde traffic tethers – COG complex	Cog1	CG4848	5.633e-38	-1.60	n.d.
	Cog2	ldlCp/CG6177	7.74e-101	-1.27	n.d.
	Cog3	Cog3/CG3248	3.817e-77	-1.43	n.d.
	Cog4	CG7456	7.34e-160	-1.44	n.d.
	Cog5	fws/CG6549	5.463e-60	-1.22	n.d.
	Cog6	CG1968	6.83e-153	-1.26	n.d.
	Cog7	Cog7/CG31040	2.033e-23	-1.71	n.d.
	Cog8	CG6488	1.510e-23	-1.34	n.d.
GARP complex – Endosomes to late Golgi traffic tethers	Vps51	CG15087	5.05e-169	No change	n.d.
	Vps52	CG7371	0	No change	n.d.
	Vps53	CG3338	1.054e-31	No change	n.d.
	Vps54	scat/CG3766	1.003e-70	No change	n.d.