

OptiPrep™ Reference List RS15

Purification of subcellular organelles and membrane compartments from *Saccharomyces cerevisiae* – a bibliography

This Reference List covers all published papers that have reported the use of iodixanol gradients for the purification of organelles and membrane compartments from yeast (*Saccharomyces cerevisiae*) spheroplasts. For detailed protocols please refer to the following **OptiPrep™ Application Sheets**, which can be accessed from the following section: “**Subcellular Membranes (Non-mammalian)**”.

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|--|---------------------------|
| Endosomes, endoplasmic reticulum, Golgi, TGN and vacuoles | see Application Sheet S53 |
| Membrane trafficking (vacuole, Cvt vesicles etc) | see Application Sheet S52 |
| Mitochondria | see Application Sheet S17 |
| Peroxisomes | see Application Sheet S57 |

See also Reference List RS09 “Lipid rich detergent-resistant membranes from non-mammalian sources – a bibliography”, this contains a section on yeast analysis.

See also Reference List RS13 “Resolution of soluble cytosolic proteins from membrane vesicles and organelles – a bibliography”; this contains a section on yeast analysis.

Both RS09 and RS13 have sections on yeast.

In the following bibliography the published papers have been sorted according to the **principal membrane compartments under study or research topic** and listed alphabetically according to first author. **Key words are highlighted in blue.**

1. Autophagosomes/autophagic vacuoles

- Cohen-Kaplan, V.**, Livneh, I., Kwon, Y.T. and Ciechanover, A. (2019) *Monitoring stress-induced autophagic engulfment and degradation of the 26S proteasome in mammalian cells* Meth. Enzymol., **619**, 337-366
- Gao, J.**, Reggiori, F. and Ungermann, C. (2018) *A novel in vitro assay reveals SNARE topology and the role of Ykt6 in autophagosome fusion with vacuoles* J. Cell Biol., **217**, 3670–3682
- Ishihara, N.**, Hamasaki, M., Yokota, S., Suzuki, K., Kamada, Y., Kihara, A., Yoshimori, T., Noda, T. and Ohsumi, Y. (2001) *Autophagosome requires specific early Sec proteins for its formation and NSF/SNARE for vacuolar fusion* Mol. Biol. Cell, **12**, 3690-3702
- Kametaka, S.**, Okano, T., Ohsumi, M. and Ohsumi, Y. (1998) *Apg14p and Apg6/Vps30p form a protein complex essential for autophagy in the yeast Saccharomyces cerevisiae* J. Biol. Chem., **273**, 22284-22291
- Kim, J.**, Huang, W-P., Stromhaug, P.E. and Klionsky, D.J. (2002) *Convergence of multiple autophagy and cytoplasm to vacuole components to a perivacuolar membrane compartment prior to de novo vesicle formation* J. Biol. Chem., **277**, 763-773
- Meiling-Wesse, K.**, Barth, H., Voss, C., Eskelinen, E-L., Epple, U.D. and Thumm, M. (2004) *Atg21 is required for effective recruitment of Atg8 to the preautophagosomal structure during the Cvt pathway* J. Biol. Chem., **279**, 37741-37759
- Shintani, T.**, Suzuki, K., Kamada, Y., Noda, T. and Ohsumi, Y. (2001) *Apg2p functions in autophagosome formation on the perivacuolar structure* J. Biol. Chem., **276**, 30452-30460
- Suzuki, K.**, Nakamura, S., Morimoto, M., Fujii, K., Noda, N.N., Inagaki, F. and Ohsumi, Y. (2014) *Proteomic profiling of autophagosome cargo in Saccharomyces cerevisiae* PloS One, **9**: e91651
- Wang, C-W.**, Kim, Huang, W-P., Abeliovich, H., Stromhaug, P.E., Dunn, W.A. and Klionsky, D.J. (2001) *Apg2 is a novel protein required for the cytoplasm to vacuole targeting, autophagy, and pexophagy pathways* J. Biol. Chem., **276**, 30442-30451
- Yamamoto, H.**, Kakuta, S., Watanabe, T.M., Kitamura, A., Sekito, T., Kondo-Kakuta, C., Ichikawa, R., Kinjo, M. and Ohsumi, Y. (2012) *Atg9 vesicles are an important membrane source during early steps of autophagosome formation* J. Cell Biol., **198**, 219–233

2. Cvt vesicles plus endosomes/Golgi/ER/TGN/vacuole (see also Section 12)

- Chantalat, S.**, Park, S-K., Hua, Z., Liu, K., Gobin, R., Peyroche, A., Rambourg, A., Graham, T. and Jackson, C.L. (2004) *The Arf activator Gea2p and P-type ATPase Drs2p interact at the Golgi in Saccharomyces cerevisiae* J. Cell Sci., **117**, 711-722

- Dove, S.K.**, Piper, R.C., McEwen, R.K., Yu, J.W., King, M.C., Hughes, D.C., Thuring, J., Holmes, A.B., Cooke, F.T., Michell, R.H., Parker, P.J. and Lemmon, M.A. (2004) *Svp1p defines a family of phosphatidylinositol 3,5-bisphosphate effectors* EMBO J., **23**, 1922-1933
- Guan, J.**, Stromhaug, P.E., George, M.D., Habibzadeh-Tari, P., Bevan, A., Dunn, W.A. and Klionsky, D.J. (2001) *Cvt18/Gsa12 is required for cytoplasm-to-vacuole transport, pexophagy, and autophagy in Saccharomyces cerevisiae and Pichia pastoris* Mol. Biol. Cell, **12**, 3821-3838
- Kim, J.**, Kamada, Y., Stromhaug, P.E., Guan J., Hefner-Gravink, A., Baba, M., Scott, S.V., Ohsumi, Y., Dunn, W.A. and Klionsky, D.J. (2001) *Cvt9/Gsa9 functions in sequestering selective cytosolic cargo destined for the vacuole* J. Cell Biol., **153**, 381-396
- Mitsui, K.**, Koshimura, Y., Yoshikawa, Y., Matsushita, M. and Kanazawa, H. (2011) *The endosomal Na⁺/H⁺ exchanger contributes to multivesicular body formation by regulating the recruitment of ESCRT-0 Vps27p to the endosomal membrane* J. Biol. Chem., **286**, 37625–37638
- Sakakibara, K.**, Eiyama, A., Suzuki, S.W., Sakoh-Nakatogawa, M., Okumura, N., Tani, M., Hashimoto, A., Nagumo, S., Kondo-Okamoto, N. et al (2015) *Phospholipid methylation controls Atg32-mediated mitophagy and Atg8 recycling* EMBO J., **134**, 2703-2719
- Shiffert, S.L.**, Vaughn, M.B., Huynh, D., Kaplan, J. and McVey Ward, D. (2004) *Bph1p, the Saccharomyces cerevisiae homologue of CHS1/beige, functions in cell wall formation and protein sorting* Traffic, **5**, 700-710
- Teter, S.A.**, Eggerton, K.P., Scott, S.V., Kim, J., Fischer, A.M. and Klionsky, D.J. (2001) *Degradation of lipid vesicles in the yeast vacuole requires function of Cvt17, a putative lipase* J. Biol. Chem., **276**, 2083-2087
- Urbanowski, J.L.** and Piper, R.C. (2001) *Ubiquitin sorts proteins into the intraluminal degradative compartment of the late-endosome/vacuole* Traffic, **2**, 622-630
- Wang, C-W.**, Stromhaug, P.E., Shima, J. and Klionsky, J. (2002) *The Ccz1-Mon1 protein complex is required for the late step of multiple vacuole delivery pathways* J. Biol. Chem., **277**, 47917-47927
- Wang, C-W.**, Stromhaug, P.E., Kauffman, E.J., Weisman, L.S. and Klionsky, D.J. (2003) *Yeast homotypic vacuole fusion requires the Ccz1-Mon1 complex during the tethering/docking stage* J. Cell Biol., **163**, 973-985

3. Cvt vesicles plus vacuole/vacuolar vesicles

- Satyanarayana, C.**, Schroder-Kohne, S., Craig, E.A., Schu, P.V. and Horst, M. (2000) *Cytosolic Hsp70s are involved in the transport of aminopeptidase 1 from the cytoplasm into the vacuole* FEBS Lett., **470**, 232-238
- Scott, S.V.**, Baba, M., Ohsumi, Y. and Klionsky, D.J. (1997) *Aminopeptidase I is targeted to the vacuole by a nonclassical vesicular mechanism* J. Cell Biol., **138**, 37-44

4. Cytosolic proteins: resolution from membrane vesicles and organelles: see MS-17

5. Endoplasmic reticulum

- Diaz, A.**, Gallei, A. and Ahlquist, P. (2012) *Bromovirus RNA replication compartment formation requires concerted action of Ia's self-interacting RNA capping and helicase domains* J. Virol., **86**, 821–834
- Welker, S.**, Rudolph, B., Frenzel, E., Hagn, F., Liebisch, G., Schmitz, G., Scheuring, J., Kerth, A., Blume, A., Weinkauff, S., Haslbeck, M., Kessler, H. and Buchner, J. (2010) *Hsp12 is an intrinsically unstructured stress protein that folds upon membrane association and modulates membrane function* Mol. Cell, **39**, 507–520

6. Endoplasmic reticulum/Golgi

- Chen, J.**, Korostyshevsky, D., Lee, S. and Perlstein, E.O. (2012) *Accumulation of an antidepressant in vesiculogenic membranes of yeast cells triggers autophagy* PLoS One, **7**: e34024
- Kumanovics, A.**, Poruk, K.E., Osborn, K.A., Ward, D.M. and Kaplan, J. (2006) *YKE4 (YIL023C) encodes a bidirectional zinc transporter in the endoplasmic reticulum of Saccharomyces cerevisiae* J. Biol. Chem., **281**, 22566-22574
- Sakakibara, K.**, Eiyama, A., Suzuki, S.W., Sakoh-Nakatogawa, M., Okumura, N., Tani, M., Hashimoto, A., Nagumo, S., Kondo-Okamoto, N. et al (2015) *Phospholipid methylation controls Atg32-mediated mitophagy and Atg8 recycling* EMBO J., **134**, 2703-2719
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- Wang, Y.**, Lilley, K.S. and Oliver, S.G. (2014) *A protocol for the subcellular fractionation of Saccharomyces cerevisiae using nitrogen cavitation and density gradient centrifugation* Yeast, **31**, 127–135

7. Endosomes

- Chen, J.**, Korostyshevsky, D., Lee, S. and Perlstein, E.O. (2012) *Accumulation of an antidepressant in vesiculogenic membranes of yeast cells triggers autophagy* PLoS One, **7**: e34024
- Suzuki, K.**, Nakamura, S., Morimoto, M., Fujii, K., Noda, N.N., Inagaki, F. and Ohsumi, Y. (2014) *Proteomic profiling of autophagosomal cargo in Saccharomyces cerevisiae* PLoS One, **9**: e91651

Welker, S., Rudolph, B., Frenzel, E., Hagn, F., Liebisch, G., Schmitz, G., Scheuring, J., Kerth, A., Blume, A., Weinkauff, S., Haslbeck, M., Kessler, H. and Buchner, J. (2010) *Hsp12 is an intrinsically unstructured stress protein that folds upon membrane association and modulates membrane function* Mol. Cell, **39**, 507–520

8. Exosomes

Rodrigues, M.L., Oliveira, D.L., Vargas, G., Girard-Dias, W., Franzen, A.J., Frasés, S., Miranda, K. and Nimrichter, L. (2016) *Analysis of yeast extracellular vesicles* In Unconventional Protein Secretion: Methods and Protocols, Methods Mol. Biol., **1459** (ed. Pompa, A. and De Marchis, F.), Springer Science+Business Media New York, pp 175-190

9. Fractionation technology

Wang, Y., Lilley, K.S. and Oliver, S.G. (2014) *A protocol for the subcellular fractionation of Saccharomyces cerevisiae using nitrogen cavitation and density gradient centrifugation* Yeast, **31**, 127–135

10. Mitochondria (see also 11. Nucleic acids and ribosomes)

10-1 Co-enzyme Q

He, C.H., Xie, L.X., Allan, C.M., Tran, U.P.C. and Clarke, C.F. (2014) *Coenzyme Q supplementation or over-expression of the yeast Coq8 putative kinase stabilizes multi-subunit Coq polypeptide complexes in yeast coq null mutants* Biochim. Biophys. Acta, **1841**, 630–644

He, C.H., Black, D.S., Nguyen, T.P.T., Wang, C., Srinivasan, C. and Clarke, C.F. (2015) *Yeast Coq9 controls deamination of coenzyme Q intermediates that derive from para-aminobenzoic acid* Biochim. Biophys. Acta, **1851**, 1227–1239

Xie, L.X., Ozeir, M., Tang, J.Y., Chen, J.Y., Jaquinod, S.-K., Fontecave, M., Clarke, C.F. Pierrel, F. (2012) *Overexpression of the Coq8 kinase in Saccharomyces cerevisiae coq null mutants allows for accumulation of diagnostic intermediates of the coenzyme Q₆ biosynthetic pathway* J. Biol. Chem., **287**, 23571–23581

10-2 Energy metabolism

Nishimura, A., Nasuno, R., Yoshikawa, Y., Jung, M., Ida, T., Matsunaga, T., Morita, M., Takagi, H., Motohashi, H. and Akaike, T. (2019) *Mitochondrial cysteinyl-tRNA synthetase is expressed via alternative transcriptional initiation regulated by energy metabolism in yeast cells* J. Biol. Chem., **294**, 13781–13788

10-3 Iron analysis/transport

Chen, O.S. and Kaplan J. (2000) *CCCI suppresses mitochondrial damage in the yeast model of Friedreich's ataxia by limiting mitochondrial iron accumulation* J. Biol. Chem., **275**, 7626-7632

Chen, O.S. and Kaplan, J. (2001) *YFH1-mediated iron homeostasis is independent of mitochondrial respiration* FEBS Lett., **509**, 131-134

Chen, O.S., Hemenway, S. and Kaplan, J. (2002) *Genetic analysis of iron citrate toxicity in yeast: implications for mammalian iron homeostasis* Proc. Natl. Acad. Sci., USA, **99**, 16922-16927

Crisp, R.J., Pollington, A., Galea, C., Jaron, S., Yamaguchi-Iwai, Y. and Kaplan, J. (2003) *Inhibition of heme biosynthesis prevents transcription of iron uptake genes in yeast* J. Biol. Chem., **278**, 45499-45506

Lindahl, P.A. Garber Morales, J., Miao, R. and Holmes-Hampton, G. (2009) *Isolation of Saccharomyces cerevisiae mitochondria for Mössbauer, EPR, and electronic absorption spectroscopic analyses* Methods Enzymol., **456**, 267-285

Radisky, D.C., Babcock, M.C. and Kaplan, J. (1999) *The yeast frataxin homologue mediates mitochondrial iron efflux* J. Biol. Chem., **274**, 4497-4499

Yun, C-W., Ferea, T., Rashford, J., Ardon, O., Brown, P.O., Botstein, D., Kaplan, J. and Philpott, C.C. (2000) *Desferrioxamine-mediated iron uptake in Saccharomyces cerevisiae. Evidence for two pathways of iron uptake* J. Biol. Chem., **275**, 10709-10715

10-4 Lipid metabolism/transport/

Kannan, M., Lahiri, S., Liu, L-K., Choudhary, V. and Prinz, W.A. (2017) *Phosphatidylserine synthesis at membrane contact sites promotes its transport out of the ER* J. Lipid Res., **58**, 553–562

Lahiri, S., Chao, J.T., Tavassoli, S., Wong, A.K.O., Choudhary, V. et al (2014) *A conserved endoplasmic reticulum membrane protein complex (EMC) facilitates phospholipid transfer from the ER to mitochondria* PLoS Biol., **12**: e1001969

Sakakibara, K., Eiyama, A., Suzuki, S.W., Sakoh-Nakatogawa, M., Okumura, N., Tani, M., Hashimoto, A., Nagumo, S., Kondo-Okamoto, N. et al (2015) *Phospholipid methylation controls Atg32-mediated mitophagy and Atg8 recycling* EMBO J., **134**, 2703-2719

Tamura, Y., Harada, Y., Nishikawa, S-I, Yamano, K., Kamiya, M., Shiota, T., Kuroda, T., Kuge, O., Sesaki, H., Imai, K., Tomii, K. and Endo, T. (2013) *Tam41 is a CDP-diacylglycerol synthase required for cardiolipin biosynthesis in mitochondria* Cell Metab., **17**, 709–718

10-5 Mitophagy

Sakakibara, K., Eiyama, A., Suzuki, S.W., Sakoh-Nakatogawa, M., Okumura, N., Tani, M., Hashimoto, A., Nagumo, S., Kondo-Okamoto, N. et al (2015) *Phospholipid methylation controls Atg32-mediated mitophagy and Atg8 recycling* EMBO J., **134**, 2703-2719

Vigié, P., Cougouilles, E., Bhatia-Kissová, I., Salin, B., Blancard, C. and Camougrand, N. (2019) *The mitochondrial phosphatidylserine decarboxylase Psd1 is involved in nitrogen starvation-induced mitophagy in yeast* J. Cell Sci., **132**: jcs221655

10-6 Protein complexes

Chatterjee, N., Pabla, R. and Siede, W. (2013) *Role of polymerase η in mitochondrial mutagenesis of Saccharomyces cerevisiae* Biochem. Biophys. Res. Comm., **431**, 270–273

Gold, V.A.M., Brandt, T., Cavellini, L., Cohen, M.M., Ieva, R. and van der Laan, M. (2017) *Analysis of mitochondrial membrane protein complexes by electron cryo-tomography* In Mitochondria: Practical Protocols, Methods in Mol. Biol., **1567**, (ed. Mokranjac, D. and Perocchi, F.) Springer Science+Business Media, New York, pp 315-336

Gold, V.A.M., Ieva, R., Walter, A., Pfanner, N., van der Laan, M. and Kühlbrandt, W. (2014) *Visualizing active membrane protein complexes by electron cryotomography* Nat. Commun., **5**: 4129

10-7 Proteome

Nightingale, D.J.H., Oliver, S.G. and Lilley, K.S. (2019) *Mapping the Saccharomyces cerevisiae spatial proteome with high resolution using hyperLOPIT* In Yeast Systems Biology: Methods and Protocols, Methods in Molecular Biology, vol. **2049** (ed. Oliver, S.G. and Castrillo, J.I.), Springer Science+Business Media LLC New York, pp 165-190

10-8 Stress proteins

Welker, S., Rudolph, B., Frenzel, E., Hagn, F., Liebisch, G., Schmitz, G., Scheuring, J., Kerth, A., Blume, A., Weinkauff, S., Haslbeck, M., Kessler, H. and Buchner, J. (2010) *Hsp12 is an intrinsically unstructured stress protein that folds upon membrane association and modulates membrane function* Mol. Cell, **39**, 507–520

11. Nucleic acids and ribosomes

Chang, W., Zaarour, R.F., Reck-Peterson, S., Rinn, J., Singer, R.H., Snyder, M., Novick, P. and Mooseker, M.S. (2008) *Myo2p, a class V myosin in budding yeast, associates with a large ribonucleic acid–protein complex that contains mRNAs and subunits of the RNA-processing body* RNA, **14**, 491-502

Gold, V.A.M., Chroscicki, P., Bragoszewski, P. and Chacinska, A. (2017) *Visualization of cytosolic ribosomes on the surface of mitochondria by electron cryo-tomography* EMBO Rep., **18**, 1786-1800

Meeusen, S., Tieu, Q., Wong, E., Weiss, E., Schieltz, D., Yates, J.R. and Nunnari, J. (1999) *Mgm101p is a novel component of the mitochondrial nucleoid that binds DNA and is required for the repair of oxidatively damaged mitochondrial DNA* J. Cell Biol., **145**, 291-304

12. Organelle contact sites

Toulmay, A. and Prinz, W.A. (2012) *A conserved membrane-binding domain targets proteins to organelle contact sites* J. Cell Sci., **125**, 49–58

13. Peroxisomes

Antonenkov, V.D., Mindthoff, S., Grunau, S., Erdmann, R. and Hiltunen, J.K. (2009) *An involvement of yeast peroxisomal channels in transmembrane transfer of glyoxylate cycle intermediates* Int. J. Biochem. Cell Biol., **41**, 2546–2554

Cramer, J., Effelsberg, D., Girzalsky, W. and Erdmann, R. (2015) *Isolation of peroxisomes from yeast* Cold Spring Harb. Protoc; doi:10.1101/pdb.top074500

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Debelyy, M.O., Platta, H.W., Saffian, D., Hensel, A., Thoms, S., Meyer, H.E., Warscheid, B., Girzalsky, W. and Erdmann, R. (2011) *Uhp15p, a ubiquitin hydrolase associated with the peroxisomal export machinery* J. Biol. Chem., **286**, 28223–28234

Effelsberg, D., Cruz-Zaragoza, L.D., Schliebs, W. and Erdmann, R. (2016) *Pex9p is a new yeast peroxisomal import receptor for PTS1-containing proteins* J. Cell Sci., **129**, 4057-4066

Effelsberg, D., Cruz-Zaragoza, L.D., Tonillo, J., Schliebs, W. and Erdmann, R. (2015) *Role of Pex21p for piggyback import of Gpd1p and Pnc1p into peroxisomes of Saccharomyces cerevisiae* J. Biol. Chem., **290**, 25333–25342

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- Einwachter, H.**, Sowinski, S., Kunau, W-H. and Schliebs, W. (2001) *Yarrowia lipolytica Pex20p, Saccharomyces cerevisiae Pex18p/Pex 21p and mammalian Pex5pL fulfil a common function in the early steps of the peroxisomal PTS2 import pathway* EMBO Rep., **2**, 1035-1039
- Grunau, S.**, Mindthoff, S., Rottensteiner, H., Sormunen, R.T., Hiltunen, J.K., Erdmann, R. and Antonenkov, V.D. (2009) *Channel-forming activities of peroxisomal membrane proteins from the yeast Saccharomyces cerevisiae* FEBS J., **276**, 1698–1708
- Grunau, S.**, Lay, D., Mindthoff, S., Platta, H.W., Girzalsky, W., Just, W.W. and Erdmann, R. (2011) *The phosphoinositide 3-kinase Vps34p is required for pexophagy in Saccharomyces cerevisiae* Biochem. J. **434**, 161–170
- Kerssen, D.**, Hambruch, E., Klaas, W., Platta, H.W., de Kruijff, B., Erdmann, R., Kunau, W-H. and Schliebs, W. (2006) *Membrane association of the cycling peroxisome import receptor Pex5p* J. Biol. Chem., **281**, 27003-27015
- Mindthoff, S.**, Grunau, S., Steinfort, L.L., Girzalsky, W., Hiltunen, J.K., Erdmann, R. and Antonenkov, V.D. (2016) *Peroxisomal Pex11 is a pore-forming protein homologous to TRPM channels* Biochim. Biophys. Acta, **1863**, 271–283
- Oeljeklaus, S.**, Reinartz, B.S., Wolf, J., Wiese, S., Tonillo, J., Podwojski, K., Kuhlmann, K., Stephan, C. et al (2012) *Identification of core components and transient interactors of the peroxisomal importomer by dual-track stable isotope labeling with amino acids in cell culture analysis* J. Proteome Res. 2012, **11**, 2567–2580
- Platta, H.W.**, Grunau, S., Rosenkrantz, K., Girzalsky, W. and Erdmann, R. (2005) *Functional role of the AAA peroxins in dislocation of the cycling PTS1 receptor back to the cytosol* Nat. Cell Biol., **7**, 817-822
- Schäfer, A.**, Kerssen, D., Veenhuis, M., Kunau, W-H. and Schliebs, W. (2004) *Functional similarity between the peroxisomal PTS2 receptor binding protein Pex18p and the N-terminal half of the PTS1 receptor Pex5p* Mol. Cell Biol., **24**, 8895-8906
- Thoms, S.**, Debelyy, M.O., Nau, K., Meyer, H.E. and Erdmann, R. (2008) *Lpx1p is a peroxisomal lipase required for normal peroxisome morphology* FEBS J., **275**, 504-514
- Welker, S.**, Rudolph, B., Frenzel, E., Hagn, F., Liebisch, G., Schmitz, G., Scheuring, J., Kerth, A., Blume, A., Weinkauff, S., Haslbeck, M., Kessler, H. and Buchner, J. (2010) *Hsp12 is an intrinsically unstructured stress protein that folds upon membrane association and modulates membrane function* Mol. Cell, **39**, 507–520
- Wróblewska, J.P.**, Cruz-Zaragoza, L.D., Yuan, W., Schummer, A., Chuartzman, S.G., de Boer, R., Oeljeklaus, S., Schuldiner, M. et al (2017) *Saccharomyces cerevisiae cells lacking Pex3 contain membrane vesicles that harbor a subset of peroxisomal membrane proteins* BBA Mol. Cell Res., **1864**, 656–1667

14. Plasma membrane

- Wang, Y.**, Lilley, K.S. and Oliver, S.G. (2014) *A protocol for the subcellular fractionation of Saccharomyces cerevisiae using nitrogen cavitation and density gradient centrifugation* Yeast, **31**, 127–135
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15. Vacuole/pre-vacuole

- Chang, W.**, Zaarour, R.F., Reck-Peterson, S., Rinn, J., Singer, R.H., Snyder, M., Novick, P. and Mooseker, M.S. (2008) *Myo2p, a class V myosin in budding yeast, associates with a large ribonucleic acid-protein complex that contains mRNAs and subunits of the RNA-processing body* RNA, **14**, 491-502
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