

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)**”.

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 autophagosome cargo in Saccharomyces cerevisiae* PloS One, **9**: e91651

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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 Schleibs, 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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- 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