

Prof. Dr. Albert Sickmann

Leibniz-Institut für Analytische Wissenschaften – ISAS – e. V., Dortmund

E-Mail: sickmann@isas.de

Otto-Hahn-Str. 6b

44227 Dortmund

Phone: +49 231 1392-100

Fax: +49 231 1392-200



Curriculum Vitae

- *since 2008* Professor for Bioanalytics at ISAS, Dortmund
- *2007 - 2008* Professor for protein mass spectrometry at the University of Würzburg
- *2003 - 2007* Group leader at the DFG Research Centre for Experimental Biomedicine, University of Würzburg
- *2002 - 2003* Junior Professor for Protein function and Proteomics, Ruhr University, Bochum

Awards, Scholarships, Memberships, Coordination (selection)

- Analytica Research Award of the GBM (2008)
- Member of the Executive Board of the DGPF, Deutsche Gesellschaft für Proteomforschung e. V., President (2010 - 2018)
- Proteomic Forum (2015 – 2017), Conference Chairman
- Member of the EuPA Board, (2015 – 2017)
- Associate Editor, Journal of Proteome Research

Research Areas

- Bioanalytics, Protein chemistry, Systems biology, Quantitative Mass spectrometry, Post-translational modifications

Teaching

- Ruhr-University Bochum (Faculty of Medicine)
- TU Dortmund University (Department of Biochemical and Chemical Engineering (BCI))
- University of Aberdeen, Scotland (Department of Chemistry, School of Natural & Computing Sciences (NCS))

Most important publications (2005-2016)

(total number 196, around 7500 citations, H-Factor: 50)

Schmidt, O.; A.B. Harbauer, A.B.; Rao, S.; Eylich, B.; Zahedi, R. P.; Stojanovski, D.; Schonfisch, B.; Guiard, B.; Sickmann, A.; Pfanner, N.; Meisinger, C.:

Regulation of Mitochondrial Protein Import by Cytosolic Kinases **Cell**, 2011

Vögtle, F. N.; Wortelkamp, S.; Zahedi, R. P.; Becker, D.; Leidhold, C.; Gevaert, K.; Kellermann, J.; Voos, W.; Sickmann, A.; Pfanner, N.; Meisinger, C.:

Global analysis of the mitochondrial N-proteome identifies a processing peptidase critical for protein stability **Cell**. 139(2) (2009) 428-39

Meisinger, C.; Sickmann, A.; Pfanner, N.:

The mitochondrial proteome: from inventory to function **Cell** 134 (1) (2008) 22-4

Reinders, J.; Wagner, K.; Zahedi, R. P.; Stojanovski, D.; Eylich, B.; van der Laan, M.; Rehling, P.; Sickmann, A.; Pfanner, N.; Meisinger, C.: Profiling phosphoproteins of yeast mitochondria reveals a role of phosphorylation in assembly of the ATP synthase **Mol. Cell Proteomics** 6(11) (2007) 1896-906

Lewandrowski, U.; Moebius, J.; Walter, U.; Sickmann, A.:

Elucidation of N-glycosylation sites on human platelet protein: a glycoproteomic approach **Mol. Cell Proteomics** 5(2) (2006) 226-33

Lewandrowski, U.; Wortelkamp, S.; Lohrig, K.; Zahedi, R. P.; Wolters, D. A.; Walter, U.; Sickmann, A.: Platelet membrane proteomics: a novel repository for functional research **Blood** 114(1) (2009)

Burkhart, J. M., Gambaryan, S., Watson, S. P., Jurk, K., Walter, U., Sickmann, A., Heemskerk, J. W. M., Zahedi, R. P.: What can Proteomics tell us about platelets? **Circ. Res.** 114 (2014) 1204-1219

Vaudel, M., Burkhart, J. M., Zahedi, R. P., Oveland, E., Berven, F. S., Sickmann, A., Martens, L., Barsnes, H.: PeptideShaker enables reanalysis of MS-derived proteomics data sets **Nat. Biotech.** 33 (1) (2015) 22-4