

Selected Publications

Elisa Luquet, Christoph Biesemann, Annie Munier, and **Etienne Herzog**. Purification of synaptosome populations using Fluorescence Activated Synaptosome Sorting. *Methods Mol Biol*, vol. 1538, 2017. ISBN 978-1-4939-6688-2.

Schreiner D, Savas JN, **Herzog E**, Brose N & de Wit J. Synapse biology in the 'circuit-age'-paths toward molecular connectomics. *Curr Opin Neurobiol*, 2016, 42: 102–110

Rothman JS, Kocsis L, **Herzog E**, Nusser Z & Silver RA. Physical determinants of vesicle mobility and supply at a central synapse. *eLife*, 2016, 5: e15133.

Biesemann C, Grønborg M, Luquet E, Wichert SP, Bernard V, Bungers S.R, Cooper B, Varoqueaux F, Li L, Byrne JA, Urlaub H, Jahn O, Brose N*, and **Herzog E***. Proteomic screening of glutamatergic mouse brain synaptosomes isolated by fluorescence activated sorting. *The EMBO Journal*, 2014, 33 : 157–170

Herzog E*, Nadrigny F*, Silm K*, Biesemann C, Helling I, Bersot T, Steffens H, Schwartzmann R, Nägerl UV, El Mestikawy S, Rhee J, Kirchhoff F & Brose N. In Vivo Imaging of Intersynaptic Vesicle Exchange Using VGLUT1Venus Knock-In Mice. *The Journal of Neuroscience*, 2011, 31, 15544–15559.

Bonn Lecture Series in Neuroscience



Exploring the molecular diversity of central synapses in mice

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Tuesday, September 12th 2017, 16:00h
Epileptology, Seminar Room, Ground Floor

The brain connectome is made of several functional classes of synapses (excitatory, inhibitory, modulatory) each category may be further classified in subcategories (GABAergic, glycinergic ...). In the end, synapses within each brain circuit may present molecular adaptations relevant to support specific functional features. Since the pioneering work of Whittaker in the 1960's, neuroscientists have used enriched preparations of synaptic particles called synaptosomes to gather a wealth of knowledge about synapse structure, composition, and function. Yet, our current view of the molecular synapse is largely biased to an average synapse mostly contributed by the 2 major populations (glutamatergic and GABAergic).

We recently established a novel Fluorescence Activated Synaptosome Sorting method (FASS) that substantially improves conventional synaptosome enrichment protocols and enables high-resolution biochemical analysis of specific synapse subpopulations. In the present talk I will expose results gathered through the mass spectrometric analysis of VGLUT1 glutamatergic synapses in physiology and pathology. I will also present new developments that allow the refinement of the FASS approach to more discrete populations of synapses of diverse phenotype and origin.