

# Colloquia in Cellular Signaling

Venue: Medical University Vienna, Center for Physiology and Pharmacology,  
Institute of Pharmacology, Waehringerstrasse 13a, 1090 Vienna, "**Leseraum**".  
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**Friday 09.06.2017**

**16:00**

**Host: T. Stockner**

## **Mapping protein conformations using DEER/EPR spectroscopy**

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### **Abstract:**

For many proteins, flexibility and motion form the basis of their function. In our lab, we quantify the conformational landscapes of proteins and their changes upon interaction with ligands and other proteins. Using Double Electron-Electron Resonance (DEER) spectroscopy, a form of Electron Paramagnetic Resonance (EPR) spectroscopy, we directly measure absolute distances and distance distributions within proteins. From the data, we build quantitative structural models of the protein's intrinsic flexibility, conformational substates, and the structural changes induced by ligands and binding partners. We are also active in the development of improved DEER methodologies. In this presentation, we summarize our work on HCN, a hyperpolarization-activated ion channel involved in the regulation of the heartbeat [1-4]. Its activity is modulated by the binding of cyclic nucleotides such as cyclic AMP. We present a DEER-based structural model for the conformational transition induced by ligand binding, as well as DEER-derived insight into the energetics and the kinetics of the ligand binding and the conformational transition. In addition, we present results on the topology of the complex between HCN and TRIP8b, a structurally poorly characterized accessory protein.

[1] M. C. Puljung et al, *Proc. Natl. Acad. Sci. USA* **2014**, 111, 9816-9821. [[link](#)]

[2] H. A. DeBerg et al, *Structure* **2015**, 23, 734-744. [[link](#)]

[3] H. A. DeBerg et al, *J. Biol. Chem.* **2016**, 291, 371-281. [[link](#)]

[4] A. Collauto et al, *submitted* **2017**.