

Neuroscience Colloquium Summer Semester 2011

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Modeling intellectual disability in Drosophila: targeted and systematic approaches

Massive efforts are undertaken to understand the genetics of human Intellectual Disability (ID) disorders. More than 400 human ID genes have been identified to date, and we are now at the point where functional studies have to catch up with gene identification. This is a big challenge, but very worthwhile for two reasons. First, functional studies into Fragile X Syndrome and a few other ID disorders have identified first therapeutic strategies. Second, there is accumulating evidence that ID genes/proteins form molecular networks. ID research can therefore identify key modules that control brain development and cognition. My lab uses ID genes and the fruitfly *Drosophila melanogaster* as a model organism to gain in depth knowledge of mechanisms that wire our brains and to translate this knowledge back to humans. I will speak about two projects that already uncovered highly specialized (epigenetic and synaptic) functions of uncharacterised ID genes, unravelled unanticipated common molecular connections between them and contributed to the identification of novel ID causing mutations. I will further speak about our ongoing efforts to systematically characterize ID genes in *Drosophila*. Our goal is to provide conceptual advance in our understanding of brain development in health and disease and to significantly contribute to the development of novel diagnostic and therapeutic strategies for the large and still growing group of ID disorders.

Location: BCCN lecture theater,
Bernstein Center for Computational Neuroscience
Humboldt-Universität zu Berlin
Philippstr. 13, Haus 6

Date: Friday, June 3rd, 4:00 p.m.

Host: Christina Zube/Stephan Sigrist

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