BEN LEHNER

Biography

Ben Lehner is an ICREA Research Professor at the EMBL-CRG Systems Biology Program at the Centre for Genomic Regulation. He has a degree and a PhD from the University of Cambridge and was a post-doctoral fellow at the Wellcome Trust Sanger Institute. The main interest of his lab is the genetics and biology of individuals: can we make accurate predictions about how individuals differ from their genome sequences, and why is this often impossible? The lab is funded by the ERC, the EU, and grants from the Spanish and Catalan governments. He was awarded the Banco Sabadell Prize for Biomedical Sciences, the City of Barcelona Prize for Science, the FEBBS Anniversary Prize and is an EMBO Young Investigator.

Project

European Research Council Starting Grant
Project acronym: 2-HIT
Project full title: Genetic interaction networks: from C. elegans to human diseases

Overview
Most hereditary diseases in humans are genetically complex, resulting from combinations of mutations in multiple genes. However synthetic interactions between genes are very difficult to identify in population studies because of a lack of statistical power and we fundamentally do not understand how mutations interact to produce phenotypes. *C. elegans* is a unique animal in which genetic interactions can be rapidly identified *in vivo* using RNA interference, and we recently used this system to construct the first genetic interaction network for any animal, focused on signal transduction genes. The first objective of this proposal is to extend this work and map a comprehensive genetic interaction network for this model metazoan. This project will provide the first insights into the global properties of animal genetic interaction networks, and a comprehensive view of the functional relationships between genes in an animal. The second objective of the proposal is to use *C. elegans* to develop and validate experimentally integrated gene networks that connect genes to phenotypes and predict genetic interactions on a genome-wide scale. The methods that we develop and validate in *C. elegans* will then be applied to predict phenotypes and interactions for human genes. The final objective is to dissect the molecular mechanisms underlying genetic interactions, and to understand how these interactions evolve. The combined aim of these three objectives is to generate a framework for understanding and predicting how mutations interact to produce phenotypes, including in human disease.