

## **Large scale fitness landscape of a protein-coding gene**

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The relationship between genotype and phenotype, the fitness landscape, is one of the most useful abstractions in evolutionary biology. However, to date few experimental assays of the fitness landscape have been performed because of the inherent complications with a systematic high-throughput surveys of an astronomical number of genotypes. In my talk I will present new data on the fitness landscape of an evolutionarily-relevant section of the fitness landscape from His3 - a conditionally essential enzyme from baker's yeast. We find that the fitness landscape is influenced by epistatic interactions, including those that do not seem to conform to simple unidimensional rules. The understanding of a fitness landscape on a large scale may lead to a better understanding of how to design proteins with specific functions.