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OTHER PROGRAM AFFILIATIONS

Cancer

Infection and Immunity

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With the advent of personal genomic medicine a detailed understanding of gene function has never been more important. In to the future, our health may be monitored by regular “omics” measurements overlaid on our individual genomes. Each of us carries numerous “disease” mutations and countless further genetic variation, with mostly unknown consequences. My lab studies RNA metabolism: the birth, life and death of RNA molecules. A growing list of RNA-metabolic enzymes and binding proteins are implicated in intellectual disability, neuronal disorders and other diseases. I am motivated by a conviction that through the combined use of next generation technologies and evolutionary conservation in model organisms we can significantly accelerate discovery of basic gene function and the network-effect of loss-of-function mutations. And, that the impact that these mutations have on gene expression networks will have direct relevance to human health.

Research Projects

1. **Investigating coding and non-coding RNA expression**
2. **Investigating the switch from silence to activation of translation**
3. **An Investigation into the host-pathogen synapse**

Selected significant publications:

1. Archer SK, Shirokikh NE, **Beilharz TH**, Preiss T. 2016. Dynamics of ribosome scanning and recycling revealed by translation complex profiling. *Nature* doi: 10.1038/nature18647 [Epub ahead of print].
2. Harrison PF, Powell DR, Clancy JL, Preiss T, Boag PR, Traven A, Seemann T, **Beilharz TH**. 2015. PAT-seq: a method to study the integration of 3’-UTR dynamics with gene expression in the eukaryotic transcriptome. *RNA* 21:1502-10.
3. Janicke A, Vancuylenberg J, Boag PR, Traven A, **Beilharz TH**. 2012. ePAT: A simple method to tag adenylated RNA to measure poly(A)-tail length and other 3’ RACE applications. *RNA* 18: 1289-1295
4. **Beilharz TH**, Humphreys DT, Clancy JL, Thermann R, Martin DI, Hentze MW, Preiss T. 2009. microRNA-mediated messenger RNA deadenylation contributes to translational repression in mammalian cells. *PloS* one 4: e6783
5. **Beilharz TH**, Preiss T. 2007. Widespread use of poly(A) tail length control to accentuate expression of the yeast transcriptome. *RNA* 13: 982-997