

## Hosting group information for applicants

Name of DKFZ research division/group:

**Division of Regulatory Genomics and Cancer Evolution (B270)**

Contact person: **Duncan Odom (d.odom@dkfz.de)**

Group homepage: <https://www.dkfz.de/en/regulatorische-genomik/index.php>

Please visit our website for further information on our research and recent publications.

### RESEARCH PROFILE AND PROJECT TOPICS:

Dr Odom's laboratory studies how genetic sequence information shapes the cell's DNA regulatory landscape and thus the trajectory of cancer genome evolution. To date, their use of interspecies comparisons of matched functional genomic data has resulted in fundamental discoveries, including the extensive and rapid turn-over of tissue-specific transcription factor binding (Schmidt et al Science 2010, Stefflova et al Cell 2013), insulator elements (Schmidt et al Cell 2012), polymerase occupancies (Kutter et al Nature Genetics 2011), and enhancer activities (Villar et al Cell 2015) during organismal evolution, as well as the mechanisms underlying this regulatory plasticity (Wilson et al Science 2008). To demonstrate that genetic sequences were the major determinant of transcription and transcriptional regulation, the Odom lab re-purposed a fascinating aneuploidy mouse model of Down syndrome (previously developed by collaborators) that carries an almost complete copy of human chromosome 21 (Ward et al Molecular Cell 2013). Profiling the functional behaviour of a human chromosome in a mouse nucleus provided an elegant and powerful demonstration that cis-acting sequences have a greater impact than trans influences on transcription factor binding, chromatin state, and gene expression. Recently, his laboratory has begun exploiting single-cell RNA-sequencing and large-scale whole genome sequencing in understanding molecular evolution. Specifically, the Odom lab have recently used single-cell transcriptional analysis to conclusively demonstrate that ageing results in substantial increases in cell-to-cell transcriptional variability (Martinez et al Science 2017), as well as undertaken a large-scale analysis of how genetic and epigenetic differences between alleles can fundamentally alter the location and intensity of mutagenesis during tumour evolution.

Postdoctoral opportunities are available to work particularly in the areas of single-cell functional genomics, and the influence of genetic sequence variation on cancer genome evolution. Successful candidates should be highly versant with a diversity of modern genomics methods, and able to perform basic computational biology to facilitate interaction with dedicated computational collaborators.



CONNECTING THE DOTS.  
TO ADVANCE RESEARCH CAREERS

International Postdoc Program  
[www.dkfz.de/postdoc](http://www.dkfz.de/postdoc)