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Our group is integrated into a multidisciplinary research department, and we apply our knowledge to unravel novel disease intervention points. The main aim of our group is to identify potential new drug targets and the molecular pathways that they are involved in. The team has in-depth knowledge in genome-wide genetic approaches and sequencing technologies. Our general focus is on mammalian systems, using mutagenesis in cell lines, ES/iPS cell-derived progeny and primary cells, with the application of CRISPR/Cas9-mediated gene editing approaches being one of our central methods. We are constantly improving our technical know-how around genome-editing assays, starting from simple survival-based, single knock-out screens up to multi-fate readouts of individual cells with simultaneous manipulation of several genes. In combination with flow cytometry and liquid handling equipment, we apply these tools to various disease models and are able to ask specific questions around a focused set of target genes or apply genome-wide methodologies.

We are mostly interested in research questions in the fields of DNA repair, immunology, regenerative medicine, and lineage choice of various stem cell systems, and we collaborate

with other groups in these fields of expertise. Ultimately, we are trying to find molecules that allow us to manipulate cells in such a way that they contribute to attenuate or even cure diseases. We believe that combining latest state-of-the-art methods with relevant scientific questions will lead us to new interesting discoveries.

Selected Publications

Nannocystin?A: an elongation factor 1 inhibitor from Myxobacteria with differential anti-cancer properties. [2]
Krastel P, Roggo S, Schirle M, Ross NT, Perruccio F, Aspesi P Jr, Aust T, Buntin K, Estoppey D, Liechty B, Mapa F, Memmert K, Miller H, Pan X, Riedl R, Thibaut C1, Thomas J, Wagner T, Weber E, Xie X, Schmitt EK, Hoepfner D.
Angew Chem Int Ed Engl. 2015, 54, 10149-54.

Decatransin, a new natural product inhibiting protein translocation at the Sec61/SecYEG translocon. [3]
Junne T, Wong J, Studer C, Aust T, Bauer BW, Beibel M, Bhullar B, Bruccoleri R, Eichenberger J, Estoppey D, Hartmann N, Knapp B, Krastel P, Melin N, Oakeley EJ, Oberer L, Riedl R, Roma G, Schuierer S, Petersen F, Tallarico JA, Rapoport TA, Spiess M, Hoepfner D.
J Cell Sci. 2015, 128, 1217-29.

High-resolution chemical dissection of a model eukaryote reveals targets, pathways and gene functions. [4]
Hoepfner D, Helliwell SB, Sadlish H, Schuierer S, Filipuzzi I, Brachat S, Bhullar B, Plikat U, Abraham Y, Altorfer M, Aust T, Baeriswyl L, Cerino R, Chang L, Estoppey D, Eichenberger J, Frederiksen M, Hartmann N, Hohendahl A, Knapp B, Krastel P, Melin N, Nigsch F, Oakeley EJ, Petitjean V, Petersen F, Riedl R, Schmitt EK, Staedtler F, Studer C, Tallarico JA, Wetzel S, Fishman MC, Porter JA, Movva NR.
Microbiol Res. 2014, 169, 107-20.

Click here [5] for additional publications.

Links
[1] https://www.novartis.com/our-science/postdoc-program/research-themes/pathways-biology/dominic-hoepfner-phd
[2] http://www.ncbi.nlm.nih.gov/pubmed/26179970
[3] http://www.ncbi.nlm.nih.gov/pubmed/25616894%20
[4] http://www.ncbi.nlm.nih.gov/pubmed/24360837
[5] http://www.ncbi.nlm.nih.gov/pubmed/?term=hoepfner+d