Overview: HP-L's offered in SoSe 2016 – Modules "Biolab" and "Working in Bioscience"

Definition: A 'Biolab' or 'Working in Bioscience' lab internship – duration: minimum 6 weeks in the lab (extensible) – should consist of a small scientific project. The experimental work must be recorded by a protocol report which has to be written in the style of a master thesis, consisting of title page, abstract, introduction, materials and methods, results, discussion and references.

"Biolab" (only for MBS students with Major Cancer Biology) – "Working in Bioscience" (also for MBS-Students from other Majors) – "and for other interested students"

"Leistungsnachweis/Mode of Examination": for Major Cancer Biology students to fulfill Module Biolab: The experimental work has to be recorded and the protocol will be graded by the instructor on a scale from 0 - 100 points

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<tr>
<th>Lfd Nr.</th>
<th>Term</th>
<th>Type</th>
<th>Supervisor(s)</th>
<th>Duration and date</th>
<th>Title and Description</th>
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<tbody>
<tr>
<td>1</td>
<td>every semester</td>
<td>Biolab</td>
<td>Amir Abdollahi, Sara Chibliak, Ivana Dokic, Sophie Domhan, Christian Schwager, Philipp Seidel, Peter Hofner, Ali Nowrouzi, Martin Niklas, Quanxiang Wei, Ute Wirkner</td>
<td>to be arranged</td>
<td>Tumor microenvironment, radiation oncology and translational cancer research</td>
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<td>WiB (also for Major: MCB)</td>
<td>also for Master Molecular Biotechnology also for Master Translational Medical Research</td>
<td>9:00-18:00</td>
<td>The main focus of our lab is to investigate the role of tumor-stroma communication in development of tumor resistance to multimodal therapies and rational design of novel therapy strategies. For a recent overview please read: Abdollahi and Folkman. Evading tumor evasion: Current concepts and perspectives of anti-angiogenic cancer therapy. Drug Resist Updat. 2010 (download @ <a href="http://angiogenesis.dkfz.de/papers/abdollahi_drugresist_2010.pdf">http://angiogenesis.dkfz.de/papers/abdollahi_drugresist_2010.pdf</a>). We seek for candidates with an excellent scientific record and strong motivation in multidisciplinary projects. Solid background in basic cell and molecular biology techniques are requested. Experiences in the field of tumor angiogenesis and tumor microenvionment, radiation biology, genome/transcripome and epigenetic analysis (microarrays based mRNA, miRNA, SNP, CGH and promoter methylation studies), analysis of large data sets generated with high-throughput methods (basic statistics, R, SQL), functional genomics (RNAi or pharmacological in-vitro and in-vivo screens), proteomics (expression, purification, phosphorylation and protein-protein interaction analysis) are advantageous for the evaluation of our laboratory. Special skills with animal experimentation, including transgenic mouse models, surgical orthotopic tumor implantation, intravital microscopy or other invasive or non-invasive imaging tools (MRI, CT-scan, PET and ultrasound) are advantageous for the evaluation of the applicant. Our team is integrated in Heidelberg Ion Therapy Center and National Center for Tumor diseases (NCT) which offer state-of-the-art research facilities and a supportive multidisciplinary environment. For more information about our group please visit: <a href="http://www.molecularoncology.de">www.molecularoncology.de</a></td>
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<td>2</td>
<td>SoSe2016</td>
<td>Biolab for Major Cancer Biology students only</td>
<td>Helmut Augustin, Iris Augustin, Marco Breinig</td>
<td>9:00-18:00 INF 580 (TP3) 1</td>
<td>Methods in angiogenesis research&lt;br&gt;The term angiogenesis describes the growth of new blood vessels from existing vessels. This process is responsible for essential biological functions such as embryonic development, the female reproductive cycle, wound healing and tissue repair processes. Pathological conditions in which angiogenesis is active are malignant neoplasm/tumor and additional diseases such as cardiovascular diseases, diabetes, multiple sclerosis or autoimmune disorders. The aim of the underlying course is to provide an overview of endothelial cell biology and to gain experience in several standard angiogenesis assays.</td>
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<td>3</td>
<td>SoSe2016</td>
<td>WiB (also for Majors: MCB, Systems Biology)</td>
<td>Michael Boutros, Anna-Lisa Böttcher</td>
<td>9:00-18:00 INF 580 (TP3) 1</td>
<td>Wnt signaling in cancer&lt;br&gt;Wnt signaling has been implicated in cancerogenesis. In current projects we are dissecting the Wnt signaling pathway in developmental and pathological conditions. One particular focus is on skin biology and associated tumors. In further projects we are analyzing the Wnt signaling pathway in transgenic mice lines. We also investigate novel candidate genes involved in tumor cell migration and invasion that contribute to metastasis. For this we use different cell based assays including organotypic cultures as well as mouse studies. References: Augustin et al., The Journal of Experimental Medicine, 2013; Augustin et al., EMBO Molecular Medicine, 2012.</td>
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<td>4</td>
<td>SoSe2016</td>
<td>WiB (also for Majors: MCB, Systems Biology)</td>
<td>Michael Boutros, Max Billmann, Iris Augustin</td>
<td>9:00-18:00 INF 580 (TP3) 1</td>
<td>High-throughput methods to dissect cancer signaling pathways&lt;br&gt;We offer a practical in high-throughput screening methods. These include genomic technologies as well as cell biology and genetics in model systems like Drosophila and human cells. In particular we use cell-based RNA interference (RNAi) technologies to systematically identify pathway-specific genes and pathway networks to dissect their role in development and carcinogenesis. We are currently setting up novel genetic engineering tools for high-throughput research, which build upon the recently introduced CRISPR/CAS9 system. Methods will include (high-throughput) cloning (standard as well as sequence and ligation independent multi-fragment cloning), cell culture work (cell lines, stable transfection, selection) and standard molecular biology methods. Programing skills (e.g. R) are of advantage but not mandatory. References: Horn et al., Nature Methods, 2011; Sandmann et al., Current Opinion in Genetics and Development, 2012; Heigwer et al., Nucleic Acids Res. 2013.</td>
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<td>5</td>
<td>SoSe2016</td>
<td>WiB (also for Majors: MCB, Systems Biology)</td>
<td>Michael Boutros, Oksana Voloshanenko</td>
<td>9:00-18:00 INF 580 (TP3) 1</td>
<td>Wnt signaling in Drosophila&lt;br&gt;Signaling networks control key decisions during development of organisms and deregulation of signal transduction pathways has been linked with carcinogenesis. To understand the complex biological networks, our research centers at dissecting how signals are secreted, received and transmitted. We offer a practical course for the systematic analysis of Wnt signaling and secretion using Drosophila as a model system. The Drosophila midgut, that is analogous to the mammalian small intestine, is used here to study the differentiation and maintenance of intestinal stem cells (ISCs) in the gut. Therefore we use large-scale in vivo RNAI screening approaches to identify factors involved in a proper tissue homeostasis with a special focus on the Wnt signal transduction cascade. Candidate genes have to be further characterized by different ex vivo (Drosophila cells) and in vivo (Drosophila wing imaginal discs) approaches. References: Gross et al., Nature Cell Biology, 2012; Zhou et al., Developmental Biology, 2014.</td>
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<td>6</td>
<td>SoSe2016</td>
<td>WiB (also for Majors: MCB, Systems Biology)</td>
<td>Michael Boutros, Oksana Voloshanenko</td>
<td>9:00-18:00 INF 580 (TP3) 1</td>
<td>Wnt signaling pathway&lt;br&gt;The Wnt signaling pathway is one of evolutionarily conserved signal transduction pathways used extensively during animal development, from Hydra to humans. The aim of the project will be to characterize the role of novel regulators possibly involved in canonical or non-canonical Wnt signaling or proteins, which regulate Wnt's secretion. The following techniques will be applied as part of the practical: gene editing by CRISPR/Cas9, gene silencing by siRNA, luciferase reporter systems, Western Blotting. Reference: Voloshanenko et al., Nature Communications, 2013</td>
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<td>SoSe2016</td>
<td>• Biolab for Major Cancer Biology students only</td>
<td>Adelheid Cerwenka, Jing Ni, Margareta Correia, Ana Stojanovic</td>
<td>to be arranged</td>
<td><strong>Innate Immunity and Cancer</strong> <a href="http://www.dkfz.de/en/innateimmun/index.php">http://www.dkfz.de/en/innateimmun/index.php</a></td>
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<td><a href="mailto:a.cerwenka@dkfz.de">a.cerwenka@dkfz.de</a></td>
<td>09:00-18:00</td>
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<td>DKFZ, INF 280, 7. OG</td>
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<td>8.</td>
<td>SoSe2016</td>
<td>• Biolab • WIB (also for Major: MCB) and other interested students</td>
<td>Angel Cid</td>
<td>to be arranged</td>
<td><strong>Targeted tumor vaccines and liposomes</strong></td>
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<td><a href="mailto:a.cid@dkfz.de">a.cid@dkfz.de</a></td>
<td>9.00-17.00</td>
<td>Project 1. Targeted tumor vaccines</td>
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<td>DKFZ, HH, INF 280, H2.07.057</td>
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<td>Construction and characterization of recombinant fusion proteins designed to induce T cell responses against cells infected by human papillomavirus (HPV) types 16 and 18, which cause precancerous lesions leading to cervical cancer.</td>
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<td>Project 2. Targeted liposomes</td>
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<td>Preparation and characterization of liposomes conjugated with single-chain antibodies binding to surface proteins overexpressed in cancer cells.</td>
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<td>9.</td>
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<td>• Biolab • WIB (also for Major: MCB)</td>
<td>Tobias P. Dick</td>
<td>to be arranged</td>
<td><strong>Redox regulation of signal transduction</strong></td>
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<td>semester</td>
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<td><a href="mailto:t.dick@dkfz.de">t.dick@dkfz.de</a></td>
<td>9.00-18.00</td>
<td>Please refer to our website for topics and references.</td>
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<td>DKFZ, INF 280, H2.02</td>
<td>1</td>
<td><a href="http://www.dkfz.de/en/redoxregulation/inhalte/researchinterests/startres.html">http://www.dkfz.de/en/redoxregulation/inhalte/researchinterests/startres.html</a></td>
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<td>10.</td>
<td>SoSe2016</td>
<td>• Biolab • WIB (also for Major: MCB)</td>
<td>Sven Diederichs</td>
<td>6-8 weeks; date to be arranged</td>
<td><strong>non-coding RNA biology</strong></td>
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<td><a href="mailto:s.diederichs@dkfz.de">s.diederichs@dkfz.de</a></td>
<td>full-time</td>
<td>Many non-protein-coding RNAs (ncRNAs) can exert important functions in the cell. One class of ncRNAs, microRNAs, are novel important post-transcriptional regulators of gene expression. Many microRNAs play prominent roles in tumorigenesis by targeting oncogenes or tumor suppressor genes. In our young and motivated group, you will study the biogenesis of microRNAs or the function of other non-coding RNAs as well as their dysregulation and role in cancer. The most important methods in our lab that you could learn are cell culture, transfection, RT-PCR &amp; qPCR, luciferase assays, cloning using topoisomerase or Gateway methodology, mutagenesis, microRNA target prediction, splicing analysis, cellular phenotype analysis of e.g. proliferation or apoptosis. Website: <a href="http://www.diederichslab.org">www.diederichslab.org</a></td>
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<td>SoSe2016</td>
<td>• Biolab • WIB (also for other Majors)</td>
<td>Markus Feuerer</td>
<td>to be arranged</td>
<td><strong>Molecular mechanisms involved in development and function of regulatory immune cells</strong></td>
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<td><a href="mailto:m.feuerer@dkfz.de">m.feuerer@dkfz.de</a></td>
<td>9.00-18.00</td>
<td>Quite recently, Foxp3 expressing regulatory T cells (Tregs) have emerged as critical control elements within the immune system, being of essential importance for the maintenance of self-tolerance, the limitation of excessive anti-pathogen responses and for the control of immune homeostasis. This project is part of a bigger picture that aims to decipher and compare the molecular control mechanisms involved in the development and function of Tregs that emerge along the respective pathways. <a href="http://www.dkfz.de/en/immuntoleranz/index.html">http://www.dkfz.de/en/immuntoleranz/index.html</a></td>
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<td>12.</td>
<td>every</td>
<td>• Biolab • WIB (also for other Majors) and other interested students</td>
<td>Andreas Fischer</td>
<td>to be arranged</td>
<td><strong>Notch signaling in angiogenesis and vascular tumors</strong></td>
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<td><a href="mailto:a.fischer@dkfz.de">a.fischer@dkfz.de</a></td>
<td>full-time</td>
<td>Our laboratory is interested in how Delta Notch signaling coordinates blood vessel differentiation in normal tissue and how this pathway affects tumor angiogenesis, vascular malformations and vascular tumors. Other projects address the role of Notch signaling for tissue homeostasis e.g. vascular permeability control and the influence of endothelial cells on metabolism. We apply a large repertoire of cellular methods in cell biology, molecular biology as well as mouse models.</td>
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<td>13.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Richard Gabriel, Manfred Schmidt, Christof von Kalle</td>
<td><a href="mailto:richard.gabriel@nct-heidelberg.de">richard.gabriel@nct-heidelberg.de</a></td>
<td>8 weeks; date to be arranged</td>
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<td>INF 581 (TP4) 4th floor, 4.301</td>
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<td>14.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Violaine Goidts, Emma Phillips</td>
<td><a href="mailto:v.goidts@dkfz.de">v.goidts@dkfz.de</a></td>
<td>to be arranged</td>
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<td>for Major Cancer Biology students only</td>
<td>Tel. 06221 42-4635</td>
<td>full-time</td>
<td>DKFZ, TP3, INF 580, 1.205</td>
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<td>15.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Ingrid Herr and co-workers</td>
<td><a href="mailto:secr@exchi.uni-heidelberg.de">secr@exchi.uni-heidelberg.de</a></td>
<td>to be arranged</td>
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<td>for Major Cancer Biology students</td>
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<td>16.</td>
<td>every semester</td>
<td>Biolab</td>
<td>Ilse Hofmann</td>
<td><a href="mailto:i.hofmann@dkfz.de">i.hofmann@dkfz.de</a></td>
<td>to be arranged</td>
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<td>SoSe2016</td>
<td>Biolab</td>
<td>Michael Knop</td>
<td><a href="mailto:m.knop@zmbh.uni-heidelberg.de">m.knop@zmbh.uni-heidelberg.de</a></td>
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<td>18.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Dorde Komljenovic, Klaus Braun, Mark E. Ladd</td>
<td><a href="mailto:d.komljenovic@dkfz.de">d.komljenovic@dkfz.de</a></td>
<td>to be arranged</td>
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<td>for Major Cancer Biology students only</td>
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<td>09:00-18:00</td>
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| 19.   | every semester | ☑ Biolab WIB (also for other Majors) and other interested students | Rajiv Kumar  
Tel. 06221 42-1806 | 8 weeks; date to be arranged  
08:00-17:00  
DKFZ, TP3, INF 580, Rm 3.206  
2 | Somatic mutations and effect in melanoma and other cancers  
Role somatic mutations in human cancers effect on gene expression. Please refer to the website http://www.dkfz.de/en/molgen_epidemiology/mitarbeiter/rajiv.html |
| 20.   | every semester | ☑ Biolab WIB (also for Major: Infectious Diseases) | Martin Löchelt  
Tel. 06221 42-4933 | to be arranged  
to be arranged  
ATV, 2.108  
1-2 | Foamy viruses: Molecular biology, epidemiology and vector development  
The student will work on a sub-project that is integrated in our ongoing research which deals with 1. the host-virus interaction of foamy viruses, 2. molecular mechanisms of counteracting interspecies and zoonotic events (virus restriction and counter-defense) or 3. with all aspects of vector development for gene transfer or vaccination. The student will use state-of-the-art cell biology, virology and molecular biology methods. For further information see also our web page at http://www.dkfz.de/en/f020/groups/loechelt/index.html |
| 21.   | SoSe2016 | ☑ Biolab for Major Cancer Biology students only | Justo Lorenzo Bermejo, Dominique Scherer  
lorenzo@imbi.uni-heidelberg.de  
Tel. 06221 56-4180 | 6-8 weeks; date to be arranged  
9:00-18:00  
IMBI, INF 305, 1st floor, Rm 126  
1-2 | Statistical analysis of genetic data: Applied bioinformatics with R  
The statistical analysis of genetic data plays today a major role in life sciences. A basic knowledge of biostatistics is essential for a successful academic career and many biotech/pharmaceutical companies are actively recruiting staff with an appropriate training. This internship aims to provide participants with an overview of standard methods, statistical software and current developments in applied statistical genetics. After an introduction into the field including the R project for statistical computing, participants will gain hands-on experience in R programming. Previous programming experience is not required, but exposure to genetic or epigenetic data (DNA sequence, micro-RNA or mRNA expression, methylation data) is advantageous. The two instructors are members of the Statistical Genetic Group at the Institute of Medical Biometry and Informatics, University of Heidelberg. Please visit www.biometrie.uni-heidelberg.de/StatisticalGenetics for a brief description of the group activities. |
| 22.   | SoSe2016 | ☑ Biolab WIB (also for Major: MCB) and other interested students | Mona Malz, Nikolas Gunkel  
m.malz@dkfz.de  
Tel. 06221 42-3433 | to be arranged  
9.00-18.00  
DKFZ, TP3  
1 | Cancer drug discovery  
Our group is active in four areas of cancer drug discovery: 1) Target Identification and Validation; 2) Assay Development and Screening; 3) Synthetic Organic Chemistry, and 4) Biological Testing. These activities are combined to discover specific inhibitors and to establish candidate drugs for clinical testing. During your internship, you will actively collaborate in one of our running drug discovery portfolio projects. This may encompass target validation procedures (analyze the cancer relevant phenotype after knockdown and/or overexpression of the target), development and validation of cell-based assays for primary high-throughput screening and secondary assays, cellular testing of new compounds (e.g. EC50 determination, synergy screens), and if desired medicinal chemistry. For more information don't hesitate to contact Mona Malz (m.malz@dkfz.de) or visit our website: http://www.dkfz.de/en/drugs/index.php |
| 23.   | every semester | ☑ Biolab WIB (also for Major: Infectious Diseases) | Antonio Marchini  
a.marchini@dkfz.de  
Tel. 06221 42-4964 | to be arranged  
full-time  
DKFZ, ATV, A2.208  
1 | Development of novel Parvovirus-based anti-cancer therapies  
We genetically modify rodent oncolytic parvoviruses (PVs) with the aim to improve their antineoplastic activity. PVs of a second generation are then tested alone or in combination with other anti-cancer agents. Molecular Biology, Cell Biology and Virology methods are used for the characterization of the novel therapies. The student will work in a small project integrated into the research activities of our Team. |
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<th>Duration and date</th>
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<td>24</td>
<td>every</td>
<td>Biolab, WIB</td>
<td>Ana Martin-Villalba, Susanne Kleber, and PhD students in the group</td>
<td>to be arranged</td>
<td>Analysing the role of the CD95/CD95L-system in different scenarios of the central nervous system</td>
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<tr>
<td></td>
<td>semester</td>
<td>(also for Majors: Neuroscience, MCB, Dev. Biol.)</td>
<td><a href="mailto:a.martin-villalba@dkfz.de">a.martin-villalba@dkfz.de</a></td>
<td>10.00-18.00</td>
<td>Stem cells\nOur lab is interested in the function and regulation of neural stem cells in the developing and adult brain. In the adult brain there are two regions harbouring neural stem/progenitor cells (NPCs) that continuously generate new neurons, the dentate gyrus of the hippocampus (DG) and the subventricular zone of the lateral ventricles (SVZ). Newborn neurons of the hippocampus are involved in learning and memory. Stem cells in the SVZ generate interneurons involved in fine tuning of olfaction. In the diseased brain, NPCs can be activated to repair the brain. Over-activation of these cells can result in tumour formation. To envisage ways to repair the CNS or block tumor formation the lab studies cell proliferation, and differentiation in the developing and healthy, tumorigenic, and regenerating adult CNS. Our laboratory has identified CD95 as a receptor signaling survival and neuronal differentiation in the naive and ischemic brain (Corsini et al., Cell Stem Cell 2009).\nAxonal regeneration\nSantiago Ramón y Cajal made several fundamental observations that have defined the perception of axonal regeneration in the central nervous system (CNS) of the past decades. While during development and in the peripheral nervous system, regeneration of nerve fibers does occur, in the adult CNS they do not regenerate. Right after injury, transected axons in the brain and spinal cord extend short distances, but shortly afterwards regeneration is halted and growth cones turn into retraction bulbs (Cajal, 1928). Our laboratory tries to envisage new ways to coax axons towards regeneration using models of crush- and transection-injury of the spinal cord.\nSignaling\nCD95 was first described as the inducer of apoptosis and it is still mostly known as the &quot;death receptor&quot;. However, research in our group questions this dogma. We showed in several cancer cell lines and primary cell types that CD95 does not act as an apoptosis inducer but rather triggers migration, invasion and differentiation. We have deciphered molecular events originating from CD95 in glioma, neural stem cells and immune cells. Currently, we are investigating corresponding pathways in differentiating neurons and pancreatic cancer. Those findings imply CD95 as a therapeutic target for treating spreading of glioblastoma, neurodegenerative disorders as well as inflammation after spinal cord injury (Kleber et al., Cancer Cell, 2008; Corsini et al., Cell Stem Cell 2009; Sancho Martinez and Martin-Villalba, Cell Cycle, 2009; Letellier et al., Immunity, 2010). Furthermore, by identification of cell-type specific adapters of CD95 signaling we enlarged a potential spectrum of pharmacological intervention.\nhttp://www.dkfz.de/en/neurobiologie-von-gehirntumoren/index.html</td>
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<tr>
<td>25</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Michael Milsom\<a href="mailto:nmichael.milsom@dkfz.de">nmichael.milsom@dkfz.de</a></td>
<td>8 weeks; date to be arranged</td>
<td>Stem cells, DNA damage and ageing\nCancer is one of several diseases whose incidence dramatically increases with advancing age. The Experimental Hematology group is broadly interested in understanding the mechanisms which govern this phenomenon and predominantly focusses upon the hematopoietic system as a model to study ageing. Specifically, we are interested in characterizing the biological changes that take place in hematopoietic stem cells during ageing and how these alterations impact upon hematopoietic function and the process of leukemogenesis. This Biolab rotation will involve working with experimental mice. For further details on the work program and associated literature, please visit <a href="https://www.dkfz.de/en/experimentelle-haematologie/index.php">https://www.dkfz.de/en/experimentelle-haematologie/index.php</a></td>
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<td>Nr</td>
<td>Term</td>
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<td>Supervisor(s)</td>
<td>Duration and date</td>
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<tr>
<td>26</td>
<td>every semester</td>
<td>Biology</td>
<td>Norbert Mücke, Jörg Langowski</td>
<td>to be arranged</td>
<td>TP3</td>
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<tr>
<td>27</td>
<td>every semester</td>
<td>Biology</td>
<td>Christoph Plass, Dieter Weichenhan, Daniel Lipka, Annika Baude</td>
<td>to be arranged</td>
<td>DKFZ, HH, INF 280, 3. OG</td>
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<td>28</td>
<td>every semester</td>
<td>Biology</td>
<td>Odilia Popanda</td>
<td>to be arranged</td>
<td>DKFZ, HH, INF 280, H02.03.071</td>
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<td>29</td>
<td>every semester</td>
<td>Biology</td>
<td>Angelika Riemer</td>
<td>6-8 weeks, date to be arranged</td>
<td>DKFZ, ATV, INF 242</td>
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<td>Supervisor(s)</td>
<td>Duration and date</td>
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<td>30.</td>
<td>every</td>
<td>Biolab</td>
<td>Marcel Schilling, Ursula Klingmüller</td>
<td>to be arranged</td>
<td>Analysis of information processing in by an integrative receptor and signaling-pathway model</td>
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<td></td>
<td>semester</td>
<td>(also for other Majors)</td>
<td><a href="mailto:m.schilling@dkfz.de">m.schilling@dkfz.de</a></td>
<td>to be arranged</td>
<td>The hormone Erythropoietin (Epo) is the key regulator of erythropoiesis and regulates cell survival via the JAK2/STAT5 signaling pathway. We have recently demonstrated that information processing by EpoR and JAK2 at the plasma membrane is linear over a broad range of ligand concentrations and that the activation of STAT5 is directly linked to survival of erythroid progenitor cells. However, the mode of signal processing throughout the JAK2/STAT5 pathway remains elusive. The aim of this project is to combine these previously established models and calibrate the resulting mathematical model with quantitative data. Data generation will be performed by quantitative immunoblotting and qRT-PCR. Identifiability analysis of model parameters, model reduction and experimental design can be performed. Depending on the qualifications of the student, the focus of this lab practical will be on the experimental side, the modeling aspects or a combination of both methods. <a href="http://www.dkfz.de/en/systembiologie/index.php">http://www.dkfz.de/en/systembiologie/index.php</a></td>
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<td>WiB</td>
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<td>DFKZ, HH, INF 280, H1.05.040</td>
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<td>31.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Manfred Schmidt, Cynthia Bartholomä, Stefan Wilkening</td>
<td>to be arranged</td>
<td>Vector biosafety analyses in preclinical and clinical gene therapy studies</td>
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<td></td>
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<td>(for Major Cancer Biology students only)</td>
<td><a href="mailto:manfred.schmidt@nct-heidelberg.de">manfred.schmidt@nct-heidelberg.de</a></td>
<td>9-18</td>
<td>The main focus of the Schmidt group is set on the efficiency and safety of gene transfer vector systems and their application in clinical gene therapy. The linear amplification mediated (LAM)-PCR technology, developed in our lab, detects viral integration sites in the human genome in minimal amounts of clinical samples, allowing the dissection of vector integrations that may lead to genotoxicity, as a side effect of gene therapy. For nearly all world-wide successful gene therapy studies, with the aim to cure immunodeficiencies, the group surveyed the clonal composition of the hematopoietic system after transplantation. These studies also provided precious insights into the biology of stem cells, physiology of hematopoietic (and other tissue) regeneration and development of malignancies. Moreover, the integration site analysis, combined with next generation sequencing and bioinformatical data management, serves as a highly valuable platform for more than 40 national and international collaborative projects, which investigate molecular mechanisms underlying gene and molecular therapeutical studies. <a href="http://www.nct-heidelberg.de/forschung/nct-clinical-and-translational-research-programs-groups/molecular-diagnostics/section-molecular-and-gene-therapy-schmidt.html">http://www.nct-heidelberg.de/forschung/nct-clinical-and-translational-research-programs-groups/molecular-diagnostics/section-molecular-and-gene-therapy-schmidt.html</a></td>
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<td>(also for other Majors)</td>
<td><a href="mailto:stephanie.laufs@nct-heidelberg.de">stephanie.laufs@nct-heidelberg.de</a></td>
<td>DFKZ, TP4, INF 581, Rm 4.303</td>
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<td>32.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Manfred Schmidt, Stephanie Laufs, Cynthia Bartholomä, Wei Wang</td>
<td>8 weeks; date to be arranged</td>
<td>Subgenomic sequencing of wtHIV in vivo</td>
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<td></td>
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<td>(for Major Cancer Biology students only)</td>
<td><a href="mailto:stephanie.laufs@nct-heidelberg.de">stephanie.laufs@nct-heidelberg.de</a></td>
<td>9.00-17.00</td>
<td>Practical will include basic studies on HIV-1 biology with a special emphasis on genomic integration. Methods will include linker-PCR/PCR/qPCR techniques and high throughput sequencing</td>
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<td>(also for other Majors)</td>
<td><a href="mailto:stephanie.laufs@nct-heidelberg.de">stephanie.laufs@nct-heidelberg.de</a></td>
<td>DFKZ, TP4, INF 581, 4th floor</td>
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<td>33.</td>
<td>SoSe2016</td>
<td>Biolab</td>
<td>Holger Sültmann</td>
<td>to be arranged</td>
<td>Transcriptome analysis</td>
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<td>(also for other Majors)</td>
<td><a href="mailto:h.sueltmann@dkfz.de">h.sueltmann@dkfz.de</a></td>
<td>9-18</td>
<td>The goal of the practical course is to identify and investigate the expression patterns of different RNA species (mRNA, miRNA, lncRNA) in solid tumors and body fluids using high throughput genomic technologies. Selected candidate miRNAs and genes are characterized in cancer cell line models by intervention experiments and functional assays. The methods comprise microarray / low-density array analysis, total RNA isolation and QC, qRT-PCR/ddPCR, cell culture, transfection experiments and cellular assays. <a href="http://www.dkfz.de/en/krebsgenomforschung/">www.dkfz.de/en/krebsgenomforschung/</a></td>
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<td>WiB</td>
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<td>NCT, INF 460</td>
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<td>34.</td>
<td>every</td>
<td>Biolab</td>
<td>Aurelio Teleman</td>
<td>to be arranged</td>
<td>Regulation of cell growth and metabolism in cancer</td>
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<td></td>
<td>semester</td>
<td>(also for other Majors)</td>
<td><a href="mailto:a.teleman@dkfz.de">a.teleman@dkfz.de</a></td>
<td>B1.314</td>
<td>We are interested in studying the cancer signaling pathways that regulate cell growth and metabolism. To grow, cells need to synthesize all the necessary metabolic building blocks by activating the relevant metabolic pathways. Thus we study both signaling pathways (such as insulin, PI3K and TOR) and metabolic pathways. The lab uses a wide range of techniques, from cell culture and biochemical approaches to in vivo genetics and organismal phenotyping.</td>
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<td>Duration and date</td>
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| 35. | every semester | • Biolab  
• WiB (also for other Majors)  
also for BSc Biosciences  
also for BSc and MSc Molecular Biotechnology | Guy Ungerechts, Christine Engeland  
christine.engeland@nct-heidelberg.de | to be arranged  
to be arranged  
NCT, INF 460, 2. OG, 02.127 | 1 | Oncolytic Measles viruses for cancer therapy  
The group "Virotherapy" (Dr. Dr. Guy Ungerechts, Dept. of Translational Oncology, NCT) is engineering and characterizing oncolytic Measles virus vectors for novel cancer therapies with the goal of translation toward clinical Phase I studies.  
Link "http://www.nct-heidelberg.de/de/forschung/Neue_Therapeutika/virotherapie/virotherapie.php" |
| 36. | SoSe2016 | • Biolab  
• WiB (also for Major: MCB, Dev. Biol., Systems Biology) | Alexandros Vegiopoulos  
a.vegiopoulos@dkfz.de | to be arranged  
9.00-18.00  
DKFZ, HH, INF 280, H1.01.043 | 1 | Stem cell and tissue responses to metabolic stress  
Methodology: Culture and manipulation (RNAi) of primary adipose tissue stem cells. Quantitative fluorescence microscopy. Molecular (RNA, protein) and metabolic profiling of cells and tissues. Mouse physiology/metabolism. |
| 37. | SoSe2016 | • Biolab  
• WiB (also for other Majors) | Stefan Wiemann  
s.wiemann@dkfz.de | to be arranged  
9.00-18.00  
DKFZ, TP3, INF 580 | 1 | Qualitative and quantitative analysis of cellular signaling |