Collaborations

CEDAD Cologne
Center for Molecular Medicine Cologne (CMMC)
Nephrolab Cologne / Kidney Research Center Cologne (KRCC)
Max-Planck-Institut für Stoffwechselforschung
Albertus Magnus Center for Early Career Researchers
Graduate School for Biological Sciences (GSfBS)
Interdisciplinary Program Molecular Medicine at the University of Cologne (IPMM)
Graduiertenschule Human- und Zahnmedizin (GSHZ)
Deutsche Forschungsgemeinschaft (DFG)

Core facilities

Histopathology, Institute of Pathology

Histopathology is the main connecting cross-disciplinary subject in medicine, and enables the direct visualization of tissue changes. This technique has the unique capacity to analyze a marker at the single cell/tissue level while preserving the morphological context. Formalin-fixed and paraffin-embedded (FFPE) human as well as mouse material will be used for a morphology-based description of the different tissue components using histochemical, immunohistochemical, as well as in situ, technologies (RNAscope).

Immunohistochemistry (IHC) allows the detection of cell-associated or non-cell fixed proteins, modern in situ hybridization (ISH) technologies enable the reliable and specific detection of mRNA, miRNA, and lncRNA within the tissue environment context. Dual ISH and IHC stainings will be used for the identification of cytokines and their cellular origin. Furthermore, the Nanostring technology enables the expression profiling of more than 500 inflammation- and immunology-related genes on human or mouse FFPE material.
1. **Histopathology**: Standard tissue preparation on FFPE material or frozen material using different histochemical stainings.

2. **Immunohistochemistry**: Standard detection of different proteins on slides in the preserved tissue context.

3. **RNAscope**: Specific detection of mRNA, miRNA, and IncRNA within the tissue environment.

4. **Nanostring platform**: Inflammation- and immunology-related expression profiling of more than 500 genes on human or mouse FFPE material.

**Internal resources**: Immunohistochemical detection platforms (Bond MAX by Leica, Benchmark by Ventana, Dako Stainer); RNAscope platform including dual ISH-IHC staining (Ventana Discovery XT); Nanostring platform.

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Quantitative Proteomics, CMMC/CECAD

MS-based [proteomics](#) is routinely used to investigate the composition and dynamics of cellular organelles, protein complexes, and signaling pathways. Contemporary shotgun proteomics utilizes site-specific proteases to perform protein digestion and the resulting peptide mixture is then subjected to mass spectrometry. Modern high resolution mass spectrometers, such as quadrupole Orbitraps, consist of a selection quadrupole, a high-efficiency C-trap and higher-energy collisional dissociation (HCD) octopole collision cell that allows for a rapid and sensitive fragmentation of peptides.

Another challenge for proteomics is the identification of peptides with post-translational modifications (PTMs) from cells and tissues since biological relevant modifications are often of low abundance. To identify those PTMs by MS, several modification enrichment strategies were developed.

1. **Quantitative proteomics** (using LFQ, SILAC, and ITRAQ): protein quantification in cell culture and living animals with SILAC labeling, protein extraction, and protein/peptide separation.

2. **Protein-protein interaction studies**: Protein-protein interactions is based on the enrichment of bait proteins using a specific antibody analyzed by liquid chromatography tandem mass spectrometry (LC-MS/MS) and quantified by an intensity-based label-free quantification.

3. **PTM mapping - Enrichment of post-translational modifications**: For the enrichment of ubiquitination sites (ubiquitin remnants), tryptic peptides from cells/tissue will be immunoprecipitated with an ubiquitin remnant motif antibody and then analyzed by mass spectrometry.

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**Molecular imaging** allows the visualization of different physiological or pathophysiological processes at the molecular level with high resolution and extraordinary sensitivity. This detection requires the preparation of molecular probes that enable the non-invasive detection of small molecular alterations in preclinical models. The molecular imaging probes are injected into the animal model and interact specifically with its molecular target and specifically display the expression of, e.g. enzymes or receptor systems. A molecular imaging probe typically comprises a signal agent, a targeting moiety, and a linker connecting the targeting moiety and the signal agent. The signal agent usually produces signal for that subsequently allow imaging. A PET imaging probe requires a positron-emitting radionuclide as the label. The signal agent is a radionuclide produced at a cyclotron. These PET nuclides are then incorporated via labeling chemistry into biomolecules suitable for PET imaging. After tracer development, the novel imaging probes can be evaluated in preclinical settings. After successful biological evaluation, the probe is produced on a preparative scale using automation processes.

For the whole process, i.e. target identification, probe design, radiolabeling, preclinical evaluation, and automation, the following infrastructure is required and provided:

1. **Cyclotron**: Radionuclide production in cooperation with Forschungszentrum Jülich.
2. **Radiochemistry laboratories**: Radiochemical developments to prepare imaging agents.
3. **Small animal imaging facility**: Biological in vivo and in vitro evaluation of imaging probes.
4. **Hot-cells and automated synthesis modules**: For the production on a preparative scale, leaded-shielded hot cells are required that enable us to handle high radioactivity amounts.

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**Functional Genomics; Cologne Center for Genomics [CCG]**

Next generation sequencing (NGS) methods are currently revolutionizing the field of genome research. They enable researchers to decode DNA and RNA sequences at an unprecedented depth and level of detail. The **Cologne Center for Genomics** set up cutting-edge NGS technologies to assist all life scientists of the University of Cologne in their bio-medical research efforts.

1. **Genomics - Whole genome shotgun sequencing (WGS)**: Random fragments of a complete genome are sequenced using PCR-free library preparation.
2. **Transcriptomics - RNA-seq**: Reverse transcribed cDNA fragments from total RNA of any organism are sequenced.
3. **Epigenomics - ChIP-seq/RIP-seq**: DNA or RNA fragments extracted by chromatin immunoprecipitation are sequenced.

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