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BMFZ Core Labs Newsletter #02-2021

Dear Reader,

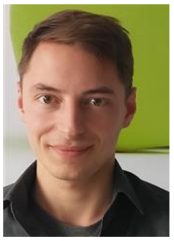
The GTL and MPL teams wish you and your colleagues and families a pleasent Advent season, Merry Christmas, a Happy New Year, and a relaxing break!

Please feel free to contact the Genomics and Transcriptomics Laboratory (GTL) for any questions regarding DNA or RNA analyses and the Molecular Proteomics Laboratory (MPL) for any protein-related questions. We look forward to supporting you and appreciate your feedback!

Yours,
The GTL and MPL Teams

Meet the Teams - New Members

Tassilo Wollenweber



Daniel Rickert

Katharina Schmitz

In June 2021, Tassilo Wollenweber joined the GTL Team as new NGS / PacBio expert

In July 2021, Daniel Rickert joined the GTL Team as new WGGC Bioinformatician

In October 2021, Katharina Schmitz joined the GTL Team as new WGGC Scientific Officer

Eva Bruns

Marc Driessen

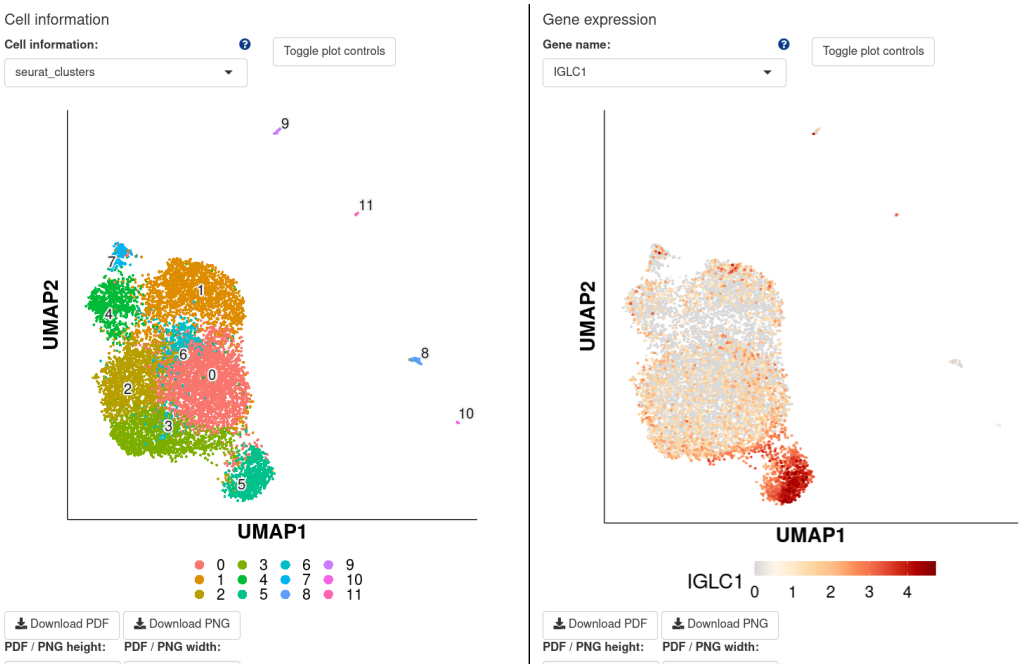
Stella Pauls

In May 2021, **Eva Bruns** joined the MPL team as new technical assistant

In June 2021, **Marc Driessen** joined the MPL team as new postdoc

In August 2021, **Stella Pauls** joined the MPL team as new postdoc

This Month's Featured Technologies



Shiny App

With increasing popularity of Single Cell RNA Sequencing the GTL Team was looking for a way to allow researches to explore their single cell data sets after analysis on their own in an easy and intuitive way without the need for any knowledge with command line tools and/or R.

In order to achieve this the GTL has set up a Virtual ShinyApp Server hosted at the ZIM. After data analysis has been performed at the GTL, the data is uploaded to this ShinyApp Server and can then be accessed by cooperation partners via web browser. The ShinyApp allows user to interactively explore the results of their analysis including cell information and the clustering itself. Furthermore it is possible to visualize the expression pattern of all genes, the distribution of continuous cell information using violin plots / box plots, the composition of different clusters / groups of cells using proportion plots and the expression of multiple genes using bubbleplots and heatmaps. All plots generated can also be exported and saved.

Contact **Tobias Lautwein** for more information >

Proteomics Goes Multiplexing

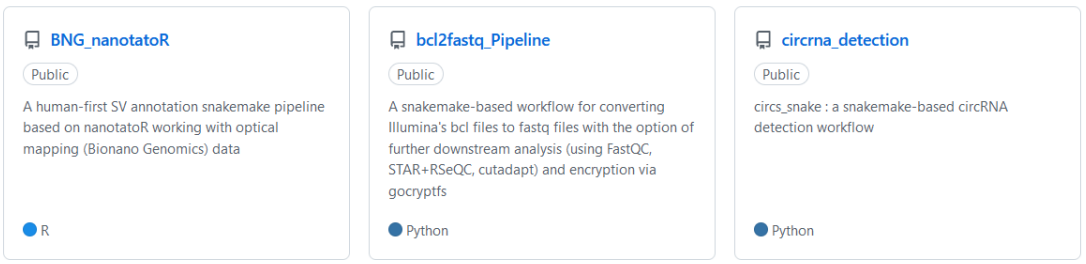
In recent years, new isotope tags have been introduced for quantitative mass spectrometry. Now multiplexing of up to 18 samples using tandem mass tags (TMT) is possible without compromising protein identification and quantification. This not only increases the sample throughput, but also improves the accuracy of protein quantification as well as the statistics due to almost no missing values. In combination with protein fractionation, e.g. by high pH fractionation, deep proteomic analyses with routinely more than 5,000 proteins are possible (for more information see Li et al., 2021). Currently, the MPL is adapting its service portfolio for multiplex analyses using TMT labeling.

Contact **Anja Stefanski** for more information >

Snakemake Pipelines

The WGGC Düsseldorf recently opened up first workflows and tools including demultiplexing with data quality checks, a collaborator-facing RNA data plotting R-shiny instance, Bionano SV annotation and more for everyone to participate, use and contribute: WGGC GitHub.

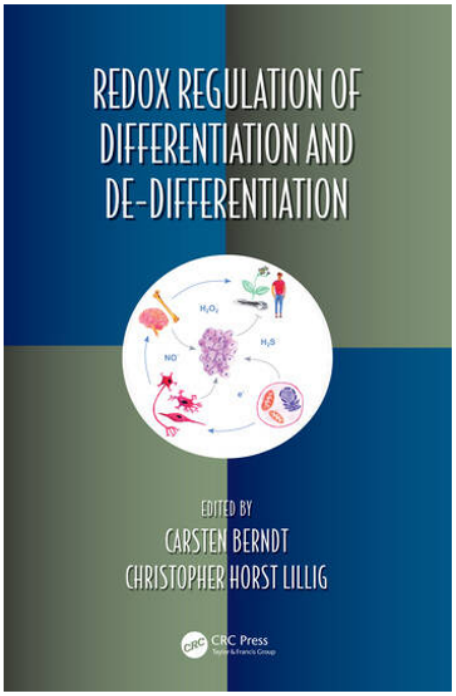
Human or mouse bulk total paired-end RNA sequencing projects that were sequenced on any Illumina machine are now eligible for additional circular RNA (circRNA) detection. We recently established an opensource snakemake workflow called circs [1] CircRNA -only projects (RNAseR digested total RNA) are also welcome!

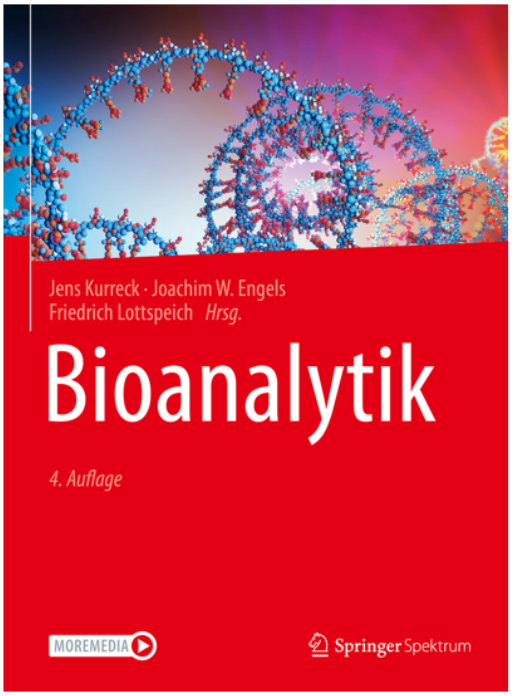


[1] Rickert, D., Bartl, J., Picard, D. et al. Circular RNA profiling distinguishes medulloblastoma groups and shows aberrant RMST overexpression in WNT medulloblastoma. Acta Neuropathol 141, 975–978 (2021). https://doi.org/10.1007/s00401-021-02306-2

Contact **Daniel Rickert** for more information >

Research Highlights





MPL members contributed to book publications

Members of the MPL recently contributed to two books. In **'Redox Regulation of Differentiation and De-differentiation'** edited by Carsten Berndt and Christopher Host Lillig (ISBN 978-0367895662), Gereon Poschmann contributed a chapter describing state of the art redox proteomics techniques, available tools and probes as well as important caveats in sample preparation and experimental design.

Furthermore, MPL members contributed an updated chapter about the analysis of protein post-translational modifications to the 4th edition of the German version **"Bioanalytik"** edited by Jens Kurreck, Joachim Engels and Friedrich Lottspeich (ISBN 978-3662617069). Bionalytik is the standard piece of literature giving an excellent overview of currently available methods available for the analysis of biomolecules. These includes also mass spectrometry and the analysis of post-translational protein modifications. In the current edition phosphorylation and oxidation of cysteine residues are exemplarily highlighted. 'Bioanalytik' will be available on 26. December 2021.

Contact **Gereon Poschmann** for more information >

More From The Labs

WEST GERMAN
GENOME CENTER

West German Genome Center Extension

The West German Genome Center (WGGC) initiative was funded for another two years until the end of 2023! The WGGC is a collaborative endeavour of universities Düsseldorf, Cologne and Bonn together with multipe other institutions from NRW and Saarland, dedicated to providing and developing cutting-edge genome and transcriptome sequencing techniques. The GTL is one of its three sequencing facilities and is specialized on long read sequencing techniques. The WGGC is one of four central DFG-funded German sequencing facilities.

Contact **Lena Peitzmann or Katharina Schmitz**
for more information >

Single-pot, solid-phase-enhanced sample-preparation (SP3)

The MPL is constantly working on improving sample preparation for mass spectrometry-based protein analysis. In this context, the SP3 method has proven to be a major advance in terms of sample throughput, ease of use and reproducibility (for more information see Hughes et al., 2014). Currently, the SP3 method is used in projects dealing with low sample volume (microdissected tissue samples, conditioned medium (<500 µl), etc.) and in combination with thermal proteome profiling. The MPL is pleased to provide its partners with access to this advanced sample preparation protocol.

Contact **Anja Stefanski** for more information >

Quality Assurance

According to the certification to DIN EN ISO 9001:2015 the GTL regularly performs external quality assessments. We use the EQA schemes of the following providers: European Molecular Genetics Quality Network (EMQN) for DNA Sequencing NGS (vGermline) and Referenzinstitut für Bioanalytik (RfB) for Sanger DNA-Sequencing. The quality assurance measures for long read sequencing with Oxford Nanopore are perfomed by an interlaboratory exchange of control samples.

Contact **Sibylle Scheuring** for more informaton >

Sample Information Sheet

We need a couple of information allowing us to perform the MS analysis in due. Please download the sample Information sheet and fill in all required information.

Please also note the GTL's updated sample requirements sheet!

Download the MPL sample information sheet >

Sequel IIe Upgrade

(high fidelity) output per SMRT Cell (8M). The low error rate of 0.1% combined with long fragments of 15 – 20 kb (HiFi) gives rise to several advanced workflows. From *de novo* genome assemblies to single nucleotide variant detection to amplicon sequencing and isoform detection: The PacBio platform covers a wide variety of applications. Furthermore, the upgraded “Sequel IIe” adds onboard computational power, enabling the consensus HiFi read generation from subreads without a mandatory connection to the HPC (high performance computing). In addition, the latest SMRT Link Software release v10.1 updates the Iso-Seq analysis application for multiplexed samples and incorporates an improved genome assembly pipeline.

Contact **Tassilo Wollenweber** for more information >

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...IT systems are maintained at the GTL and MPL labs!

Need anything?

Please contact us if you have any suggestions, feedback, questions or would like to work with us on a project!

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