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**Deciphering glomerular pathophysiology by proteome-
metabolome integration**

Our overall research goal is to understand the fundamental mechanisms of glomerular kidney disease. To this end, we use integration of mass-spectrometry based proteome and metabolome analyses in order to pinpoint the precise mechanisms determining glomerular fate and tissue heterogeneity. This is followed by functional studies in a hypothesis-driven manner combined with quantitative modelling. In order to gain a deep understanding of glomerular (patho-)physiology, we use a highly interdisciplinary approach that converges omics data with renal pathology, human genetics and clinical nephrology. Recent advances have allowed us to (1) understand molecular mechanisms of disease causing mutations, mechanical signaling and metabolic shifts (2) inhibit disease-triggering and propagating pathways by genetic or pharmacological interventions in animal models, and (3) develop novel tools and knowledge bases for stratification of renal biopsies of patients.

Time: Thursday 28th March, 17:15h
Location: Raum VKL 4.0.04
Institut für Physiologie
Universität Regensburg

The seminar is video transmitted to:
Pathologie Universitätsklinikum Erlangen,
Krankenhausstr. 8-10
Oberer Hörsaal, Raum A 2.150