

Information to be requested from all CA17104 participants:



Indicate your Working Group(s) in COST Action17104:	WG1
First Name:	Thomas
Surname:	Mohr
Department	
Primary Institution	ScienceConsult – DI Thomas KG
Address of Primary Institution	Enzianweg 10a, 2353 Guntramsdorf, Austria
Other institutions	Medical University of Vienna
Telephone:	+43223656793
e-mail:	Thomas.mohr@mohrkeg.co.at
Link to webpage with biography:	<i>https://www.mohrkeg.co.at</i>

Link to webpage with group description:	https://www.mohrkeg.co.at
------------------------------------------------	-------------------------------------------------------------------

Orcid ID or Scopus ID	https://orcid.org/0000-0002-1933-847X
Linkedin	https://www.linkedin.com/in/thomas-mohr-87aa757f/
Expertise relevant for this COST Action:	<ul style="list-style-type: none"> • Application of Omics analysis methods (microarray, RNASeq and proteomics) with a focus on network and pathway analysis methods such as co-expression network analysis (WGCNA), Gene Set Enrichment Analysis, Signaling Pathway Impact Analysis, Machine Learning, Detection of Hub Genes. • Statistical design and analysis of experiments • Statistical analysis (SPSS, GraphPad Prism, R, Bioconductor, FlowJo) • Extensive wetlab experience to bridge to molecular biologists: Cell isolation and culture techniques (implementation as well as practice): Isolation of endothelial cells, epithelial cells, fibroblasts, peripheral blood monocytes. 3D culture (matrigel embedding). High density culture (hollow fiber reactor). Co-culture techniques and protein-free cell culture, ELISA, FACS and Immunocytochemical and PCR techniques (implementation as well as practice), Confocal microscopy Functional assays (cell migration, formation of 3D structures, matrigel-based cell invasion assays)
Available facilities to conduct work, relevant for this COST Action:	<ul style="list-style-type: none"> • 3 Linux servers with a full computational biology software framework for R, python and OCTAVE (MATLAB) • Workflows for the analysis of array, RNASeq and proteomics data. • KNIME Workflow environment • GALAXY Workflow environment • A git repository to facilitate reproducible biocomputing • An alfresco document storage system to facilitate information exchange. • High end laptops (octocores, 16GB RAM, 500GB SSD)

	with a full computational biology software framework.
Materials/Methods that could be shared with other members of this COST Action:	Database research, -omics analysis workflows, workflow engines, servers, computing environment

NOTE: By submitting this form to the Grant Manager of CA17104, I agree that this information can be used within the scope of this COST Action (e.g. may be included on the webpage of CA17104).