Analysis of NextGen RNA-Seq data for expression profiling and protein-binding RNAs

10.-14.10.2016 | Regensburg | H 53

Monday | 10 Oct 2016 | 17.00 - 18.00 h
Stefan Kirsch, Frauenhofer ITEM: RNA-Seq analysis: Practical and experimental considerations

Tuesday | 11 Oct 2016 | 8.30 - 9.30 h
Steve Hoffmann, Universität Leipzig: Sequence alignment

Tuesday | 11 Oct 2016 | 9.30 - 10.30 h
Nicholas Strieder, Universität Regensburg: Quality assessment and trimming of NGS data

Wednesday | 12 Oct 2016 | 8.30 - 9.30 h
Simon Anders, FIMM Helsinki: Differential gene expression

Wednesday | 12 Oct 2016 | 9.30 - 10.30 h
Rainer Spang, Universität Regensburg: Pecularities of high-throughput data analysis

Thursday | 13 Oct 2016 | 8.30 - 9.30 h
Charlotte Soneson, University of Zurich: Transcript level analysis

Thursday | 13 Oct 2016 | 9.30 - 10.30 h
Grischa Toedt, EMBL Heidelberg: Alternative splicing

Friday | 14 Oct 2016 | 8.30 -9.30 h
Markus Hafner, NIAMS/NIH, Bethesda, USA: Interrogation of RNA binding protein targets and function using CLIP

Friday | 14 Oct 2016 | 9.30 - 10.30 h
Jan Medenbach, Universität Regensburg: Ribosomal profiling

MAIN ORGANISER | Graduate Research Academy RNA Biology | www.rnabiology-regensburg.de

RNA Biology | SFB 960 | DFG Deutsche Forschungsgemeinschaft | UR