**Wissenschaftliche Publikationen**

Zech M., Jech R., Boesch S., Škorvánek M., Weber S., Wagner M., Zhao C., Jochim A., Necpál J., **Dincer Y.**, et al. (2020): "Monogenic variants in dystonia: an exome-wide sequencing study." *Lancet Neurology* 19: 908–918

Singh S., Gupta A., Zech M., Sigafoos A. N., Clark K. J., **Dincer Y.**, et al. (2020): "De novo variants of NR4A2 are associated with neurodevelopmental disorder and epilepsy." *Genetics in Medicine* 22:1413–1417

**Dincer Y.**, et al. (2018): "Multiple Integration and Data Annotation Study (MIDAS): improving next-generation sequencing data analysis by genotype-phenotype correlations." *LaboratoriumsMedizin* 42(1-2): 1-8

Avril S., **Dincer Y.**, et al. (2017): "Increased PDGFR-beta and VEGFR-2 protein levels are associated with resistance to platinum-based chemotherapy and adverse outcome of ovarian cancer patients." *Oncotarget* 8(58): 97851- 97861

**Conference Talks**

Liesfeld B., **Dincer Y.** (2019): "Upscaling genetic testing services." AWS Transformation day, München, DE

**Dincer Y.**, et al. (2019): "Differentialdiagnose Cerebralparese: Die Rolle der Genetik." Kongress FocusCP rehaKIND, Fürstenfeldbruck, DE

**Dincer Y.**, et al. (2018): "Whole-Exome sequencing for children with dyskinetic movement disorder." Neurowoche, Berlin, DE

**Conference Posters**

Brumm R., Bounda-Ndinga E., **Dincer Y.**, et al. (2019): "A concept of Integrated Diagnostics to improve patient care." Annual Meeting of the German Society of Human Genetics, Weimar, DE

Leifels L., […], **Dincer Y.**, et al. (2019): "Semi-Automatic Classification of Genetic Variants: The MIDAS CLA Module." Annual Meeting of the German Society of Human Genetics, Weimar, DE

**Dincer Y.**, et al. (2018): "Whole-exome trio sequencing in 51 patients with intellectual disability/developmental delay." Annual Meeting of the American Society of Human Genetics, San Diego, California, USA

Becker D., […], **Dincer Y.**, et al. (2018): "CNV analysis of whole exome sequencing data in a clinical diagnostic setting." Annual Meeting of the American Society of Human Genetics, San Diego, California, USA

**Dincer Y.**, et al. (2018): "MIDAS Case Report: Trio-WES of a patient with developmental delay identified a pathogenic variant in PUF60 causing rare Verheij syndrome." Annual Meeting of the German Society of Human Genetics, Münster, DE

**Dincer Y.**, et al. (2017): "MIDAS Project Status Report: Trio Whole Exome Sequencing in Patients with Intellectual Disability." Annual Meeting of the American Society of Human Genetics, Orlando, Florida, USA

Becker D., Ziegler M., **Dincer Y.**, et al. (2017): "NGS-based CNV Calling in a Clinical Diagnostic Setting." Annual Meeting of the American Society of Human Genetics, Orlando, Florida, USA

**Dincer Y.**, et al. (2017): "MIDAS Case Report: Molecular Diagnostics of Helsmoortel-Van der Aa syndrome by Exome Trio Sequencing." Annual Meeting of the German Society of Human Genetics, Bochum, DE

Brumm R., **Dincer Y.**, et al. (2017): "MIDAS – Multiple Integration of Data Annotation Software." Annual Meeting of the German Society of Human Genetics, Bochum, DE

Schulz J., Wahl D., **Dincer Y.**, et al. (2017): "MIDAS Case Report: Identification of a de novo duplication causing rare Coffin-Siris syndrome." Annual Meeting of the German Society of Human Genetics, Bochum, DE

Ziegler M., **Dincer Y.**, et al. (2016): "Next-generation sequencing (NGS) vs. Sanger sequencing: Defining quality parameters, reliability scores and thresholds to exclude false positive variants in a diagnostic setting." Annual Meeting of the American Society of Human Genetics, Vancouver, CA