Max KÃ¤ller

List of Publications by Year
in descending order

21 papers	5,057 citations	687363 13 h-index	713466 21 g-index
21 all docs	21 docs citations	21 times ranked	10499 citing authors

#	Article	IF	Citations
1	¹⁸ F-Fluorodeoxyglucose-Positron Emission Tomography Imaging Detects Response to Therapeutic Intervention and Plaque Vulnerability in a Murine Model of Advanced Atherosclerotic Diseaseâ€"Brief Report. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 2821-2828.	2.4	10
2	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. F1000Research, 2020, 9, 63.	1.6	21
3	Chromosomal genome assembly of the ethanol production strain CBS 11270 indicates a highly dynamic genome structure in the yeast species Brettanomyces bruxellensis. PLoS ONE, 2019, 14, e0215077.	2.5	8
4	Comprehensive structural variation genome map of individuals carrying complex chromosomal rearrangements. PLoS Genetics, 2019, 15, e1007858.	3.5	36
5	High throughput barcoding method for genome-scale phasing. Scientific Reports, 2019, 9, 18116.	3.3	13
6	Replicative and non-replicative mechanisms in the formation of clustered CNVs are indicated by whole genome characterization. PLoS Genetics, 2018, 14, e1007780.	3.5	28
7	Stationary and portable sequencing-based approaches for tracing wastewater contamination in urban stormwater systems. Scientific Reports, 2018, 8, 11907.	3.3	24
8	Droplet Barcode Sequencing for targeted linked-read haplotyping of single DNA molecules. Nucleic Acids Research, 2017, 45, e125-e125.	14.5	11
9	Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. Archives of Toxicology, 2017, 91, 2067-2078.	4.2	26
10	Whole-Genome Sequencing of Cytogenetically Balanced Chromosome Translocations Identifies Potentially Pathological Gene Disruptions and Highlights the Importance of Microhomology in the Mechanism of Formation. Human Mutation, 2017, 38, 180-192.	2.5	58
11	Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. Nucleic Acids Research, 2016, 44, 6756-6769.	14.5	15
12	MultiQC: summarize analysis results for multiple tools and samples in a single report. Bioinformatics, 2016, 32, 3047-3048.	4.1	4,633
13	T-cell receptorâ€"HLA-DRB1 associations suggest specific antigens in pulmonary sarcoidosis. European Respiratory Journal, 2016, 47, 898-909.	6.7	65
14	Cluster Flow: A user-friendly bioinformatics workflow tool. F1000Research, 2016, 5, 2824.	1.6	18
15	De novo assembly of Dekkera bruxellensis: a multi technology approach using short and long-read sequencing and optical mapping. GigaScience, 2015, 4, 56.	6.4	26
16	Assessment of Whole Genome Amplification for Sequence Capture and Massively Parallel Sequencing. PLoS ONE, 2014, 9, e84785.	2.5	10
17	Arrayed identification of DNA signatures. Expert Review of Molecular Diagnostics, 2007, 7, 65-76.	3.1	25
18	Comparison of PrASE and Pyrosequencing for SNP Genotyping. BMC Genomics, 2006, 7, 291.	2.8	5

#	Article	IF	Citations
19	Tag-array based HPV genotyping by competitive hybridization and extension. Journal of Virological Methods, 2005, 129, 102-112.	2.1	6
20	Detection of MC1R Polymorphisms with Protease-Mediated Allele-Specific Extension as an Alternative to Direct Sequencing. Clinical Chemistry, 2005, 51, 2388-2391.	3.2	6
21	Microarray-based AMASE as a novel approach for mutation detection. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2004, 554, 77-88.	1.0	13