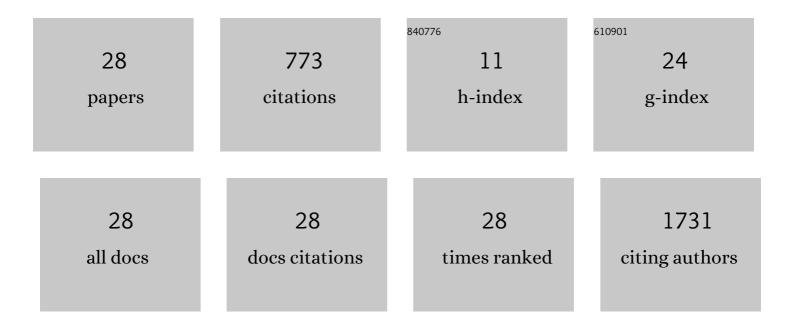
## Florian Battke

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/488840/publications.pdf Version: 2024-02-01



FLODIAN RATTE

#	Article	IF	CITATIONS
1	Biomarkers Associated with Immune-Related Adverse Events under Checkpoint Inhibitors in Metastatic Melanoma. Cancers, 2022, 14, 302.	3.7	15
2	Trio exome sequencing is highly relevant in prenatal diagnostics. Prenatal Diagnosis, 2022, 42, 845-851.	2.3	18
3	The question of WGS's clinical utility remains unanswered. European Journal of Human Genetics, 2021, 29, 722-723.	2.8	7
4	Controlling my genome with my smartphone: first clinical experiences of the PROMISE system. Clinical Research in Cardiology, 2021, , 1.	3.3	3
5	Copy number variation profiling in pharmacogenes using panel-based exome resequencing and correlation to human liver expression. Human Genetics, 2020, 139, 137-149.	3.8	9
6	Are Pathogenic Germline Variants in Metastatic Melanoma Associated with Resistance to Combined Immunotherapy?. Cancers, 2020, 12, 1101.	3.7	9
7	<p>Circulating Tumor DNA Correlates with Outcome in Metastatic Melanoma Treated by BRAF and MEK Inhibitors – Results of a Prospective Biomarker Study</p> . OncoTargets and Therapy, 2020, Volume 13, 5017-5032.	2.0	9
8	Interference With Complex IV as a Model of Age-Related Decline in Synaptic Connectivity. Frontiers in Molecular Neuroscience, 2020, 13, 43.	2.9	11
9	Sequencing for an interdisciplinary molecular tumor board in patients with advanced breast cancer: experiences from a case series. Oncotarget, 2020, 11, 3279-3285.	1.8	2
10	Tumor mutation burden and circulating tumor DNA in combined CTLA-4 and PD-1 antibody therapy in metastatic melanoma – results of a prospective biomarker study. , 2019, 7, 180.		137
11	Targeted gene sequencing in 6994 individuals with neurodevelopmental disorder with epilepsy. Genetics in Medicine, 2019, 21, 2496-2503.	2.4	45
12	Molecular tumor analysis and liquid biopsy: a feasibility investigation analyzing circulating tumor DNA in patients with central nervous system lymphomas. BMC Cancer, 2019, 19, 192.	2.6	32
13	A New Panel-Based Next-Generation Sequencing Method for ADME Genes Reveals Novel Associations of Common and Rare Variants With Expression in a Human Liver Cohort. Frontiers in Genetics, 2019, 10, 7.	2.3	37
14	My Genome Belongs to Me: Controlling Third Party Computation on Genomic Data. Proceedings on Privacy Enhancing Technologies, 2019, 2019, 108-132.	2.8	6
15	Rare Variants in Neurodegeneration Associated Genes Revealed by Targeted Panel Sequencing in a German ALS Cohort. Frontiers in Molecular Neuroscience, 2016, 9, 92.	2.9	41
16	The Maternal Transcriptome of the Crustacean Parhyale hawaiensis Is Inherited Asymmetrically to Invariant Cell Lineages of the Ectoderm and Mesoderm. PLoS ONE, 2013, 8, e56049.	2.5	23
17	REVEALvisual eQTL analytics. Bioinformatics, 2012, 28, i542-i548.	4.1	0
18	iHAT: interactive Hierarchical Aggregation Table for Genetic Association Data. BMC Bioinformatics, 2012, 13, S2.	2.6	16

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#	Article	IF	CITATIONS
19	An eQTL biological data visualization challenge and approaches from the visualization community. BMC Bioinformatics, 2012, 13, S8.	2.6	9
20	iHAT: Interactive hierarchical aggregation table. , 2011, , .		2
21	TIALA — Time series alignment analysis. , 2011, , .		4
22	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	2.5	17
23	The PII protein GlnK is a pleiotropic regulator for morphological differentiation and secondary metabolism in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2011, 92, 1219-1236.	3.6	34
24	<i>GaggleBridge</i> : collaborative data analysis. Bioinformatics, 2011, 27, 2612-2613.	4.1	4
25	Mayday - integrative analytics for expression data. BMC Bioinformatics, 2010, 11, 121.	2.6	102
26	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 10.	2.8	171
27	Integrative systems biology visualization with MAYDAY. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	9
28	Post-Hybridization Quality Measures for Oligos in Genome-Wide Microarray Experiments. Lecture Notes in Computer Science, 2008, , 64-75.	1.3	1