Florian Battke

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/488840/publications.pdf

Version: 2024-02-01

28 papers 773 citations

840776 11 h-index 610901 24 g-index

28 all docs 28 docs citations

28 times ranked

1731 citing authors

#	Article	IF	CITATIONS
1	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11 , 10 .	2.8	171
2	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
3	Mayday - integrative analytics for expression data. BMC Bioinformatics, 2010, 11, 121.	2.6	102
4	Targeted gene sequencing in 6994 individuals with neurodevelopmental disorder with epilepsy. Genetics in Medicine, 2019, 21, 2496-2503.	2.4	45
5	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
6	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
7	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
8	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
9	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
10	Trio exome sequencing is highly relevant in prenatal diagnostics. Prenatal Diagnosis, 2022, 42, 845-851.	2.3	18
11	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	2.5	17
12	iHAT: interactive Hierarchical Aggregation Table for Genetic Association Data. BMC Bioinformatics, 2012, 13, S2.	2.6	16
13	Biomarkers Associated with Immune-Related Adverse Events under Checkpoint Inhibitors in Metastatic Melanoma. Cancers, 2022, 14, 302.	3.7	15
14	Interference With Complex IV as a Model of Age-Related Decline in Synaptic Connectivity. Frontiers in Molecular Neuroscience, 2020, 13, 43.	2.9	11
15	An eQTL biological data visualization challenge and approaches from the visualization community. BMC Bioinformatics, 2012, 13, S8.	2.6	9
16	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
17	Are Pathogenic Germline Variants in Metastatic Melanoma Associated with Resistance to Combined Immunotherapy?. Cancers, 2020, 12, 1101.	3.7	9
18	<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

#	Article	IF	Citations
19	Integrative systems biology visualization with MAYDAY. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	9
20	The question of WGS's clinical utility remains unanswered. European Journal of Human Genetics, 2021, 29, 722-723.	2.8	7
21	My Genome Belongs to Me: Controlling Third Party Computation on Genomic Data. Proceedings on Privacy Enhancing Technologies, 2019, 2019, 108-132.	2.8	6
22	TIALA & amp; #x2014; Time series alignment analysis., 2011,,.		4
23	<i>GaggleBridge</i> : collaborative data analysis. Bioinformatics, 2011, 27, 2612-2613.	4.1	4
24	Controlling my genome with my smartphone: first clinical experiences of the PROMISE system. Clinical Research in Cardiology, 2021, , 1.	3.3	3
25	iHAT: Interactive hierarchical aggregation table. , 2011, , .		2
26	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
27	Post-Hybridization Quality Measures for Oligos in Genome-Wide Microarray Experiments. Lecture Notes in Computer Science, 2008, , 64-75.	1.3	1
28	REVEALvisual eQTL analytics. Bioinformatics, 2012, 28, i542-i548.	4.1	0