Max Robinson

List of Publications by Year in descending order

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840776 794594 19 706 11 19 citations h-index g-index papers 31 31 31 1059 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Quality control of large genome datasets. Human Genetics and Genomics Advances, 2022, 3, 100123.	1.7	1
2	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. Nature Metabolism, 2021, 3, 274-286.	11.9	278
3	Modulating innate immune activation states impacts the efficacy of specific $\hat{Al^2}$ immunotherapy. Molecular Neurodegeneration, 2021, 16, 32.	10.8	4
4	The geometry of clinical labs and wellness states from deeply phenotyped humans. Nature Communications, 2021, 12, 3578.	12.8	19
5	Microglia show differential transcriptomic response to ${\hat {\sf Al}^2}$ peptide aggregates ex vivo and in vivo. Life Science Alliance, 2021, 4, e202101108.	2.8	17
6	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. Scientific Reports, 2019, 9, 9807.	3.3	10
7	NormExpression: An R Package to Normalize Gene Expression Data Using Evaluated Methods. Frontiers in Genetics, 2019, 10, 400.	2.3	9
8	Sex, obesity, diabetes, and exposure to particulate matter among patients with severe asthma: Scientific insights from a comparative analysis of open clinical data sources during a five-day hackathon. Journal of Biomedical Informatics, 2019, 100, 103325.	4.3	22
9	O3â€03â€01: MECHANISTIC AND DIRECTIONAL TRANSCRIPTIONAL REGULATORY NETWORKS IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P1014.	0.8	0
10	Genotype Fingerprints Enable Fast and Private Comparison of Genetic Testing Results for Research and Direct-to-Consumer Applications. Genes, 2018, 9, 481.	2.4	3
11	Novel metrics for quantifying bacterial genome composition skews. BMC Genomics, 2018, 19, 528.	2.8	1
12	Ultrafast Comparison of Personal Genomes via Precomputed Genome Fingerprints. Frontiers in Genetics, 2017, 8, 136.	2.3	13
13	Genomic architecture of inflammatory bowel disease in five families with multiple affected individuals. Human Genome Variation, 2016, 3, 15060.	0.7	14
14	Identification of copy number variants in whole-genome data using Reference Coverage Profiles. Frontiers in Genetics, 2015, 6, 45.	2.3	18
15	Systematic measurement of transcription factor-DNA interactions by targeted mass spectrometry identifies candidate gene regulatory proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3645-3650.	7.1	31
16	Optimal Scaling of Digital Transcriptomes. PLoS ONE, 2013, 8, e77885.	2.5	44
17	Index-ion Triggered MS2 Ion Quantification: A Novel Proteomics Approach for Reproducible Detection and Quantification of Targeted Proteins in Complex Mixtures. Molecular and Cellular Proteomics, 2011, 10, M110.005611.	3.8	26
18	A New Method for Straightening DNA Molecules for Optical Restriction Mapping. Nucleic Acids Research, 1997, 25, 1064-1070.	14.5	93

#	Article	IF	CITATIONS
19	Sensitivity and Selectivity in Protein Similarity Searches: A Comparison of Smith–Waterman in Hardware to BLAST and FASTA. Genomics, 1996, 38, 179-191.	2.9	79