

Jeremy Leipzig

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

34
papers

3,783
citations

27
h-index

37
g-index

37
ext. papers

4,295
ext. citations

11.1
avg, IF

5.12
L-index

#	Paper	IF	Citations
34	The role of metadata in reproducible computational research. <i>Patterns</i> , 2021 , 2, 100322	5.1	12
33	Biodiversity Image Quality Metadata Augments Convolutional Neural Network Classification of Fish Species. <i>Communications in Computer and Information Science</i> , 2021 , 3-12	0.3	1
32	A comparison of survival analysis methods for cancer gene expression RNA-Sequencing data. <i>Cancer Genetics</i> , 2019 , 235-236, 1-12	2.3	7
31	Computational Pipelines and Workflows in Bioinformatics 2019 , 1151-1162		
30	Mitochondrial DNA Variation Dictates Expressivity and Progression of Nuclear DNA Mutations Causing Cardiomyopathy. <i>Cell Metabolism</i> , 2019 , 29, 78-90.e5	24.6	35
29	Mitochondrial energy deficiency leads to hyperproliferation of skeletal muscle mitochondria and enhanced insulin sensitivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2705-2710	11.5	52
28	Association Between Mitochondrial DNA Haplogroup Variation and Autism Spectrum Disorders. <i>JAMA Psychiatry</i> , 2017 , 74, 1161-1168	14.5	33
27	Predicting the pathogenicity of novel variants in mitochondrial tRNA with MitoTIP. <i>PLoS Computational Biology</i> , 2017 , 13, e1005867	5	51
26	A review of bioinformatic pipeline frameworks. <i>Briefings in Bioinformatics</i> , 2017 , 18, 530-536	13.4	135
25	MSeqDR: A Centralized Knowledge Repository and Bioinformatics Web Resource to Facilitate Genomic Investigations in Mitochondrial Disease. <i>Human Mutation</i> , 2016 , 37, 540-548	4.7	34
24	Phy-Mer: a novel alignment-free and reference-independent mitochondrial haplogroup classifier. <i>Bioinformatics</i> , 2015 , 31, 1310-2	7.2	41
23	Mitochondrial Disease Sequence Data Resource (MSeqDR): a global grass-roots consortium to facilitate deposition, curation, annotation, and integrated analysis of genomic data for the mitochondrial disease clinical and research communities. <i>Molecular Genetics and Metabolism</i> , 2015 , 114, 388-96	3.7	56
22	Peripheral Blood Mitochondrial DNA as a Biomarker of Cerebral Mitochondrial Dysfunction following Traumatic Brain Injury in a Porcine Model. <i>PLoS ONE</i> , 2015 , 10, e0130927	3.7	30
21	Increased frequency of de novo copy number variants in congenital heart disease by integrative analysis of single nucleotide polymorphism array and exome sequence data. <i>Circulation Research</i> , 2014 , 115, 884-896	15.7	158
20	A mitochondrial bioenergetic hypothesis for autism spectrum disorder (570.3). <i>FASEB Journal</i> , 2014 , 28, 570.3	0.9	
19	Efficient digest of high-throughput sequencing data in a reproducible report. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 11, S3	3.6	5
18	De novo mutations in histone-modifying genes in congenital heart disease. <i>Nature</i> , 2013 , 498, 220-3	50.4	591

17	A next-generation sequencing approach to study the transcriptomic changes during the differentiation of physarum at the single-cell level. <i>Gene Regulation and Systems Biology</i> , 2012 , 6, 127-37 ²		7
16	Genome-wide analysis of interferon regulatory factor I binding in primary human monocytes. <i>Gene</i> , 2011 , 487, 21-8	3.8	36
15	HTLV-1 integration into transcriptionally active genomic regions is associated with proviral expression and with HAM/TSP. <i>PLoS Pathogens</i> , 2008 , 4, e1000027	7.6	76
14	DNA bar coding and pyrosequencing to analyze adverse events in therapeutic gene transfer. <i>Nucleic Acids Research</i> , 2008 , 36, e49	20.1	87
13	DNA bar coding and pyrosequencing to identify rare HIV drug resistance mutations. <i>Nucleic Acids Research</i> , 2007 , 35, e91	20.1	187
12	HIV integration site selection: analysis by massively parallel pyrosequencing reveals association with epigenetic modifications. <i>Genome Research</i> , 2007 , 17, 1186-94	9.7	337
11	Retroviral DNA integration: viral and cellular determinants of target-site selection. <i>PLoS Pathogens</i> , 2006 , 2, e60	7.6	273
10	Selection of target sites for mobile DNA integration in the human genome. <i>PLoS Computational Biology</i> , 2006 , 2, e157	5	169
9	HIV integration site selection: targeting in macrophages and the effects of different routes of viral entry. <i>Molecular Therapy</i> , 2006 , 14, 218-25	11.7	73
8	Integration site selection by HIV-based vectors in dividing and growth-arrested IMR-90 lung fibroblasts. <i>Molecular Therapy</i> , 2006 , 13, 366-73	11.7	53
7	A role for LEDGF/p75 in targeting HIV DNA integration. <i>Nature Medicine</i> , 2005 , 11, 1287-9	50.5	489
6	Genome-wide analysis of retroviral DNA integration. <i>Nature Reviews Microbiology</i> , 2005 , 3, 848-58	22.2	335
5	Integration targeting by avian sarcoma-leukosis virus and human immunodeficiency virus in the chicken genome. <i>Journal of Virology</i> , 2005 , 79, 12035-44	6.6	73
4	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004 , 32, 3977-83	20.1	61
3	Effects of ketamine, MK-801, and amphetamine on regional brain 2-deoxyglucose uptake in freely moving mice. <i>Neuropsychopharmacology</i> , 2000 , 22, 400-12	8.7	81
2	Comparison of brain metabolic activity patterns induced by ketamine, MK-801 and amphetamine in rats: support for NMDA receptor involvement in responses to subanesthetic dose of ketamine. <i>Brain Research</i> , 1999 , 843, 171-83	3.7	98
1	Differential effects of clozapine and haloperidol on ketamine-induced brain metabolic activation. <i>Brain Research</i> , 1998 , 812, 65-75	3.7	107