## Jeremy Leipzig

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1064771/publications.pdf Version: 2024-02-01



IEDEMV | EIDZIC

#	Article	IF	CITATIONS
1	De novo mutations in histone-modifying genes in congenital heart disease. Nature, 2013, 498, 220-223.	13.7	798
2	A role for LEDGF/p75 in targeting HIV DNA integration. Nature Medicine, 2005, 11, 1287-1289.	15.2	583
3	HIV integration site selection: Analysis by massively parallel pyrosequencing reveals association with epigenetic modifications. Genome Research, 2007, 17, 1186-1194.	2.4	396
4	Genome-wide analysis of retroviral DNA integration. Nature Reviews Microbiology, 2005, 3, 848-858.	13.6	390
5	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. PLoS Pathogens, 2006, 2, e60.	2.1	310
6	Increased Frequency of De Novo Copy Number Variants in Congenital Heart Disease by Integrative Analysis of Single Nucleotide Polymorphism Array and Exome Sequence Data. Circulation Research, 2014, 115, 884-896.	2.0	229
7	DNA bar coding and pyrosequencing to identify rare HIV drug resistance mutations. Nucleic Acids Research, 2007, 35, e91.	6.5	196
8	A review of bioinformatic pipeline frameworks. Briefings in Bioinformatics, 2017, 18, bbw020.	3.2	193
9	Selection of Target Sites for Mobile DNA Integration in the Human Genome. PLoS Computational Biology, 2006, 2, e157.	1.5	191
10	Differential effects of clozapine and haloperidol on ketamine-induced brain metabolic activation. Brain Research, 1998, 812, 65-75.	1.1	112
11	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. Brain Research, 1999, 843, 171-183.	1.1	101
12	Predicting the pathogenicity of novel variants in mitochondrial tRNA with MitoTIP. PLoS Computational Biology, 2017, 13, e1005867.	1.5	93
13	HTLV-1 Integration into Transcriptionally Active Genomic Regions Is Associated with Proviral Expression and with HAM/TSP. PLoS Pathogens, 2008, 4, e1000027.	2.1	91
14	DNA bar coding and pyrosequencing to analyze adverse events in therapeutic gene transfer. Nucleic Acids Research, 2008, 36, e49-e49.	6.5	91
15	Effects of Ketamine, MK-801, and Amphetamine on Regional Brain 2-Deoxyglucose Uptake in Freely Moving Mice. Neuropsychopharmacology, 2000, 22, 400-412.	2.8	89
16	HIV Integration Site Selection: Targeting in Macrophages and the Effects of Different Routes of Viral Entry. Molecular Therapy, 2006, 14, 218-225.	3.7	83
17	Integration Targeting by Avian Sarcoma-Leukosis Virus and Human Immunodeficiency Virus in the Chicken Genome. Journal of Virology, 2005, 79, 12035-12044.	1.5	80
18	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. Nucleic Acids Research, 2004, 32, 3977-3983.	6.5	77

JEREMY LEIPZIG

#	Article	IF	CITATIONS
19	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. Molecular Genetics and Metabolism, 2015, 114, 388-396.	0.5	76
20	Mitochondrial energy deficiency leads to hyperproliferation of skeletal muscle mitochondria and enhanced insulin sensitivity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2705-2710.	3.3	73
21	Integration Site Selection by HIV-Based Vectors in Dividing and Growth-Arrested IMR-90 Lung Fibroblasts. Molecular Therapy, 2006, 13, 366-373.	3.7	57
22	Association Between Mitochondrial DNA Haplogroup Variation and Autism Spectrum Disorders. JAMA Psychiatry, 2017, 74, 1161.	6.0	57
23	Phy-Mer: a novel alignment-free and reference-independent mitochondrial haplogroup classifier. Bioinformatics, 2015, 31, 1310-1312.	1.8	55
24	Mitochondrial DNA Variation Dictates Expressivity and Progression of Nuclear DNA Mutations Causing Cardiomyopathy. Cell Metabolism, 2019, 29, 78-90.e5.	7.2	53
25	The role of metadata in reproducible computational research. Patterns, 2021, 2, 100322.	3.1	45
26	MSeqDR: A Centralized Knowledge Repository and Bioinformatics Web Resource to Facilitate Genomic Investigations in Mitochondrial Disease. Human Mutation, 2016, 37, 540-548.	1.1	42
27	Genome-wide analysis of interferon regulatory factor I binding in primary human monocytes. Gene, 2011, 487, 21-28.	1.0	41
28	Peripheral Blood Mitochondrial DNA as a Biomarker of Cerebral Mitochondrial Dysfunction following Traumatic Brain Injury in a Porcine Model. PLoS ONE, 2015, 10, e0130927.	1.1	38
29	A comparison of survival analysis methods for cancer gene expression RNA-Sequencing data. Cancer Genetics, 2019, 235-236, 1-12.	0.2	11
30	A Next-Generation Sequencing Approach to Study the Transcriptomic Changes during the Differentiation of Physarum at the Single-Cell Level. Gene Regulation and Systems Biology, 2012, 6, GRSB.S10224.	2.3	7
31	Biodiversity Image Quality Metadata Augments Convolutional Neural Network Classification of Fish Species. Communications in Computer and Information Science, 2021, , 3-12.	0.4	7
32	Efficient digest of high-throughput sequencing data in a reproducible report. BMC Bioinformatics, 2013, 14, S3.	1.2	6
33	Bamchop: A bioinformatics utility to summarize and visualize exome and other types of targeted resequencing data. , 2012, , .		0
34	Computational Pipelines and Workflows in Bioinformatics. , 2019, , 1151-1162.		0
35	A mitochondrial bioenergetic hypothesis for autism spectrum disorder (570.3). FASEB Journal, 2014, 28, 570.3.	0.2	0