Jeremy Leipzig

List of Publications by Citations

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	De novo mutations in histone-modifying genes in congenital heart disease. *Nature*, **2013**, 498, 220-3	50.4	591
33	A role for LEDGF/p75 in targeting HIV DNA integration. *Nature Medicine*, **2005**, 11, 1287-9	50.5	489
32	HIV integration site selection: analysis by massively parallel pyrosequencing reveals association with epigenetic modifications. *Genome Research*, **2007**, 17, 1186-94	9.7	337
31	Genome-wide analysis of retroviral DNA integration. *Nature Reviews Microbiology*, **2005**, 3, 848-58	22.2	335
30	Retroviral DNA integration: viral and cellular determinants of target-site selection. *PLoS Pathogens*, **2006**, 2, e60	7.6	273
29	DNA bar coding and pyrosequencing to identify rare HIV drug resistance mutations. *Nucleic Acids Research*, **2007**, 35, e91	20.1	187
28	Selection of target sites for mobile DNA integration in the human genome. *PLoS Computational Biology*, **2006**, 2, e157	5	169
27	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	15.7	158
26	A review of bioinformatic pipeline frameworks. *Briefings in Bioinformatics*, **2017**, 18, 530-536	13.4	135
25	Differential effects of clozapine and haloperidol on ketamine-induced brain metabolic activation. *Brain Research*, **1998**, 812, 65-75	3.7	107
24	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, 171-83	3.7	98
23	DNA bar coding and pyrosequencing to analyze adverse events in therapeutic gene transfer. *Nucleic Acids Research*, **2008**, 36, e49	20.1	87
22	Effects of ketamine, MK-801, and amphetamine on regional brain 2-deoxyglucose uptake in freely moving mice. *Neuropsychopharmacology*, **2000**, 22, 400-12	8.7	81
21	HTLV-1 integration into transcriptionally active genomic regions is associated with proviral expression and with HAM/TSP. *PLoS Pathogens*, **2008**, 4, e1000027	7.6	76
20	HIV integration site selection: targeting in macrophages and the effects of different routes of viral entry. *Molecular Therapy*, **2006**, 14, 218-25	11.7	73
19	Integration targeting by avian sarcoma-leukosis virus and human immunodeficiency virus in the chicken genome. *Journal of Virology*, **2005**, 79, 12035-44	6.6	73
18	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. *Nucleic Acids Research*, **2004**, 32, 3977-83	20.1	61

List of Publications

17	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, 388-96	3.7	56
16	Integration site selection by HIV-based vectors in dividing and growth-arrested IMR-90 lung fibroblasts. *Molecular Therapy*, **2006**, 13, 366-73	11.7	53
15	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	11.5	52
14	Predicting the pathogenicity of novel variants in mitochondrial tRNA with MitoTIP. *PLoS Computational Biology*, **2017**, 13, e1005867	5	51
13	Phy-Mer: a novel alignment-free and reference-independent mitochondrial haplogroup classifier. *Bioinformatics*, **2015**, 31, 1310-2	7.2	41
12	Genome-wide analysis of interferon regulatory factor I binding in primary human monocytes. *Gene*, **2011**, 487, 21-8	3.8	36
11	Mitochondrial DNA Variation Dictates Expressivity and Progression of Nuclear DNA Mutations Causing Cardiomyopathy. *Cell Metabolism*, **2019**, 29, 78-90.e5	24.6	35
10	MSeqDR: A Centralized Knowledge Repository and Bioinformatics Web Resource to Facilitate Genomic Investigations in Mitochondrial Disease. *Human Mutation*, **2016**, 37, 540-548	4.7	34
9	Association Between Mitochondrial DNA Haplogroup Variation and Autism Spectrum Disorders. *JAMA Psychiatry*, **2017**, 74, 1161-1168	14.5	33
8	Peripheral Blood Mitochondrial DNA as a Biomarker of Cerebral Mitochondrial Dysfunction following Traumatic Brain Injury in a Porcine Model. *PLoS ONE*, **2015**, 10, e0130927	3.7	30
7	The role of metadata in reproducible computational research. *Patterns*, **2021**, 2, 100322	5.1	12
6	A comparison of survival analysis methods for cancer gene expression RNA-Sequencing data. *Cancer Genetics*, **2019**, 235-236, 1-12	2.3	7
5	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, 127-37	2	7
4	Efficient digest of high-throughput sequencing data in a reproducible report. *BMC Bioinformatics*, **2013**, 14 Suppl 11, S3	3.6	5
3	Biodiversity Image Quality Metadata Augments Convolutional Neural Network Classification of Fish Species. *Communications in Computer and Information Science*, **2021**, 3-12	0.3	1
2	Computational Pipelines and Workflows in Bioinformatics **2019**, 1151-1162		
1	A mitochondrial bioenergetic hypothesis for autism spectrum disorder (570.3). *FASEB Journal*, **2014**, 28, 570.3	0.9	