Larry N Singh

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3582372/publications.pdf

Version: 2024-02-01

44 papers

2,708 citations

331538 21 h-index 289141 40 g-index

46 all docs 46 docs citations

46 times ranked

5115 citing authors

#	Article	IF	CITATIONS
1	U1 snRNP protects pre-mRNAs from premature cleavage and polyadenylation. Nature, 2010, 468, 664-668.	13.7	528
2	U1 snRNP Determines mRNA Length and Regulates Isoform Expression. Cell, 2012, 150, 53-64.	13.5	392
3	Secondary Variants in Individuals Undergoing Exome Sequencing: Screening of 572 Individuals Identifies High-Penetrance Mutations in Cancer-Susceptibility Genes. American Journal of Human Genetics, 2012, 91, 97-108.	2.6	190
4	Dysregulation of synaptogenesis genes antecedes motor neuron pathology in spinal muscular atrophy. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19348-19353.	3.3	161
5	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. Cell, 2020, 183, 1185-1201.e20.	13.5	161
6	Regulation of nuclear epigenome by mitochondrial DNA heteroplasmy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16028-16035.	3.3	108
7	Host mitochondria influence gut microbiome diversity: A role for ROS. Science Signaling, 2019, 12, .	1.6	106
8	The landscape of transcription errors in eukaryotic cells. Science Advances, 2017, 3, e1701484.	4.7	102
9	Mitochondrial DNA variation and cancer. Nature Reviews Cancer, 2021, 21, 431-445.	12.8	98
10	Specifications of the ACMG/AMP standards and guidelines for mitochondrial DNA variant interpretation. Human Mutation, 2020, 41, 2028-2057.	1.1	84
11	CTCF binding site classes exhibit distinct evolutionary, genomic, epigenomic and transcriptomic features. Genome Biology, 2009, 10, R131.	13.9	72
12	Interpreting Secondary Cardiac Disease Variants in an Exome Cohort. Circulation: Cardiovascular Genetics, 2013, 6, 337-346.	5.1	70
13	Individualized Iterative Phenotyping for Genome-wide Analysis of Loss-of-Function Mutations. American Journal of Human Genetics, 2015, 96, 913-925.	2.6	66
14	Association Between Mitochondrial DNA Haplogroup Variation and Autism Spectrum Disorders. JAMA Psychiatry, 2017, 74, 1161.	6.0	57
15	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	3.1	57
16	Role of miR-2392 in driving SARS-CoV-2 infection. Cell Reports, 2021, 37, 109839.	2.9	52
17	Assessing the reproducibility of exome copy number variations predictions. Genome Medicine, 2016, 8, 82.	3.6	44
18	Functional Diversification of Paralogous Transcription Factors via Divergence in DNA Binding Site Motif and in Expression. PLoS ONE, 2008, 3, e2345.	1.1	31

#	Article	IF	Citations
19	Integrative DNA, RNA, and Protein Evidence Connects TREML4 to Coronary Artery Calcification. American Journal of Human Genetics, 2014, 95, 66-76.	2.6	30
20	Altering the Mitochondrial Fatty Acid Synthesis (mtFASII) Pathway Modulates Cellular Metabolic States and Bioactive Lipid Profiles as Revealed by Metabolomic Profiling. PLoS ONE, 2016, 11, e0151171.	1.1	27
21	Changes at the nuclear lamina alter binding of pioneer factor Foxa2 in aged liver. Aging Cell, 2018, 17, e12742.	3.0	27
22	AKT1 Gene Mutation Levels Are Correlated with the Type of Dermatologic Lesions in Patients with Proteus Syndrome. Journal of Investigative Dermatology, 2014, 134, 543-546.	0.3	25
23	Mitochondrial DNA associations with East Asian metabolic syndrome. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, 878-892.	0.5	22
24	Mitochondrial DNA Variation and Disease Susceptibility in Primary Open-Angle Glaucoma., 2018, 59, 4598.		20
25	Assessing the capability of massively parallel sequencing for opportunistic pharmacogenetic screening. Genetics in Medicine, 2017, 19, 357-361.	1.1	15
26	Kupffer cells modulate hepatic fatty acid oxidation during infection with PR8 influenza. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2015, 1852, 2391-2401.	1.8	14
27	Estimation of the Hyperexponential Density with Applications in Sensor Networks. International Journal of Distributed Sensor Networks, 2007, 3, 311-330.	1.3	13
28	Identification of candidate genes involved in coronary artery calcification by transcriptome sequencing of cell lines. BMC Genomics, 2014, 15, 198.	1,2	13
29	Mimosa: Mixture model of co-expression to detect modulators of regulatory interaction. Algorithms for Molecular Biology, 2010, 5, 4.	0.3	12
30	Association of a functional Claudin-5 variant with schizophrenia in female patients with the 22q11.2 deletion syndrome. Schizophrenia Research, 2020, 215, 451-452.	1.1	12
31	MitoScape: A big-data, machine-learning platform for obtaining mitochondrial DNA from next-generation sequencing data. PLoS Computational Biology, 2021, 17, e1009594.	1.5	11
32	The association of mitochondrial DNA haplogroups with POAG in African Americans. Experimental Eye Research, 2019, 181, 85-89.	1,2	10
33	Correlated changes between regulatory cis elements and condition-specific expression in paralogous gene families. Nucleic Acids Research, 2010, 38, 738-749.	6.5	8
34	A New Mouse Model of Mild Ornithine Transcarbamylase Deficiency (spf-j) Displays Cerebral Amino Acid Perturbations at Baseline and upon Systemic Immune Activation. PLoS ONE, 2015, 10, e0116594.	1.1	8
35	Mitochondrial disease disrupts hepatic allostasis and lowers the threshold for immune-mediated liver toxicity. Molecular Metabolism, 2020, 37, 100981.	3.0	8
36	TREMORâ€"a tool for retrieving transcriptional modules by incorporating motif covariance. Nucleic Acids Research, 2007, 35, 7360-7371.	6.5	6

#	Article	IF	CITATIONS
37	NADH Fluorescence Lifetime Imaging Microscopy Reveals Selective Mitochondrial Dysfunction in Neurons Overexpressing Alzheimer's Disease–Related Proteins. Frontiers in Molecular Biosciences, 2021, 8, 671274.	1.6	6
38	Unlocking the Complexity of Mitochondrial DNA: A Key to Understanding Neurodegenerative Disease Caused by Injury. Cells, 2021, 10, 3460.	1.8	5
39	Hypotonia–cystinuria <i>2p21</i> deletion syndrome: Intrafamilial variability of clinical expression. Annals of Clinical and Translational Neurology, 2021, 8, 2199-2204.	1.7	3
40	Mitochondrial Etiology of Psychiatric Disorders—Reply. JAMA Psychiatry, 2018, 75, 527.	6.0	2
41	Correlated Evolution of Positions within Mammalian cis Elements. PLoS ONE, 2013, 8, e55521.	1.1	2
42	Gaussian mixture parameter estimation for cognitive radio and network surveillance applications. , 0, , \cdot		1
43	Channel and Data Estimation for Ad Hoc Networks and Cognitive Radio. International Journal of Wireless Information Networks, 2007, 14, 17-31.	1.8	0
44	Mimosa: Mixture Model of Co-expression to Detect Modulators of Regulatory Interaction. Lecture Notes in Computer Science, 2009, , 133-144.	1.0	0