

Larry N Singh

List of Publications by Year in descending order

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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	Mitochondrial DNA variation and cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 431-445.	12.8	98
2	NADH Fluorescence Lifetime Imaging Microscopy Reveals Selective Mitochondrial Dysfunction in Neurons Overexpressing Alzheimer's Disease-Related Proteins. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 671274.	1.6	6
3	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109839.	2.9	52
4	Hypotonia-cystinuria 2p21 deletion syndrome: Intrafamilial variability of clinical expression. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 2199-2204.	1.7	3
5	MitoScape: A big-data, machine-learning platform for obtaining mitochondrial DNA from next-generation sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1009594.	1.5	11
6	Unlocking the Complexity of Mitochondrial DNA: A Key to Understanding Neurodegenerative Disease Caused by Injury. <i>Cells</i> , 2021, 10, 3460.	1.8	5
7	Association of a functional Claudin-5 variant with schizophrenia in female patients with the 22q11.2 deletion syndrome. <i>Schizophrenia Research</i> , 2020, 215, 451-452.	1.1	12
8	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. <i>Cell</i> , 2020, 183, 1185-1201.e20.	13.5	161
9	Specifications of the ACMG/AMP standards and guidelines for mitochondrial DNA variant interpretation. <i>Human Mutation</i> , 2020, 41, 2028-2057.	1.1	84
10	Mitochondrial disease disrupts hepatic allostasis and lowers the threshold for immune-mediated liver toxicity. <i>Molecular Metabolism</i> , 2020, 37, 100981.	3.0	8
11	Regulation of nuclear epigenome by mitochondrial DNA heteroplasmy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16028-16035.	3.3	108
12	Host mitochondria influence gut microbiome diversity: A role for ROS. <i>Science Signaling</i> , 2019, 12, .	1.6	106
13	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	3.1	57
14	The association of mitochondrial DNA haplogroups with POAG in African Americans. <i>Experimental Eye Research</i> , 2019, 181, 85-89.	1.2	10
15	Changes at the nuclear lamina alter binding of pioneer factor Foxa2 in aged liver. <i>Aging Cell</i> , 2018, 17, e12742.	3.0	27
16	Mitochondrial Etiology of Psychiatric Disorders—Reply. <i>JAMA Psychiatry</i> , 2018, 75, 527.	6.0	2
17	Mitochondrial DNA Variation and Disease Susceptibility in Primary Open-Angle Glaucoma. , 2018, 59, 4598.		20
18	Mitochondrial DNA associations with East Asian metabolic syndrome. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 878-892.	0.5	22

#	ARTICLE	IF	CITATIONS
19	The landscape of transcription errors in eukaryotic cells. <i>Science Advances</i> , 2017, 3, e1701484.	4.7	102
20	Association Between Mitochondrial DNA Haplogroup Variation and Autism Spectrum Disorders. <i>JAMA Psychiatry</i> , 2017, 74, 1161.	6.0	57
21	Assessing the capability of massively parallel sequencing for opportunistic pharmacogenetic screening. <i>Genetics in Medicine</i> , 2017, 19, 357-361.	1.1	15
22	Altering the Mitochondrial Fatty Acid Synthesis (mtFASII) Pathway Modulates Cellular Metabolic States and Bioactive Lipid Profiles as Revealed by Metabolomic Profiling. <i>PLoS ONE</i> , 2016, 11, e0151171.	1.1	27
23	Assessing the reproducibility of exome copy number variations predictions. <i>Genome Medicine</i> , 2016, 8, 82.	3.6	44
24	A New Mouse Model of Mild Ornithine Transcarbamylase Deficiency (spf-j) Displays Cerebral Amino Acid Perturbations at Baseline and upon Systemic Immune Activation. <i>PLoS ONE</i> , 2015, 10, e0116594.	1.1	8
25	Individualized Iterative Phenotyping for Genome-wide Analysis of Loss-of-Function Mutations. <i>American Journal of Human Genetics</i> , 2015, 96, 913-925.	2.6	66
26	Kupffer cells modulate hepatic fatty acid oxidation during infection with PR8 influenza. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2015, 1852, 2391-2401.	1.8	14
27	Identification of candidate genes involved in coronary artery calcification by transcriptome sequencing of cell lines. <i>BMC Genomics</i> , 2014, 15, 198.	1.2	13
28	AKT1 Gene Mutation Levels Are Correlated with the Type of Dermatologic Lesions in Patients with Proteus Syndrome. <i>Journal of Investigative Dermatology</i> , 2014, 134, 543-546.	0.3	25
29	Integrative DNA, RNA, and Protein Evidence Connects TREML4 to Coronary Artery Calcification. <i>American Journal of Human Genetics</i> , 2014, 95, 66-76.	2.6	30
30	Interpreting Secondary Cardiac Disease Variants in an Exome Cohort. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 337-346.	5.1	70
31	Dysregulation of synaptogenesis genes antecedes motor neuron pathology in spinal muscular atrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19348-19353.	3.3	161
32	Correlated Evolution of Positions within Mammalian cis Elements. <i>PLoS ONE</i> , 2013, 8, e55521.	1.1	2
33	Secondary Variants in Individuals Undergoing Exome Sequencing: Screening of 572 Individuals Identifies High-Penetrance Mutations in Cancer-Susceptibility Genes. <i>American Journal of Human Genetics</i> , 2012, 91, 97-108.	2.6	190
34	U1 snRNP Determines mRNA Length and Regulates Isoform Expression. <i>Cell</i> , 2012, 150, 53-64.	13.5	392
35	Mimosa: Mixture model of co-expression to detect modulators of regulatory interaction. <i>Algorithms for Molecular Biology</i> , 2010, 5, 4.	0.3	12
36	U1 snRNP protects pre-mRNAs from premature cleavage and polyadenylation. <i>Nature</i> , 2010, 468, 664-668.	13.7	528

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37	Correlated changes between regulatory cis elements and condition-specific expression in paralogous gene families. <i>Nucleic Acids Research</i> , 2010, 38, 738-749.	6.5	8
38	CTCF binding site classes exhibit distinct evolutionary, genomic, epigenomic and transcriptomic features. <i>Genome Biology</i> , 2009, 10, R131.	13.9	72
39	Mimosa: Mixture Model of Co-expression to Detect Modulators of Regulatory Interaction. <i>Lecture Notes in Computer Science</i> , 2009, , 133-144.	1.0	0
40	Functional Diversification of Paralogous Transcription Factors via Divergence in DNA Binding Site Motif and in Expression. <i>PLoS ONE</i> , 2008, 3, e2345.	1.1	31
41	TREMOR—a tool for retrieving transcriptional modules by incorporating motif covariance. <i>Nucleic Acids Research</i> , 2007, 35, 7360-7371.	6.5	6
42	Estimation of the Hyperexponential Density with Applications in Sensor Networks. <i>International Journal of Distributed Sensor Networks</i> , 2007, 3, 311-330.	1.3	13
43	Channel and Data Estimation for Ad Hoc Networks and Cognitive Radio. <i>International Journal of Wireless Information Networks</i> , 2007, 14, 17-31.	1.8	0
44	Gaussian mixture parameter estimation for cognitive radio and network surveillance applications. , 0, , .		1