

Robi D Mitra

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

5,151
citations

218662

26
h-index

138468

58
g-index

70
all docs

70
docs citations

70
times ranked

8174
citing authors

#	ARTICLE	IF	CITATIONS
1	From karyotypes to precision genomics in 9p deletion and duplication syndromes. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100081.	1.7	9
2	Disentangling glial diversity in peripheral nerves at single-nuclei resolution. <i>Nature Neuroscience</i> , 2022, 25, 238-251.	14.8	35
3	Rapid and Extraction-Free Detection of SARS-CoV-2 from Saliva by Colorimetric Reverse-Transcription Loop-Mediated Isothermal Amplification. <i>Clinical Chemistry</i> , 2021, 67, 415-424.	3.2	192
4	The qBED track: a novel genome browser visualization for point processes. <i>Bioinformatics</i> , 2021, 37, 1168-1170.	4.1	4
5	High-resolution HLA typing by long reads from the R10.3 Oxford nanopore flow cells. <i>Human Immunology</i> , 2021, 82, 288-295.	2.4	28
6	Brd4-bound enhancers drive cell-intrinsic sex differences in glioblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	28
7	Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. <i>Cell</i> , 2020, 182, 992-1008.e21.	28.9	54
8	Human L1 Transposition Dynamics Unraveled with Functional Data Analysis. <i>Molecular Biology and Evolution</i> , 2020, 37, 3576-3600.	8.9	2
9	High-throughput single-cell functional elucidation of neurodevelopmental disease-associated genes reveals convergent mechanisms altering neuronal differentiation. <i>Genome Research</i> , 2020, 30, 1317-1331.	5.5	50
10	Quantitative analysis of transcription factor binding and expression using calling cards reporter arrays. <i>Nucleic Acids Research</i> , 2020, 48, e50-e50.	14.5	6
11	Dual threshold optimization and network inference reveal convergent evidence from TF binding locations and TF perturbation responses. <i>Genome Research</i> , 2020, 30, 459-471.	5.5	24
12	A viral toolkit for recording transcription factor-DNA interactions in live mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10003-10014.	7.1	17
13	Homotypic cooperativity and collective binding are determinants of bHLH specificity and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16143-16152.	7.1	27
14	Accurate Typing of Human Leukocyte Antigen Class I Genes by Oxford Nanopore Sequencing. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 428-435.	2.8	25
15	Transposase mapping identifies the genomic targets of BAP1 in uveal melanoma. <i>BMC Medical Genomics</i> , 2018, 11, 97.	1.5	10
16	Single-Cell RNA-Seq Uncovers a Robust Transcriptional Response to Morphine by Glia. <i>Cell Reports</i> , 2018, 24, 3619-3629.e4.	6.4	109
17	Massively parallel single-nucleotide mutagenesis using reversibly terminated inosine. <i>Nature Methods</i> , 2016, 13, 923-924.	19.0	14
18	Calling Card Analysis in Budding Yeast. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot086918.	0.3	2

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19	Transposon Calling Cards. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077776.	0.3	6
20	Redesign of the monomerâ€“monomer interface of Cre recombinase yields an obligate heterotetrameric complex. Nucleic Acids Research, 2015, 43, 9076-9085.	14.5	16
21	Toying with fate: Redirecting the differentiation of adrenocortical progenitor cells into gonadal-like tissue. Molecular and Cellular Endocrinology, 2015, 408, 165-177.	3.2	13
22	Amyotrophic lateral sclerosis onset is influenced by the burden of rare variants in known amyotrophic lateral sclerosis genes. Annals of Neurology, 2015, 77, 100-113.	5.3	171
23	Novel markers of gonadectomy-induced adrenocortical neoplasia in the mouse and ferret. Molecular and Cellular Endocrinology, 2015, 399, 122-130.	3.2	23
24	Origin and Consequences of the Relationship between Protein Mean and Variance. PLoS ONE, 2014, 9, e102202.	2.5	13
25	Sequencing of idiopathic pulmonary fibrosis-related genes reveals independent single gene associations. BMJ Open Respiratory Research, 2014, 1, e000057.	3.0	69
26	Transcription factor regulation and chromosome dynamics during pseudohyphal growth. Molecular Biology of the Cell, 2014, 25, 2669-2676.	2.1	11
27	Validation of a Next-Generation Sequencing Assay for Clinical Molecular Oncology. Journal of Molecular Diagnostics, 2014, 16, 89-105.	2.8	168
28	Mutation and expression analysis in medulloblastoma yields prognostic variants and a putative mechanism of disease for i17q tumors. Acta Neuropathologica Communications, 2014, 2, 74.	5.2	6
29	Synonymous ABCA3 Variants Do Not Increase Risk for Neonatal Respiratory Distress Syndrome. Journal of Pediatrics, 2014, 164, 1316-1321.e3.	1.8	6
30	PDE7B Is a Novel, Prognostically Significant Mediator of Glioblastoma Growth Whose Expression Is Regulated by Endothelial Cells. PLoS ONE, 2014, 9, e107397.	2.5	22
31	Ultralow Protein Adsorbing Coatings from Clickable PEG Nanogel Solutions: Benefits of Attachment under Salt-Induced Phase Separation Conditions and Comparison with PEG/Albumin Nanogel Coatings. Langmuir, 2013, 29, 4128-4139.	3.5	27
32	Laser capture microdissectionâ€“reduced representation bisulfite sequencing (LCM-RRBS) maps changes in DNA methylation associated with gonadectomy-induced adrenocortical neoplasia in the mouse. Nucleic Acids Research, 2013, 41, e116-e116.	14.5	38
33	ATHLATES: accurate typing of human leukocyte antigen through exome sequencing. Nucleic Acids Research, 2013, 41, e142-e142.	14.5	104
34	A systematic study of gene expression variation at single-nucleotide resolution reveals widespread regulatory roles for uAUGs. Genome Research, 2012, 22, 1089-1097.	5.5	28
35	Detection of Rare Genomic Variants from Pooled Sequencing Using SPLINTER. Journal of Visualized Experiments, 2012, , .	0.3	6
36	Single <i>ABCA3</i> Mutations Increase Risk for Neonatal Respiratory Distress Syndrome. Pediatrics, 2012, 130, e1575-e1582.	2.1	93

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37	Sensitive single-molecule protein quantification and protein complex detection in a microarray format. <i>Proteomics</i> , 2011, 11, 4731-4735.	2.2	19
38	Nanogel surface coatings for improved single-molecule imaging substrates. <i>Journal of the Royal Society Interface</i> , 2011, 8, 1400-1408.	3.4	20
39	High-throughput discovery of rare insertions and deletions in large cohorts. <i>Genome Research</i> , 2010, 20, 1711-1718.	5.5	56
40	Cardiac signaling genes exhibit unexpected sequence diversity in sporadic cardiomyopathy, revealing HSPB7 polymorphisms associated with disease. <i>Journal of Clinical Investigation</i> , 2010, 120, 280-289.	8.2	64
41	Quantification of rare allelic variants from pooled genomic DNA. <i>Nature Methods</i> , 2009, 6, 263-265.	19.0	136
42	Protein Quantification in Complex Mixtures by Solid Phase Single-Molecule Counting. <i>Analytical Chemistry</i> , 2009, 81, 7141-7148.	6.5	62
43	'Calling Cards' method for high-throughput identification of targets of yeast DNA-binding proteins. <i>Nature Protocols</i> , 2008, 3, 1569-1577.	12.0	14
44	Long-range polony haplotyping of individual human chromosome molecules. <i>Nature Genetics</i> , 2006, 38, 382-387.	21.4	97
45	Accurate Multiplex Polony Sequencing of an Evolved Bacterial Genome. <i>Science</i> , 2005, 309, 1728-1732.	12.6	1,189
46	Advanced sequencing technologies: methods and goals. <i>Nature Reviews Genetics</i> , 2004, 5, 335-344.	16.3	499
47	Digital quantitative measurements of gene expression. <i>Biotechnology and Bioengineering</i> , 2004, 86, 117-124.	3.3	22
48	Fluorescent in situ sequencing on polymerase colonies. <i>Analytical Biochemistry</i> , 2003, 320, 55-65.	2.4	159
49	Parallel competition analysis of <i>Saccharomyces cerevisiae</i> strains differing by a single base using polymerase colonies. <i>Nucleic Acids Research</i> , 2003, 31, 84e-84.	14.5	17
50	Digital genotyping and haplotyping with polymerase colonies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5926-5931.	7.1	141
51	Single Molecule Profiling of Alternative Pre-mRNA Splicing. <i>Science</i> , 2003, 301, 836-838.	12.6	93
52	A computational analysis of whole-genome expression data reveals chromosomal domains of gene expression. <i>Nature Genetics</i> , 2000, 26, 183-186.	21.4	485
53	In situ localized amplification and contact replication of many individual DNA molecules. <i>Nucleic Acids Research</i> , 1999, 27, 34e-34.	14.5	202
54	Fluorescence resonance energy transfer between blue-emitting and red-shifted excitation derivatives of the green fluorescent protein. <i>Gene</i> , 1996, 173, 13-17.	2.2	307

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55	Single Cell RNAseq Uncovers a Robust Transcriptional Response to Morphine by Oligodendrocytes. SSRN Electronic Journal, 0, , .	0.4	0