Robi D Mitra

List of Publications by Year in descending order

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55 papers

5,151 citations

218677
26
h-index

58 g-index

70 all docs

70 docs citations

times ranked

70

8174 citing authors

#	Article	IF	CITATIONS
1	Accurate Multiplex Polony Sequencing of an Evolved Bacterial Genome. Science, 2005, 309, 1728-1732.	12.6	1,189
2	Advanced sequencing technologies: methods and goals. Nature Reviews Genetics, 2004, 5, 335-344.	16.3	499
3	A computational analysis of whole-genome expression data reveals chromosomal domains of gene expression. Nature Genetics, 2000, 26, 183-186.	21.4	485
4	Fluorescence resonance energy transfer between blue-emitting and red-shifted excitation derivatives of the green fluorescent protein. Gene, 1996, 173, 13-17.	2.2	307
5	In situ localized amplification and contact replication of many individual DNA molecules. Nucleic Acids Research, 1999, 27, 34e-34.	14.5	202
6	Rapid and Extraction-Free Detection of SARS-CoV-2 from Saliva by Colorimetric Reverse-Transcription Loop-Mediated Isothermal Amplification. Clinical Chemistry, 2021, 67, 415-424.	3,2	192
7	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
8	Validation of a Next-Generation Sequencing Assay for Clinical Molecular Oncology. Journal of Molecular Diagnostics, 2014, 16, 89-105.	2.8	168
9	Fluorescent in situ sequencing on polymerase colonies. Analytical Biochemistry, 2003, 320, 55-65.	2.4	159
10	Digital genotyping and haplotyping with polymerase colonies. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5926-5931.	7.1	141
11	Quantification of rare allelic variants from pooled genomic DNA. Nature Methods, 2009, 6, 263-265.	19.0	136
12	Single-Cell RNA-Seq Uncovers a Robust Transcriptional Response to Morphine by Glia. Cell Reports, 2018, 24, 3619-3629.e4.	6.4	109
13	ATHLATES: accurate typing of human leukocyte antigen through exome sequencing. Nucleic Acids Research, 2013, 41, e142-e142.	14.5	104
14	Long-range polony haplotyping of individual human chromosome molecules. Nature Genetics, 2006, 38, 382-387.	21.4	97
15	Single Molecule Profiling of Alternative Pre-mRNA Splicing. Science, 2003, 301, 836-838.	12.6	93
16	Single <i>ABCA3</i> Mutations Increase Risk for Neonatal Respiratory Distress Syndrome. Pediatrics, 2012, 130, e1575-e1582.	2.1	93
17	Sequencing of idiopathic pulmonary fibrosis-related genes reveals independent single gene associations. BMJ Open Respiratory Research, 2014, 1, e000057.	3.0	69
18	Cardiac signaling genes exhibit unexpected sequence diversity in sporadic cardiomyopathy, revealing HSPB7 polymorphisms associated with disease. Journal of Clinical Investigation, 2010, 120, 280-289.	8.2	64

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19	Protein Quantification in Complex Mixtures by Solid Phase Single-Molecule Counting. Analytical Chemistry, 2009, 81, 7141-7148.	6.5	62
20	High-throughput discovery of rare insertions and deletions in large cohorts. Genome Research, 2010, 20, 1711-1718.	5 . 5	56
21	Self-Reporting Transposons Enable SimultaneousÂReadout of Gene Expression and TranscriptionÂFactor Binding in Single Cells. Cell, 2020, 182, 992-1008.e21.	28.9	54
22	High-throughput single-cell functional elucidation of neurodevelopmental disease–associated genes reveals convergent mechanisms altering neuronal differentiation. Genome Research, 2020, 30, 1317-1331.	5.5	50
23	Laser capture microdissection–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
24	Disentangling glial diversity in peripheral nerves at single-nuclei resolution. Nature Neuroscience, 2022, 25, 238-251.	14.8	35
25	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
26	High-resolution HLA typing by long reads from the R10.3 Oxford nanopore flow cells. Human Immunology, 2021, 82, 288-295.	2.4	28
27	Brd4-bound enhancers drive cell-intrinsic sex differences in glioblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	28
28	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
29	Homotypic cooperativity and collective binding are determinants of bHLH specificity and function. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16143-16152.	7.1	27
30	Accurate Typing of Human Leukocyte Antigen Class I Genes by Oxford Nanopore Sequencing. Journal of Molecular Diagnostics, 2018, 20, 428-435.	2.8	25
31	Dual threshold optimization and network inference reveal convergent evidence from TF binding locations and TF perturbation responses. Genome Research, 2020, 30, 459-471.	5. 5	24
32	Novel markers of gonadectomy-induced adrenocortical neoplasia in the mouse and ferret. Molecular and Cellular Endocrinology, 2015, 399, 122-130.	3.2	23
33	Digital quantitative measurements of gene expression. Biotechnology and Bioengineering, 2004, 86, 117-124.	3.3	22
34	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
35	Nanogel surface coatings for improved single-molecule imaging substrates. Journal of the Royal Society Interface, 2011, 8, 1400-1408.	3.4	20
36	Sensitive singleâ€molecule protein quantification and protein complex detection in a microarray format. Proteomics, 2011, 11, 4731-4735.	2.2	19

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37	Parallel competition analysis of Saccharomyces cerevisiae strains differing by a single base using polymerase colonies. Nucleic Acids Research, 2003, 31, 84e-84.	14.5	17
38	A viral toolkit for recording transcription factor–DNA interactions in live mouse tissues. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10003-10014.	7.1	17
39	Redesign of the monomer–monomer interface of Cre recombinase yields an obligate heterotetrameric complex. Nucleic Acids Research, 2015, 43, 9076-9085.	14.5	16
40	'Calling Cards' method for high-throughput identification of targets of yeast DNA-binding proteins. Nature Protocols, 2008, 3, 1569-1577.	12.0	14
41	Massively parallel single-nucleotide mutagenesis using reversibly terminated inosine. Nature Methods, 2016, 13, 923-924.	19.0	14
42	Origin and Consequences of the Relationship between Protein Mean and Variance. PLoS ONE, 2014, 9, e102202.	2.5	13
43	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
44	Transcription factor regulation and chromosome dynamics during pseudohyphal growth. Molecular Biology of the Cell, 2014, 25, 2669-2676.	2.1	11
45	Transposase mapping identifies the genomic targets of BAP1 in uveal melanoma. BMC Medical Genomics, 2018, 11, 97.	1.5	10
46	From karyotypes to precision genomics in 9p deletion and duplication syndromes. Human Genetics and Genomics Advances, 2022, 3, 100081.	1.7	9
47	Detection of Rare Genomic Variants from Pooled Sequencing Using SPLINTER. Journal of Visualized Experiments, 2012, , .	0.3	6
48	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
49	Synonymous ABCA3 Variants Do Not Increase Risk for Neonatal Respiratory Distress Syndrome. Journal of Pediatrics, 2014, 164, 1316-1321.e3.	1.8	6
50	Transposon Calling Cards. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077776.	0.3	6
51	Quantitative analysis of transcription factor binding and expression using calling cards reporter arrays. Nucleic Acids Research, 2020, 48, e50-e50.	14.5	6
52	The qBED track: a novel genome browser visualization for point processes. Bioinformatics, 2021, 37, 1168-1170.	4.1	4
53	Calling Card Analysis in Budding Yeast. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot086918.	0.3	2
54	Human L1 Transposition Dynamics Unraveled with Functional Data Analysis. Molecular Biology and Evolution, 2020, 37, 3576-3600.	8.9	2

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