Mitali Mukerji

List of Publications by Year
in descending order

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92 papers	3,744 citations	172207 29 h-index	143772 57 g-index
105 all docs	105 docs citations	105 times ranked	4978 citing authors

#	Article	IF	Citations
1	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	6.0	557
2	Genome-wide prediction of G4 DNA as regulatory motifs: Role in Escherichia coli global regulation. Genome Research, 2006, 16, 644-655.	2.4	287
3	Genetic landscape of the people of India: a canvas for disease gene exploration. Journal of Genetics, 2008, 87, 3-20.	0.4	282
4	EGLN1 involvement in high-altitude adaptation revealed through genetic analysis of extreme constitution types defined in Ayurveda. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18961-18966.	3.3	152
5	Whole genome expression and biochemical correlates of extreme constitutional types defined in Ayurveda. Journal of Translational Medicine, 2008, 6, 48.	1.8	150
6	Alu repeat analysis in the complete human genome: trends and variations with respect to genomic composition. Bioinformatics, 2004, 20, 813-817.	1.8	123
7	CAG repeat instability at SCA2 locus: anchoring CAA interruptions and linked single nucleotide polymorphisms. Human Molecular Genetics, 2001, 10, 2437-2446.	1.4	121
8	Complex Patterns of Genomic Admixture within Southern Africa. PLoS Genetics, 2013, 9, e1003309.	1.5	94
9	Nonrandom Distribution of Alu Elements in Genes of Various Functional Categories: Insight from Analysis of Human Chromosomes 21 and 22. Molecular Biology and Evolution, 2003, 20, 1420-1424.	3.5	81
10	Evidence of a Common Founder for SCA12 in the Indian Population. Annals of Human Genetics, 2005, 69, 528-534.	0.3	71
11	Characterization of the negative elements involved in silencing the bgl operon of Escherichia coli : possible roles for DNA gyrase, Hâ€NS, and CRPâ€“cAMP in regulation. Molecular Microbiology, 1997, 24, 617-627.	1.2	70
12	Western Indian Rural Gut Microbial Diversity in Extreme Prakriti Endo-Phenotypes Reveals Signature Microbes. Frontiers in Microbiology, 2018, 9, 118.	1.5	68
13	SNPs in stress-responsive rice genes: validation, genotyping, functional relevance and population structure. BMC Genomics, 2012, 13, 426.	1.2	64
14	Hypoxia Response in Asthma. American Journal of Respiratory Cell and Molecular Biology, 2012, 47, 1-10.	1.4	62
15	Genomic insights into ayurvedic and western approaches to personalized medicine. Journal of Genetics, 2016, 95, 209-228.	0.4	59
16	Ayurgenomics: A New Way of Threading Molecular Variability for Stratified Medicine. ACS Chemical Biology, 2011, 6, 875-880.	1.6	56
17	Human satellite-III non-coding RNAs modulate heat shock-induced transcriptional repression. Journal of Cell Science, 2016, 129, 3541-3552.	1.2	53
18	Transcriptional activation of the Escherichia coli bgl operon: negative regulation by DNA structural elements near the promoter. Molecular Microbiology, 1995, 17, 1085-1092.	1.2	48

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19	Evolution and distribution of RNA polymerase II regulatory sites from RNA polymerase III dependant mobile Alu elements. BMC Evolutionary Biology, 2004, 4, 37.	3.2	46
20	Finding Alu in primate genomes with AF-1. Bioinformation, 2009, 3, 287-288.	0.2	45
21	MLC1 Gene Is Associated with Schizophrenia and Bipolar Disorder in Southern India. Biological Psychiatry, 2005, 58, 16-22.	0.7	44
22	Comparative Genomics of Hostâ€“Symbiont and Free-Living Oceanobacillus Species. Genome Biology and Evolution, 2017, 9, 1175-1182.	1.1	44
23	Comparative analysis of the alveolar microbiome in COPD, ECOPD, Sarcoidosis, and ILD patients to identify respiratory illnesses specific microbial signatures. Scientific Reports, 2021, 11, 3963.	1.6	42
24	IndiGenomes: a comprehensive resource of genetic variants from over 1000 Indian genomes. Nucleic Acids Research, 2021, 49, D1225-D1232.	6.5	39
25	Combined genetic effects of EGLN1 and VWF modulate thrombotic outcome in hypoxia revealed by Ayurgenomics approach. Journal of Translational Medicine, 2015, 13, 184.	1.8	38
26	Ayurgenomics for stratified medicine: TRISUTRA consortium initiative across ethnically and geographically diverse Indian populations. Journal of Ethnopharmacology, 2017, 197, 274-293.	2.0	38
27	Traditional Knowledge-based Medicine: A Review of History, Principles, and Relevance in the Present Context of P4 Systems Medicine. Progress in Preventive Medicine (New York, N Y), 2017, 2, e0011.	0.7	38
28	Integrated genomic view of SARS-CoV-2 in India. Wellcome Open Research, 2020, 5, 184.	0.9	36
29	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. PLoS ONE, 2017, 12, e0185380.	1.1	35
30	Heat shock factor binding in Alu repeats expands its involvement in stress through an antisense mechanism. Genome Biology, 2011, 12, R117.	13.9	34
31	SCA-LSVD: A repeat-oriented locus-specific variation database for genotype to phenotype correlations in spinocerebellar ataxias. Human Mutation, 2009, 30, 1037-1042.	1.1	32
32	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 111-120.	2.6	32
33	Differential serum cytokine levels are associated with cytokine gene polymorphisms in north Indians with active pulmonary tuberculosis. Infection, Genetics and Evolution, 2011, 11, 1015-1022.	1.0	31
34	IGVBrowser-a genomic variation resource from diverse Indian populations. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq022-baq022.	1.4	30
35	Complex phenotypes in an Indian family with homozygous SCA2 mutations. Annals of Neurology, 2004, 55, 130-133.	2.8	29
36	Deletion of the APOBEC3B gene strongly impacts susceptibility to falciparum malaria. Infection, Genetics and Evolution, 2012, 12, 142-148.	1.0	29

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37	Transcriptome-wide expansion of non-coding regulatory switches: evidence from co-occurrence of Alu exonization, antisense and editing. Nucleic Acids Research, 2013, 41, 2121-2137.	6.5	29
38	Founder Haplotype for Machado-Joseph Disease in the Indian Population. Archives of Neurology, 2005, 62, 637.	4.9	28
39	Post-zygotic de novo trinucleotide repeat expansion at spinocerebellar ataxia type 7 locus: evidence from an Indian family. Journal of Human Genetics, 2005, 50, 155-157.	1.1	26
40	ALU-ring elements in the primate genomes. Genetica, 2005, 124, 273-289.	0.5	26
41	From 'JUNK' to Just Unexplored Noncoding Knowledge: the case of transcribed Alus. Briefings in Functional Genomics, 2011, 10, 294-311.	1.3	26
42	Adhatoda Vasica attenuates inflammatory and hypoxic responses in preclinical mouse models: potential for repurposing in COVID-19-like conditions. Respiratory Research, 2021, 22, 99.	1.4	24
43	Extensive Copy Number Variations in Admixed Indian Population of African Ancestry: Potential Involvement in Adaptation. Genome Biology and Evolution, 2014, 6, 3171-3181.	1.1	23
44	Novel mutations in typical and atypical genetic loci through exome sequencing in autosomal recessive cerebellar ataxia families. Clinical Genetics, 2014, 86, 335-341.	1.0	22
45	MtSNPscore: a combined evidence approach for assessing cumulative impact of mitochondrial variations in disease. BMC Bioinformatics, 2009, 10, S7.	1.2	21
46	Targeted exome sequencing in anti-factor H antibody negative HUS reveals multiple variations. Clinical and Experimental Nephrology, 2018, 22, 653-660.	0.7	21
47	Cryptic genes: Evolutionary puzzles. Journal of Genetics, 1997, 76, 147-159.	0.4	20
48	Diverse Facets of COMT: From a Plausible Predictive Marker to a Potential Drug Target for Schizophrenia. Current Molecular Medicine, 2011, 11, 732-743.	0.6	20
49	Alu-miRNA interactions modulate transcript isoform diversity in stress response and reveal signatures of positive selection. Scientific Reports, 2016, 6, 32348.	1.6	20
50	From diversity to delivery: the case of the Indian Genome Variation initiative. Nature Reviews Genetics, 2008, 9, S9-S14.	7.7	18
51	North and South Indian Populations Share a Common Ancestral Origin of Friedreich's Ataxia but Vary in Age of GAA Repeat Expansion. Annals of Human Genetics, 2010, 74, 202-210.	0.3	18
52	Whole exome and targeted gene sequencing to detect pathogenic recessive variants in early onset cerebellar ataxia. Clinical Genetics, 2019, 96, 566-574.	1.0	18
53	Myg1 exonuclease couples the nuclear and mitochondrial translational programs through RNA processing. Nucleic Acids Research, 2019, 47, 5852-5866.	6.5	18
54	Spatio-temporal dynamics of intra-host variability in SARS-CoV-2 genomes. Nucleic Acids Research, 2022, 50, 1551-1561.	6.5	18

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55	Origin and Instability of GAA Repeats: Insights from Alu Elements. Journal of Biomolecular Structure and Dynamics, 2002, 20, 253-263.	2.0	17
56	Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. Human Genetics, 2012, 131, 131-143.	1.8	17
57	Infantile Onset Spinocerebellar Ataxia 2 (SCA2). Journal of Child Neurology, 2014, 29, 139-144.	0.7	17
58	Population Diversity and Adaptive Evolution in Keratinization Genes: Impact of Environment in Shaping Skin Phenotypes. Molecular Biology and Evolution, 2015, 32, 555-573.	3.5	17
59	SMARCA2 and THAP11: potential candidates for polyglutamine disorders as evidenced from polymorphism and protein-folding simulation studies. Journal of Human Genetics, 2004, 49, 596-602.	1.1	16
60	Insights into the mutational history and prevalence of SCA1 in the Indian population through anchored polymorphisms. Human Genetics, 2005, 118, 107-114.	1.8	16
61	Molecular analysis of Friedreich's ataxia locus in the Indian population. Acta Neurologica Scandinavica, 2000, 102, 227-229.	1.0	14
62	SCA 1, SCA 2 & SCA 3/MJD mutations in ataxia syndromes in southern India. Indian Journal of Medical Research, 2007, 126, 465-70.	0.4	13
63	Ancestral Variations of the PCDHG Gene Cluster Predispose to Dyslexia in a Multiplex Family. EBioMedicine, 2018, 28, 168-179.	2.7	12
64	Spinocerebellar ataxia 7 (SCA7) in Indian population: predilection of ATXN7-CAG expansion mutation in an ethnic population. Indian Journal of Medical Research, 2015, 141, 187.	0.4	12
65	Investigation of mitochondrial DNA variations among Indian Friedreich's ataxia (FRDA) patients. Mitochondrion, 2015, 25, 1-5.	1.6	11
66	Generation of three spinocerebellar ataxia type-12 patients derived induced pluripotent stem cell lines (IGIBi002-A, IGIBi003-A and IGIBi004-A). Stem Cell Research, 2018, 31, 216-221.	0.3	11
67	Non-random genomic divergence in repetitive sequences of human and chimpanzee in genes of different functional categories. Molecular Genetics and Genomics, 2007, 277, 441-455.	1.0	8
68	Frequency spectrum of rare and clinically relevant markers in multiethnic Indian populations (ClinIndb): A resource for genomic medicine in India. Human Mutation, 2020, 41, 1833-1847.	1.1	8
69	Adhatoda vasica rescues the hypoxia-dependent severe asthma symptoms and mitochondrial dysfunction. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L757-L769.	1.3	8
70	Next-Generation Sequencing for Congenital Nephrotic Syndrome: A Multi-Center Cross-Sectional Study from India. Indian Pediatrics, 2021, 58, 445-451.	0.2	8
71	Multiple Alu exonization in 3â€™UTR of a primate specific isoform of CYP20A1 creates a potential miRNA sponge. Genome Biology and Evolution, 2021, 13, .	1.1	8
72	Genetic Risk Prediction of COVID-19 Susceptibility and Severity in the Indian Population. Frontiers in Genetics, 2021, 12, 714185.	1.1	8

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73	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. Pharmacogenomics, 2021, 22, 603-618.	0.6	7
74	Transcriptome analysis and connectivity mapping of Cissampelos pareira L. provides molecular links of ESR1 modulation to viral inhibition. Scientific Reports, 2021, 11, 20095.	1.6	7
75	A Complete Association of an intronic SNP rs6798742 with Origin of Spinocerebellar Ataxia Type 7â€CAG Expansion Loci in the Indian and Mexican Population. Annals of Human Genetics, 2017, 81, 197-204.	0.3	6
76	VitiVar: A locus specific database of vitiligo associated genes and variations. Gene: X, 2019, 721, 100018.	2.3	6
77	A Genomeâ€Wide Search for Nonâ€UGT1A1 Markers Associated with Unconjugated Bilirubin Level Reveals Significant Association with a Polymorphic Marker Near a Gene of the Nucleoporin Family. Annals of Human Genetics, 2012, 76, 33-41.	0.3	5
78	First Degree Relatives of Patients with Celiac Disease Harbour an Intestinal Transcriptomic Signature that Might Protect them from Enterocyte Damage. Clinical and Translational Gastroenterology, 2018, 9, e195.	1.3	5
79	Utilizing linkage disequilibrium information from Indian Genome Variation Database for mapping mutations: SCA12 case study. Journal of Genetics, 2009, 88, 55-60.	0.4	4
80	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. Journal of Genetics, 2018, 97, 589-609.	0.4	4
81	Baseline cell proliferation rates and response to UV differ in lymphoblastoid cell lines derived from healthy individuals of extreme constitution types. Cell Cycle, 2021, 20, 903-913.	1.3	3
82	Whole Exome Sequencing in Healthy Individuals of Extreme Constitution Types Reveals Differential Disease Risk: A Novel Approach towards Predictive Medicine. Journal of Personalized Medicine, 2022, 12, 489.	1.1	3
83	Genomics and Big Data Analytics in Ayurvedic Medicine. Progress in Preventive Medicine (New York, N Y) Tj ETQq1 1 0.784314 rgBT /Ov	0.7	2
84	Genomics and Traditional Indian Ayurvedic Medicine. , 2016, , 271-292.		1
85	Dissecting Human Microbiome for Personalized Therapy. , 2022, , 274-285.		1
86	An Alu insertion map of the Indian population: identification and analysis in 1021 genomes of the IndiGen project. NAR Genomics and Bioinformatics, 2022, 4, lqac009.	1.5	1
87	Recent Admixture in an Indian Population of African Ancestry. American Journal of Human Genetics, 2011, 89, 344.	2.6	0
88	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges. , 2018, , 71-95.		0
89	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. Journal of Genetics, 2018, 97, 589-609.	0.4	0
90	Next-Generation Sequencing for Congenital Nephrotic Syndrome: A Multi-Center Cross-Sectional Study from India. Indian Pediatrics, 2021, 58, 445-451.	0.2	0

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91	Genetic epidemiology of autoinflammatory disease variants in Indian population from 1029 whole genomes. Journal of Genetic Engineering and Biotechnology, 2021, 19, 183.	1.5	0
92	Landscape of Variability in Chemosensory Genes Associated With Dietary Preferences in Indian Population: Analysis of 1029 Indian Genomes. Frontiers in Genetics, 0, 13, .	1.1	0