

Mitali Mukerji

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

92
papers

2,919
citations

25
h-index

52
g-index

105
ext. papers

3,419
ext. citations

5.6
avg, IF

4.89
L-index

#	Paper	IF	Citations
92	Spatio-temporal dynamics of intra-host variability in SARS-CoV-2 genomes.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	4
91	Dissecting Human Microbiome for Personalized Therapy 2022 ,		1
90	An insertion map of the Indian population: identification and analysis in 1021 genomes of the IndiGen project.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac009	3.7	
89	Genetic Risk Prediction of COVID-19 Susceptibility and Severity in the Indian Population. <i>Frontiers in Genetics</i> , 2021 , 12, 714185	4.5	1
88	Transcriptome analysis and connectivity mapping of <i>Cissampelos pareira</i> L. provides molecular links of ESR1 modulation to viral inhibition. <i>Scientific Reports</i> , 2021 , 11, 20095	4.9	1
87	Multiple Alu Exonization in 3'UTR of a Primate-Specific Isoform of CYP20A1 Creates a Potential miRNA Sponge. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	5
86	IndiGenomes: a comprehensive resource of genetic variants from over 1000 Indian genomes. <i>Nucleic Acids Research</i> , 2021 , 49, D1225-D1232	20.1	12
85	<i>Adhatoda Vasica</i> attenuates inflammatory and hypoxic responses in preclinical mouse models: potential for repurposing in COVID-19-like conditions. <i>Respiratory Research</i> , 2021 , 22, 99	7.3	7
84	Baseline cell proliferation rates and response to UV differ in lymphoblastoid cell lines derived from healthy individuals of extreme constitution types. <i>Cell Cycle</i> , 2021 , 20, 903-913	4.7	1
83	rescues the hypoxia-dependent severe asthma symptoms and mitochondrial dysfunction. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021 , 320, L757-L769	5.8	4
82	Next-Generation Sequencing for Congenital Nephrotic Syndrome: A Multi-Center Cross-Sectional Study from India. <i>Indian Pediatrics</i> , 2021 , 58, 445-451	1.2	4
81	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. <i>Pharmacogenomics</i> , 2021 , 22, 603-618	2.6	0
80	Comparative analysis of the alveolar microbiome in COPD, ECOPD, Sarcoidosis, and ILD patients to identify respiratory illnesses specific microbial signatures. <i>Scientific Reports</i> , 2021 , 11, 3963	4.9	12
79	Next-Generation Sequencing for Congenital Nephrotic Syndrome: A Multi-Center Cross-Sectional Study from India. <i>Indian Pediatrics</i> , 2021 , 58, 445-451	1.2	
78	Genetic epidemiology of autoinflammatory disease variants in Indian population from 1029 whole genomes.. <i>Journal of Genetic Engineering and Biotechnology</i> , 2021 , 19, 183	3.1	
77	Integrated genomic view of SARS-CoV-2 in India. <i>Wellcome Open Research</i> , 2020 , 5, 184	4.8	25
76	Frequency spectrum of rare and clinically relevant markers in multiethnic Indian populations (ClinIndb): A resource for genomic medicine in India. <i>Human Mutation</i> , 2020 , 41, 1833-1847	4.7	5

75	Myg1 exonuclease couples the nuclear and mitochondrial translational programs through RNA processing. <i>Nucleic Acids Research</i> , 2019 , 47, 5852-5866	20.1	8
74	VitiVar: A locus specific database of vitiligo associated genes and variations. <i>Gene: X</i> , 2019 , 3, 100018	2.1	3
73	Whole exome and targeted gene sequencing to detect pathogenic recessive variants in early onset cerebellar ataxia. <i>Clinical Genetics</i> , 2019 , 96, 566-574	4	10
72	Ancestral Variations of the PCDHG Gene Cluster Predispose to Dyslexia in a Multiplex Family. <i>EBioMedicine</i> , 2018 , 28, 168-179	8.8	9
71	Targeted exome sequencing in anti-factor H antibody negative HUS reveals multiple variations. <i>Clinical and Experimental Nephrology</i> , 2018 , 22, 653-660	2.5	8
70	Western Indian Rural Gut Microbial Diversity in Extreme Endo-Phenotypes Reveals Signature Microbes. <i>Frontiers in Microbiology</i> , 2018 , 9, 118	5.7	31
69	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. <i>Journal of Genetics</i> , 2018 , 97, 589-609	1.2	2
68	Generation of three spinocerebellar ataxia type-12 patients derived induced pluripotent stem cell lines (IGiBi002-A, IGiBi003-A and IGiBi004-A). <i>Stem Cell Research</i> , 2018 , 31, 216-221	1.6	6
67	First Degree Relatives of Patients with Celiac Disease Harbour an Intestinal Transcriptomic Signature that Might Protect them from Enterocyte Damage. <i>Clinical and Translational Gastroenterology</i> , 2018 , 9, 195	4.2	2
66	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges 2018 , 71-95		
65	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. <i>Journal of Genetics</i> , 2018 , 97, 589-609	1.2	
64	Comparative Genomics of Host-Symbiont and Free-Living Oceanobacillus Species. <i>Genome Biology and Evolution</i> , 2017 , 9, 1175-1182	3.9	18
63	A Complete Association of an intronic SNP rs6798742 with Origin of Spinocerebellar Ataxia Type 7-CAG Expansion Loci in the Indian and Mexican Population. <i>Annals of Human Genetics</i> , 2017 , 81, 197-204	2.2	6
62	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. <i>PLoS ONE</i> , 2017 , 12, e0185380	3.7	13
61	Ayurgenomics for stratified medicine: TRISUTRA consortium initiative across ethnically and geographically diverse Indian populations. <i>Journal of Ethnopharmacology</i> , 2017 , 197, 274-293	5	20
60	Traditional Knowledge-based Medicine: A Review of History, Principles, and Relevance in the Present Context of P4 Systems Medicine. <i>Progress in Preventive Medicine (New York, N Y)</i> , 2017 , 2, e0011	0.7	23
59	Human satellite-III non-coding RNAs modulate heat-shock-induced transcriptional repression. <i>Journal of Cell Science</i> , 2016 , 129, 3541-3552	5.3	30
58	Alu-miRNA interactions modulate transcript isoform diversity in stress response and reveal signatures of positive selection. <i>Scientific Reports</i> , 2016 , 6, 32348	4.9	12

57 Genomics and Traditional Indian Ayurvedic Medicine **2016**, 271-292

56 Genomic insights into ayurvedic and western approaches to personalized medicine. *Journal of Genetics*, **2016**, 95, 209-28 1.2 38

55 Investigation of mitochondrial DNA variations among Indian Friedreich's ataxia (FRDA) patients. *Mitochondrion*, **2015**, 25, 1-5 4.9 8

54 Population diversity and adaptive evolution in keratinization genes: impact of environment in shaping skin phenotypes. *Molecular Biology and Evolution*, **2015**, 32, 555-73 8.3 14

53 Combined genetic effects of EGLN1 and VWF modulate thrombotic outcome in hypoxia revealed by Ayurgenomics approach. *Journal of Translational Medicine*, **2015**, 13, 184 8.5 25

52 Spinocerebellar ataxia 7 (SCA7) in Indian population: predilection of ATXN7-CAG expansion mutation in an ethnic population. *Indian Journal of Medical Research*, **2015**, 141, 187-98 2.9 11

51 Novel mutations in typical and atypical genetic loci through exome sequencing in autosomal recessive cerebellar ataxia families. *Clinical Genetics*, **2014**, 86, 335-41 4 15

50 Extensive copy number variations in admixed Indian population of African ancestry: potential involvement in adaptation. *Genome Biology and Evolution*, **2014**, 6, 3171-81 3.9 9

49 Infantile onset spinocerebellar ataxia 2 (SCA2): a clinical report with review of previous cases. *Journal of Child Neurology*, **2014**, 29, 139-44 2.5 15

48 Complex patterns of genomic admixture within southern Africa. *PLoS Genetics*, **2013**, 9, e1003309 6 72

47 Transcriptome-wide expansion of non-coding regulatory switches: evidence from co-occurrence of Alu exonization, antisense and editing. *Nucleic Acids Research*, **2013**, 41, 2121-37 20.1 19

46 Deletion of the APOBEC3B gene strongly impacts susceptibility to falciparum malaria. *Infection, Genetics and Evolution*, **2012**, 12, 142-8 4.5 25

45 Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. *Human Genetics*, **2012**, 131, 131-43 6.3 13

44 SNPs in stress-responsive rice genes: validation, genotyping, functional relevance and population structure. *BMC Genomics*, **2012**, 13, 426 4.5 55

43 A genome-wide search for non-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 2.2 4

42 Hypoxia response in asthma: differential modulation on inflammation and epithelial injury. *American Journal of Respiratory Cell and Molecular Biology*, **2012**, 47, 1-10 5.7 44

41 Heat shock factor binding in Alu repeats expands its involvement in stress through an antisense mechanism. *Genome Biology*, **2011**, 12, R117 18.3 25

40 From TUNKT to just unexplored noncoding knowledge: the case of transcribed Alus. *Briefings in Functional Genomics*, **2011**, 10, 294-311 4.9 23

39	Recent admixture in an Indian population of African ancestry. <i>American Journal of Human Genetics</i> , 2011 , 89, 111-20	11	23
38	Recent Admixture in an Indian Population of African Ancestry. <i>American Journal of Human Genetics</i> , 2011 , 89, 344	11	78
37	Ayurgenomics: a new way of threading molecular variability for stratified medicine. <i>ACS Chemical Biology</i> , 2011 , 6, 875-80	4.9	37
36	Differential serum cytokine levels are associated with cytokine gene polymorphisms in north Indians with active pulmonary tuberculosis. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 1015-22	4.5	28
35	Diverse facets of COMT: from a plausible predictive marker to a potential drug target for schizophrenia. <i>Current Molecular Medicine</i> , 2011 , 11, 732-43	2.5	16
34	North and South Indian populations share a common ancestral origin of Friedreich's ataxia but vary in age of GAA repeat expansion. <i>Annals of Human Genetics</i> , 2010 , 74, 202-10	2.2	17
33	EGLN1 involvement in high-altitude adaptation revealed through genetic analysis of extreme constitution types defined in Ayurveda. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 18961-6	11.5	122
32	IGVBrowser—a genomic variation resource from diverse Indian populations. <i>Database: the Journal of Biological Databases and Curation</i> , 2010 , 2010, baq022	5	21
31	MtSNPscore: a combined evidence approach for assessing cumulative impact of mitochondrial variations in disease. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 8, S7	3.6	17
30	SCA-LSVD: a repeat-oriented locus-specific variation database for genotype to phenotype correlations in spinocerebellar ataxias. <i>Human Mutation</i> , 2009 , 30, 1037-42	4.7	25
29	Utilizing linkage disequilibrium information from Indian Genome Variation Database for mapping mutations: SCA12 case study. <i>Journal of Genetics</i> , 2009 , 88, 55-60	1.2	4
28	Mapping human genetic diversity in Asia. <i>Science</i> , 2009 , 326, 1541-5	33.3	444
27	Finding Alu in primate genomes with AF-1. <i>Bioinformatics</i> , 2009 , 3, 287-8	1.1	43
26	Whole genome expression and biochemical correlates of extreme constitutional types defined in Ayurveda. <i>Journal of Translational Medicine</i> , 2008 , 6, 48	8.5	106
25	Genetic landscape of the people of India: a canvas for disease gene exploration. <i>Journal of Genetics</i> , 2008 , 87, 3-20	1.2	259
24	Non-random genomic divergence in repetitive sequences of human and chimpanzee in genes of different functional categories. <i>Molecular Genetics and Genomics</i> , 2007 , 277, 441-55	3.1	7
23	SCA 1, SCA 2 & SCA 3/MJD mutations in ataxia syndromes in southern India. <i>Indian Journal of Medical Research</i> , 2007 , 126, 465-70	2.9	13
22	Genome-wide prediction of G4 DNA as regulatory motifs: role in Escherichia coli global regulation. <i>Genome Research</i> , 2006 , 16, 644-55	9.7	249

21	MLC1 gene is associated with schizophrenia and bipolar disorder in Southern India. <i>Biological Psychiatry</i> , 2005 , 58, 16-22	7.9	39
20	Insights into the mutational history and prevalence of SCA1 in the Indian population through anchored polymorphisms. <i>Human Genetics</i> , 2005 , 118, 107-14	6.3	14
19	Post-zygotic de novo trinucleotide repeat expansion at spinocerebellar ataxia type 7 locus: evidence from an Indian family. <i>Journal of Human Genetics</i> , 2005 , 50, 155-157	4.3	22
18	ALU-ring elements in the primate genomes. <i>Genetica</i> , 2005 , 124, 273-89	1.5	23
17	Evidence of a common founder for SCA12 in the Indian population. <i>Annals of Human Genetics</i> , 2005 , 69, 528-34	2.2	60
16	Founder haplotype for Machado-Joseph disease in the Indian population: novel insights from history and polymorphism studies. <i>Archives of Neurology</i> , 2005 , 62, 637-40		26
15	Alu repeat analysis in the complete human genome: trends and variations with respect to genomic composition. <i>Bioinformatics</i> , 2004 , 20, 813-7	7.2	106
14	Evolution and distribution of RNA polymerase II regulatory sites from RNA polymerase III dependant mobile Alu elements. <i>BMC Evolutionary Biology</i> , 2004 , 4, 37	3	43
13	SMARCA2 and THAP11: potential candidates for polyglutamine disorders as evidenced from polymorphism and protein-folding simulation studies. <i>Journal of Human Genetics</i> , 2004 , 49, 596-602	4.3	11
12	Complex phenotypes in an Indian family with homozygous SCA2 mutations. <i>Annals of Neurology</i> , 2004 , 55, 130-3	9.4	25
11	Nonrandom distribution of alu elements in genes of various functional categories: insight from analysis of human chromosomes 21 and 22. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1420-4	8.3	72
10	Origin and instability of GAA repeats: insights from Alu elements. <i>Journal of Biomolecular Structure and Dynamics</i> , 2002 , 20, 253-63	3.6	16
9	CAG repeat instability at SCA2 locus: anchoring CAA interruptions and linked single nucleotide polymorphisms. <i>Human Molecular Genetics</i> , 2001 , 10, 2437-46	5.6	101
8	Molecular analysis of Friedreich's ataxia locus in the Indian population. <i>Acta Neurologica Scandinavica</i> , 2000 , 102, 227-9	3.8	12
7	Cryptic genes: Evolutionary puzzles. <i>Journal of Genetics</i> , 1997 , 76, 147-159	1.2	16
6	Characterization of the negative elements involved in silencing the bgl operon of Escherichia coli: possible roles for DNA gyrase, H-NS, and CRP-cAMP in regulation. <i>Molecular Microbiology</i> , 1997 , 24, 617-27	4.1	61
5	Transcriptional activation of the Escherichia coli bgl operon: negative regulation by DNA structural elements near the promoter. <i>Molecular Microbiology</i> , 1995 , 17, 1085-92	4.1	45
4	Transcriptomic Dynamics of a non-coding trinucleotide repeat expansion disorder SCA12 in iPSC derived neuronal cells: signatures of interferon induced response		1

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| 3 | Genetic differences between extreme and composite constitution types from whole exome sequences reveal actionable variations | 1 |
| 2 | Spatio-temporal dynamics of intra-host variability in SARS-CoV-2 genomes | 3 |
| 1 | Transcriptome analysis and connectivity mapping of <i>Cissampelos pareira</i> L. provides molecular links of ESR1 modulation to viral inhibition | 1 |