Mitali Mukerji

List of Publications by Citations

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	Mapping human genetic diversity in Asia. *Science*, **2009**, 326, 1541-5	33.3	444
91	Genetic landscape of the people of India: a canvas for disease gene exploration. *Journal of Genetics*, **2008**, 87, 3-20	1.2	259
90	Genome-wide prediction of G4 DNA as regulatory motifs: role in Escherichia coli global regulation. *Genome Research*, **2006**, 16, 644-55	9.7	249
89	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, 18961-6	11.5	122
88	Whole genome expression and biochemical correlates of extreme constitutional types defined in Ayurveda. *Journal of Translational Medicine*, **2008**, 6, 48	8.5	106
87	Alu repeat analysis in the complete human genome: trends and variations with respect to genomic composition. *Bioinformatics*, **2004**, 20, 813-7	7.2	106
86	CAG repeat instability at SCA2 locus: anchoring CAA interruptions and linked single nucleotide polymorphisms. *Human Molecular Genetics*, **2001**, 10, 2437-46	5.6	101
85	Recent Admixture in an Indian Population of African Ancestry. *American Journal of Human Genetics*, **2011**, 89, 344	11	78
84	Complex patterns of genomic admixture within southern Africa. *PLoS Genetics*, **2013**, 9, e1003309	6	72
83	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, 1420-4	8.3	72
82	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. *Molecular Microbiology*, **1997**, 24, 617-27	4.1	61
81	Evidence of a common founder for SCA12 in the Indian population. *Annals of Human Genetics*, **2005**, 69, 528-34	2.2	60
80	SNPs in stress-responsive rice genes: validation, genotyping, functional relevance and population structure. *BMC Genomics*, **2012**, 13, 426	4.5	55
79	Transcriptional activation of the Escherichia coli bgl operon: negative regulation by DNA structural elements near the promoter. *Molecular Microbiology*, **1995**, 17, 1085-92	4.1	45
78	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
77	Evolution and distribution of RNA polymerase II regulatory sites from RNA polymerase III dependant mobile Alu elements. *BMC Evolutionary Biology*, **2004**, 4, 37	3	43
76	Finding Alu in primate genomes with AF-1. *Bioinformation*, **2009**, 3, 287-8	1.1	43

75	MLC1 gene is associated with schizophrenia and bipolar disorder in Southern India. *Biological Psychiatry*, **2005**, 58, 16-22	7.9	39
74	Genomic insights into ayurvedic and western approaches to personalized medicine. *Journal of Genetics*, **2016**, 95, 209-28	1.2	38
73	Ayurgenomics: a new way of threading molecular variability for stratified medicine. *ACS Chemical Biology*, **2011**, 6, 875-80	4.9	37
72	Western Indian Rural Gut Microbial Diversity in Extreme Endo-Phenotypes Reveals Signature Microbes. *Frontiers in Microbiology*, **2018**, 9, 118	5.7	31
71	Human satellite-III non-coding RNAs modulate heat-shock-induced transcriptional repression. *Journal of Cell Science*, **2016**, 129, 3541-3552	5.3	30
70	Differential serum cytokine levels are associated with cytokine gene polymorphisms in north Indians with active pulmonary tuberculosis. *Infection, Genetics and Evolution*, **2011**, 11, 1015-22	4.5	28
69	Founder haplotype for Machado-Joseph disease in the Indian population: novel insights from history and polymorphism studies. *Archives of Neurology*, **2005**, 62, 637-40		26
68	Deletion of the APOBEC3B gene strongly impacts susceptibility to falciparum malaria. *Infection, Genetics and Evolution*, **2012**, 12, 142-8	4.5	25
67	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
66	Heat shock factor binding in Alu repeats expands its involvement in stress through an antisense mechanism. *Genome Biology*, **2011**, 12, R117	18.3	25
65	SCA-LSVD: a repeat-oriented locus-specific variation database for genotype to phenotype correlations in spinocerebellar ataxias. *Human Mutation*, **2009**, 30, 1037-42	4.7	25
64	Complex phenotypes in an Indian family with homozygous SCA2 mutations. *Annals of Neurology*, **2004**, 55, 130-3	9.4	25
63	Integrated genomic view of SARS-CoV-2 in India. *Wellcome Open Research*, **2020**, 5, 184	4.8	25
62	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	23
61	From JUNKTto just unexplored noncoding knowledge: the case of transcribed Alus. *Briefings in Functional Genomics*, **2011**, 10, 294-311	4.9	23
60	Recent admixture in an Indian population of African ancestry. *American Journal of Human Genetics*, **2011**, 89, 111-20	11	23
59	ALU-ring elements in the primate genomes. *Genetica*, **2005**, 124, 273-89	1.5	23
58	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	4.3	22

57	IGVBrowser--a genomic variation resource from diverse Indian populations. *Database: the Journal of Biological Databases and Curation*, **2010**, 2010, baq022	5	21
56	Ayurgenomics for stratified medicine: TRISUTRA consortium initiative across ethnically and geographically diverse Indian populations. *Journal of Ethnopharmacology*, **2017**, 197, 274-293	5	20
55	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
54	Comparative Genomics of Host-Symbiont and Free-Living Oceanobacillus Species. *Genome Biology and Evolution*, **2017**, 9, 1175-1182	3.9	18
53	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, 202-10	2.2	17
52	MtSNPscore: a combined evidence approach for assessing cumulative impact of mitochondrial variations in disease. *BMC Bioinformatics*, **2009**, 10 Suppl 8, S7	3.6	17
51	Diverse facets of COMT: from a plausible predictive marker to a potential drug target for schizophrenia. *Current Molecular Medicine*, **2011**, 11, 732-43	2.5	16
50	Cryptic genes: Evolutionary puzzles. *Journal of Genetics*, **1997**, 76, 147-159	1.2	16
49	Origin and instability of GAA repeats: insights from Alu elements. *Journal of Biomolecular Structure and Dynamics*, **2002**, 20, 253-63	3.6	16
48	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
47	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
46	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
45	Insights into the mutational history and prevalence of SCA1 in the Indian population through anchored polymorphisms. *Human Genetics*, **2005**, 118, 107-14	6.3	14
44	Recapitulation of Ayurveda constitution types by machine learning of phenotypic traits. *PLoS ONE*, **2017**, 12, e0185380	3.7	13
43	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
42	SCA 1, SCA 2 & SCA 3/MJD mutations in ataxia syndromes in southern India. *Indian Journal of Medical Research*, **2007**, 126, 465-70	2.9	13
41	Alu-miRNA interactions modulate transcript isoform diversity in stress response and reveal signatures of positive selection. *Scientific Reports*, **2016**, 6, 32348	4.9	12
40	Molecular analysis of Friedreich's ataxia locus in the Indian population. *Acta Neurologica Scandinavica*, **2000**, 102, 227-9	3.8	12

39	IndiGenomes: a comprehensive resource of genetic variants from over 1000 Indian genomes. *Nucleic Acids Research*, **2021**, 49, D1225-D1232	20.1	12
38	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	4.9	12
37	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	4.3	11
36	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
35	Whole exome and targeted gene sequencing to detect pathogenic recessive variants in early onset cerebellar ataxia. *Clinical Genetics*, **2019**, 96, 566-574	4	10
34	Ancestral Variations of the PCDHG Gene Cluster Predispose to Dyslexia in a Multiplex Family. *EBioMedicine*, **2018**, 28, 168-179	8.8	9
33	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
32	Myg1 exonuclease couples the nuclear and mitochondrial translational programs through RNA processing. *Nucleic Acids Research*, **2019**, 47, 5852-5866	20.1	8
31	Investigation of mitochondrial DNA variations among Indian Friedreich's ataxia (FRDA) patients. *Mitochondrion*, **2015**, 25, 1-5	4.9	8
30	Targeted exome sequencing in anti-factor H antibody negative HUS reveals multiple variations. *Clinical and Experimental Nephrology*, **2018**, 22, 653-660	2.5	8
29	Non-random genomic divergence in repetitive sequences of human and chimpanzee in genes of different functional categories. *Molecular Genetics and Genomics*, **2007**, 277, 441-55	3.1	7
28	Adhatoda Vasica attenuates inflammatory and hypoxic responses in preclinical mouse models: potential for repurposing in COVID-19-like conditions. *Respiratory Research*, **2021**, 22, 99	7.3	7
27	A Complete Association of an intronic SNP rs6798742 with Origin of Spinocerebellar Ataxia Type 7-CAG Expansion Loci in the Indian and Mexican Population. *Annals of Human Genetics*, **2017**, 81, 197-204	2.2	6
26	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	1.6	6
25	Multiple Alu Exonization in 3′UTR of a Primate-Specific Isoform of CYP20A1 Creates a Potential miRNA Sponge. *Genome Biology and Evolution*, **2021**, 13,	3.9	5
24	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	4.7	5
23	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
22	Utilizing linkage disequilibrium information from Indian Genome Variation Database for mapping mutations: SCA12 case study. *Journal of Genetics*, **2009**, 88, 55-60	1.2	4

21	Spatio-temporal dynamics of intra-host variability in SARS-CoV-2 genomes.. *Nucleic Acids Research*, **2022**,	20.1	4
20	rescues the hypoxia-dependent severe asthma symptoms and mitochondrial dysfunction. *American Journal of Physiology - Lung Cellular and Molecular Physiology*, **2021**, 320, L757-L769	5.8	4
19	Next-Generation Sequencing for Congenital Nephrotic Syndrome: A Multi-Center Cross-Sectional Study from India. *Indian Pediatrics*, **2021**, 58, 445-451	1.2	4
18	VitiVar: A locus specific database of vitiligo associated genes and variations. *Gene: X*, **2019**, 3, 100018	2.1	3
17	Spatio-temporal dynamics of intra-host variability in SARS-CoV-2 genomes		3
16	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. *Journal of Genetics*, **2018**, 97, 589-609	1.2	2
15	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, 195	4.2	2
14	Genetic Risk Prediction of COVID-19 Susceptibility and Severity in the Indian Population. *Frontiers in Genetics*, **2021**, 12, 714185	4.5	1
13	Transcriptome analysis and connectivity mapping of Cissampelos pareira L. provides molecular links of ESR1 modulation to viral inhibition. *Scientific Reports*, **2021**, 11, 20095	4.9	1
12	Transcriptomic Dynamics of a non-coding trinucleotide repeat expansion disorder SCA12 in iPSC derived neuronal cells: signatures of interferon induced response		1
11	Genetic differences between extreme and composite constitution types from whole exome sequences reveal actionable variations		1
10	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	4.7	1
9	Transcriptome analysis and connectivity mapping of Cissampelos pareira L. provides molecular links of ESR1 modulation to viral inhibition		1
8	Dissecting Human Microbiome for Personalized Therapy **2022**,		1
7	Pharmacogenomic landscape of COVID-19 therapies from Indian population genomes. *Pharmacogenomics*, **2021**, 22, 603-618	2.6	0
6	Genomics and Traditional Indian Ayurvedic Medicine **2016**, 271-292		
5	Understanding Genomic Variations in the Context of Health and Disease: Annotation, Interpretation, and Challenges **2018**, 71-95		
4	Paradigm for disease deconvolution in rare neurodegenerative disorders in Indian population: insights from studies in cerebellar ataxias. *Journal of Genetics*, **2018**, 97, 589-609	1.2	

List of Publications

3	Next-Generation Sequencing for Congenital Nephrotic Syndrome: A Multi-Center Cross-Sectional Study from India. *Indian Pediatrics*, **2021**, 58, 445-451	1.2
2	An insertion map of the Indian population: identification and analysis in 1021 genomes of the IndiGen project.. *NAR Genomics and Bioinformatics*, **2022**, 4, lqac009	3.7
1	Genetic epidemiology of autoinflammatory disease variants in Indian population from 1029 whole genomes.. *Journal of Genetic Engineering and Biotechnology*, **2021**, 19, 183	3.1