

# Kateryna D Makova

## List of Publications by Year in descending order

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Version: 2024-02-01

104  
papers

10,588  
citations

57758

44  
h-index

39675

94  
g-index

119  
all docs

119  
docs citations

119  
times ranked

13902  
citing authors

#	ARTICLE	IF	CITATIONS
1	Constructing a polygenic risk score for childhood obesity using functional data analysis. <i>Econometrics and Statistics</i> , 2023, 25, 66-86.	0.8	3
2	Metabolomic profiling of stool of two-year old children from the <scp>INSIGHT</scp> study reveals links between butyrate and child weight outcomes. <i>Pediatric Obesity</i> , 2022, 17, e12833.	2.8	8
3	Advanced age increases frequencies of de novo mitochondrial mutations in macaque oocytes and somatic tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118740119.	7.1	14
4	INSIGHT responsive parenting educational intervention for firstborns is associated with growth of second-born siblings. <i>Obesity</i> , 2022, 30, 183-190.	3.0	10
5	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
6	Selection and thermostability suggest G-quadruplexes are novel functional elements of the human genome. <i>Genome Research</i> , 2021, 31, 1136-1149.	5.5	20
7	Associations between stool micro-transcriptome, gut microbiota, and infant growth. <i>Journal of Developmental Origins of Health and Disease</i> , 2021, 12, 876-882.	1.4	4
8	Non-B DNA: a major contributor to small- and large-scale variation in nucleotide substitution frequencies across the genome. <i>Nucleic Acids Research</i> , 2021, 49, 1497-1516.	14.5	70
9	Pronounced somatic bottleneck in mitochondrial DNA of human hair. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190175.	4.0	29
10	Dynamic evolution of great ape Y chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26273-26280.	7.1	22
11	Age-related accumulation of de novo mitochondrial mutations in mammalian oocytes and somatic tissues. <i>PLoS Biology</i> , 2020, 18, e3000745.	5.6	62
12	Human L1 Transposition Dynamics Unraveled with Functional Data Analysis. <i>Molecular Biology and Evolution</i> , 2020, 37, 3576-3600.	8.9	2
13	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. <i>Genome Biology and Evolution</i> , 2020, 12, 842-859.	2.5	13
14	Family reunion via error correction: an efficient analysis of duplex sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 96.	2.6	10
15	Title is missing!. , 2020, 18, e3000745.		0
16	Title is missing!. , 2020, 18, e3000745.		0
17	Title is missing!. , 2020, 18, e3000745.		0
18	Title is missing!. , 2020, 18, e3000745.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 18, e3000745.		0
20	Title is missing!. , 2020, 18, e3000745.		0
21	Noise-cancelling repeat finder: uncovering tandem repeats in error-prone long-read sequencing data. <i>Bioinformatics</i> , 2019, 35, 4809-4811.	4.1	37
22	High Satellite Repeat Turnover in Great Apes Studied with Short- and Long-Read Technologies. <i>Molecular Biology and Evolution</i> , 2019, 36, 2415-2431.	8.9	43
23	DiscoverY: a classifier for identifying Y chromosome sequences in male assemblies. <i>BMC Genomics</i> , 2019, 20, 641.	2.8	16
24	Dosage regulation, and variation in gene expression and copy number of human Y chromosome ampliconic genes. <i>PLoS Genetics</i> , 2019, 15, e1008369.	3.5	19
25	Functional data analysis for computational biology. <i>Bioinformatics</i> , 2019, 35, 3211-3213.	4.1	14
26	Bottleneck and selection in the germline and maternal age influence transmission of mitochondrial DNA in human pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25172-25178.	7.1	71
27	Investigating mitonuclear interactions in human admixed populations. <i>Nature Ecology and Evolution</i> , 2019, 3, 213-222.	7.8	60
28	IWTomics: testing high-resolution sequence-based Omics™ data at multiple locations and scales. <i>Bioinformatics</i> , 2018, 34, 2289-2291.	4.1	8
29	RecoverY: k-mer-based read classification for Y-chromosome-specific sequencing and assembly. <i>Bioinformatics</i> , 2018, 34, 1125-1131.	4.1	15
30	A Population Phylogenetic View of Mitochondrial Heteroplasmy. <i>Genetics</i> , 2018, 208, 1261-1274.	2.9	41
31	High Levels of Copy Number Variation of Ampliconic Genes across Major Human Y Haplogroups. <i>Genome Biology and Evolution</i> , 2018, 10, 1333-1350.	2.5	15
32	Long-read sequencing technology indicates genome-wide effects of non-B DNA on polymerization speed and error rate. <i>Genome Research</i> , 2018, 28, 1767-1778.	5.5	55
33	Deciphering highly similar multigene family transcripts from Iso-Seq data with IsoCon. <i>Nature Communications</i> , 2018, 9, 4601.	12.8	54
34	Correcting palindromes in long reads after whole-genome amplification. <i>BMC Genomics</i> , 2018, 19, 798.	2.8	16
35	Child Weight Gain Trajectories Linked To Oral Microbiota Composition. <i>Scientific Reports</i> , 2018, 8, 14030.	3.3	39
36	Deep-Coverage MPS Analysis of Heteroplasmic Variants within the mtGenome Allows for Frequent Differentiation of Maternal Relatives. <i>Genes</i> , 2018, 9, 124.	2.4	30

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37	Y and W Chromosome Assemblies: Approaches and Discoveries. Trends in Genetics, 2017, 33, 266-282.	6.7	95
38	Functional data analysis of "Omics" data: how does the genomic landscape influence integration and fixation of endogenous retroviruses?. Contributions To Statistics, 2017, , 87-93.	0.2	0
39	Streamlined analysis of duplex sequencing data with Du Novo. Genome Biology, 2016, 17, 180.	8.8	24
40	A time- and cost-effective strategy to sequence mammalian Y Chromosomes: an application to the de novo assembly of gorilla Y. Genome Research, 2016, 26, 530-540.	5.5	99
41	Reverse Transcription Errors and RNA "DNA Differences at Short Tandem Repeats. Molecular Biology and Evolution, 2016, 33, 2744-2758.	8.9	15
42	Artifactual mutations resulting from DNA lesions limit detection levels in ultrasensitive sequencing applications. DNA Research, 2016, 23, 547-559.	3.4	51
43	Integration and Fixation Preferences of Human and Mouse Endogenous Retroviruses Uncovered with Functional Data Analysis. PLoS Computational Biology, 2016, 12, e1004956.	3.2	41
44	The effects of chromatin organization on variation in mutation rates in the genome. Nature Reviews Genetics, 2015, 16, 213-223.	16.3	199
45	Accurate typing of short tandem repeats from genome-wide sequencing data and its applications. Genome Research, 2015, 25, 736-749.	5.5	87
46	Using Statistics to Shed Light on the Dynamics of the Human Genome: A Review. Contributions To Statistics, 2015, , 69-85.	0.2	2
47	Controlling for contamination in re-sequencing studies with a reproducible web-based phylogenetic approach. BioTechniques, 2014, 56, 134-141.	1.8	22
48	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15474-15479.	7.1	201
49	Microsatellite Interruptions Stabilize Primate Genomes and Exist as Population-Specific Single Nucleotide Polymorphisms within Individual Human Genomes. PLoS Genetics, 2014, 10, e1004498.	3.5	26
50	The Intervention Nurses Start Infants Growing on Healthy Trajectories (INSIGHT) study. BMC Pediatrics, 2014, 14, 184.	1.7	105
51	Genomic Landscape of Human, Bat, and Ex Vivo DNA Transposon Integrations. Molecular Biology and Evolution, 2014, 31, 1816-1832.	8.9	30
52	Development and assessment of an optimized next-generation DNA sequencing approach for the mtgenome using the Illumina MiSeq. Forensic Science International: Genetics, 2014, 13, 20-29.	3.1	99
53	Gene Survival and Death on the Human Y Chromosome. Molecular Biology and Evolution, 2013, 30, 781-787.	8.9	67
54	The origin, evolution, and functional impact of short insertion "deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	5.5	206

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55	Segmenting the human genome based on states of neutral genetic divergence. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14699-14704.	7.1	18
56	Distinct Mutational Behaviors Differentiate Short Tandem Repeats from Microsatellites in the Human Genome. Genome Biology and Evolution, 2013, 5, 606-620.	2.5	57
57	Rescuing Alu: Recovery of New Inserts Shows LINE-1 Preserves Alu Activity through A-Tail Expansion. PLoS Genetics, 2012, 8, e1002842.	3.5	33
58	A genome-wide analysis of common fragile sites: What features determine chromosomal instability in the human genome?. Genome Research, 2012, 22, 993-1005.	5.5	150
59	Harnessing cloud computing with Galaxy Cloud. Nature Biotechnology, 2011, 29, 972-974.	17.5	100
60	A matter of life or death: How microsatellites emerge in and vanish from the human genome. Genome Research, 2011, 21, 2038-2048.	5.5	65
61	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. Genome Biology, 2011, 12, R59.	8.8	93
62	A Massively Parallel Sequencing Approach Uncovers Ancient Origins and High Genetic Variability of Endangered Przewalski's Horses. Genome Biology and Evolution, 2011, 3, 1096-1106.	2.5	51
63	DO VARIATIONS IN SUBSTITUTION RATES AND MALE MUTATION BIAS CORRELATE WITH LIFE-HISTORY TRAITS? A STUDY OF 32 MAMMALIAN GENOMES. Evolution; International Journal of Organic Evolution, 2011, 65, 2800-2815.	2.3	88
64	A genome-wide view of mutation rate co-variation using multivariate analyses. Genome Biology, 2011, 12, R27.	9.6	37
65	A computational approach to candidate gene prioritization for X-linked mental retardation using annotation-based binary filtering and motif-based linear discriminatory analysis. Biology Direct, 2011, 6, 30.	4.6	11
66	Genome analyses substantiate male mutation bias in many species. BioEssays, 2011, 33, 938-945.	2.5	106
67	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	27.8	400
68	Strong Purifying Selection at Genes Escaping X Chromosome Inactivation. Molecular Biology and Evolution, 2010, 27, 2446-2450.	8.9	35
69	The (r)evolution of SINE versus LINE distributions in primate genomes: Sex chromosomes are important. Genome Research, 2010, 20, 600-613.	5.5	48
70	What Is a Microsatellite: A Computational and Experimental Definition Based upon Repeat Mutational Behavior at A/T and GT/AC Repeats. Genome Biology and Evolution, 2010, 2, 620-635.	2.5	105
71	Evolution and Survival on Eutherian Sex Chromosomes. PLoS Genetics, 2009, 5, e1000568.	3.5	74
72	Ride the wavelet: A multiscale analysis of genomic contexts flanking small insertions and deletions. Genome Research, 2009, 19, 1153-1164.	5.5	27

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73	Evolution of X-Degenerate Y Chromosome Genes in Greater Apes: Conservation of Gene Content in Human and Gorilla, But Not Chimpanzee. <i>Journal of Molecular Evolution</i> , 2009, 68, 134-144.	1.8	25
74	Genomic Analyses of Sex Chromosome Evolution. <i>Annual Review of Genomics and Human Genetics</i> , 2009, 10, 333-354.	6.2	70
75	Coding region structural heterogeneity and turnover of transcription start sites contribute to divergence in expression between duplicate genes. <i>Genome Biology</i> , 2009, 10, R10.	9.6	33
76	Horse Domestication and Conservation Genetics of Przewalski's Horse Inferred from Sex Chromosomal and Autosomal Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 199-208.	8.9	55
77	The genome-wide determinants of human and chimpanzee microsatellite evolution. <i>Genome Research</i> , 2008, 18, 30-38.	5.5	226
78	Human-macaque comparisons illuminate variation in neutral substitution rates. <i>Genome Biology</i> , 2008, 9, R76.	9.6	54
79	A Macaque's-Eye View of Human Insertions and Deletions: Differences in Mechanisms. <i>PLoS Computational Biology</i> , 2007, 3, e176.	3.2	55
80	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007, 17, 960-964.	5.5	122
81	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
82	Mammalian Male Mutation Bias: Impacts of Generation Time and Regional Variation in Substitution Rates. <i>Journal of Molecular Evolution</i> , 2006, 63, 537-544.	1.8	48
83	Genomic Environment Predicts Expression Patterns on the Human Inactive X Chromosome. <i>PLoS Genetics</i> , 2006, 2, e151.	3.5	79
84	Strong and Weak Male Mutation Bias at Different Sites in the Primate Genomes: Insights from the Human-Chimpanzee Comparison. <i>Molecular Biology and Evolution</i> , 2006, 23, 565-573.	8.9	84
85	Oscillating Evolution of a Mammalian Locus with Overlapping Reading Frames: An XLI±s/ALEX Relay. <i>PLoS Genetics</i> , 2005, 1, e18.	3.5	39
86	Worldwide polymorphism at the MC1R locus and normal pigmentation variation in humans. <i>Peptides</i> , 2005, 26, 1901-1908.	2.4	86
87	A macaque's-eye view of human insertions and deletions: differences in mechanisms. <i>PLoS Computational Biology</i> , 2005, preprint, e176.	3.2	2
88	Insertions and Deletions Are Male Biased Too: A Whole-Genome Analysis in Rodents. <i>Genome Research</i> , 2004, 14, 567-573.	5.5	47
89	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
90	COMPARATIVE GENOMICS. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 15-56.	6.2	156

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91	DNA Polymorphism and Selection at the Melanocortin <sup>4</sup> Receptor Gene in Normally Pigmented Southern African Individuals. <i>Annals of the New York Academy of Sciences</i> , 2003, 994, 299-306.	3.8	72
92	Divergence in the Spatial Pattern of Gene Expression Between Human Duplicate Genes. <i>Genome Research</i> , 2003, 13, 1638-1645.	5.5	212
93	The KA/KS Ratio Test for Assessing the Protein-Coding Potential of Genomic Regions: An Empirical and Simulation Study. <i>Genome Research</i> , 2002, 12, 198-202.	5.5	233
94	Male-driven evolution. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 650-656.	3.3	206
95	Chromosome-wide SNPs reveal an ancient origin for <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 418, 323-324.	27.8	141
96	Strong male-driven evolution of DNA sequences in humans and apes. <i>Nature</i> , 2002, 416, 624-626.	27.8	226
97	Tetranucleotide microsatellite markers for the Brown-headed Cowbird <i>Molothrus ater</i> . <i>Journal of Avian Biology</i> , 2001, 32, 76-78.	1.2	10
98	Episodic Evolution of Growth Hormone in Primates and Emergence of the Species Specificity of Human Growth Hormone Receptor. <i>Molecular Biology and Evolution</i> , 2001, 18, 945-953.	8.9	66
99	Human DNA Sequence Variation in a 6.6-kb Region Containing the Melanocortin 1 Receptor Promoter. <i>Genetics</i> , 2001, 158, 1253-1268.	2.9	52
100	Evolution of Microsatellite Alleles in Four Species of Mice (Genus <i>Apodemus</i> ). <i>Journal of Molecular Evolution</i> , 2000, 51, 166-172.	1.8	51
101	Isolation of binary species-specific PCR-based markers and their value for diagnostic applications. <i>Gene</i> , 2000, 249, 47-51.	2.2	11
102	Increased Yield of Tri- and Tetranucleotide Heterospecific Microsatellites from Unenriched Small-Insert Libraries. <i>BioTechniques</i> , 1998, 24, 38-43.	1.8	16
103	An evolutionary view of a biomedically important gene family. <i>Peer Community in Evolutionary Biology</i> , 0, , 100104.	0.0	0
104	Exploring the Effects of Mitonuclear Interactions on Mitochondrial DNA Gene Expression in Humans. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0