

Kateryna D Makova

List of Publications by Year in descending order

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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	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
3	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
4	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010, 463, 943-947.	27.8	400
5	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
6	Strong male-driven evolution of DNA sequences in humans and apes. <i>Nature</i> , 2002, 416, 624-626.	27.8	226
7	The genome-wide determinants of human and chimpanzee microsatellite evolution. <i>Genome Research</i> , 2008, 18, 30-38.	5.5	226
8	Divergence in the Spatial Pattern of Gene Expression Between Human Duplicate Genes. <i>Genome Research</i> , 2003, 13, 1638-1645.	5.5	212
9	Male-driven evolution. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 650-656.	3.3	206
10	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013, 23, 749-761.	5.5	206
11	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15474-15479.	7.1	201
12	The effects of chromatin organization on variation in mutation rates in the genome. <i>Nature Reviews Genetics</i> , 2015, 16, 213-223.	16.3	199
13	COMPARATIVE GENOMICS. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 15-56.	6.2	156
14	A genome-wide analysis of common fragile sites: What features determine chromosomal instability in the human genome?. <i>Genome Research</i> , 2012, 22, 993-1005.	5.5	150
15	Chromosome-wide SNPs reveal an ancient origin for <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 418, 323-324.	27.8	141
16	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
17	Genome analyses substantiate male mutation bias in many species. <i>BioEssays</i> , 2011, 33, 938-945.	2.5	106
18	What Is a Microsatellite: A Computational and Experimental Definition Based upon Repeat Mutational Behavior at A/T and GT/AC Repeats. <i>Genome Biology and Evolution</i> , 2010, 2, 620-635.	2.5	105

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19	The Intervention Nurses Start Infants Growing on Healthy Trajectories (INSIGHT) study. <i>BMC Pediatrics</i> , 2014, 14, 184.	1.7	105
20	Harnessing cloud computing with Galaxy Cloud. <i>Nature Biotechnology</i> , 2011, 29, 972-974.	17.5	100
21	Development and assessment of an optimized next-generation DNA sequencing approach for the mtgenome using the Illumina MiSeq. <i>Forensic Science International: Genetics</i> , 2014, 13, 20-29.	3.1	99
22	A time- and cost-effective strategy to sequence mammalian Y Chromosomes: an application to the de novo assembly of gorilla Y. <i>Genome Research</i> , 2016, 26, 530-540.	5.5	99
23	Y and W Chromosome Assemblies: Approaches and Discoveries. <i>Trends in Genetics</i> , 2017, 33, 266-282.	6.7	95
24	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. <i>Genome Biology</i> , 2011, 12, R59.	8.8	93
25	DO VARIATIONS IN SUBSTITUTION RATES AND MALE MUTATION BIAS CORRELATE WITH LIFE-HISTORY TRAITS? A STUDY OF 32 MAMMALIAN GENOMES. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 2800-2815.	2.3	88
26	Accurate typing of short tandem repeats from genome-wide sequencing data and its applications. <i>Genome Research</i> , 2015, 25, 736-749.	5.5	87
27	Worldwide polymorphism at the MC1R locus and normal pigmentation variation in humans. <i>Peptides</i> , 2005, 26, 1901-1908.	2.4	86
28	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
29	Genomic Environment Predicts Expression Patterns on the Human Inactive X Chromosome. <i>PLoS Genetics</i> , 2006, 2, e151.	3.5	79
30	Evolution and Survival on Eutherian Sex Chromosomes. <i>PLoS Genetics</i> , 2009, 5, e1000568.	3.5	74
31	DNA Polymorphism and Selection at the Melanocortin 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
32	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
33	Genomic Analyses of Sex Chromosome Evolution. <i>Annual Review of Genomics and Human Genetics</i> , 2009, 10, 333-354.	6.2	70
34	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
35	Gene Survival and Death on the Human Y Chromosome. <i>Molecular Biology and Evolution</i> , 2013, 30, 781-787.	8.9	67
36	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

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37	A matter of life or death: How microsatellites emerge in and vanish from the human genome. <i>Genome Research</i> , 2011, 21, 2038-2048.	5.5	65
38	Age-related accumulation of de novo mitochondrial mutations in mammalian oocytes and somatic tissues. <i>PLoS Biology</i> , 2020, 18, e3000745.	5.6	62
39	Investigating mitonuclear interactions in human admixed populations. <i>Nature Ecology and Evolution</i> , 2019, 3, 213-222.	7.8	60
40	Distinct Mutational Behaviors Differentiate Short Tandem Repeats from Microsatellites in the Human Genome. <i>Genome Biology and Evolution</i> , 2013, 5, 606-620.	2.5	57
41	A Macaque's-Eye View of Human Insertions and Deletions: Differences in Mechanisms. <i>PLoS Computational Biology</i> , 2007, 3, e176.	3.2	55
42	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
43	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
44	Human-macaque comparisons illuminate variation in neutral substitution rates. <i>Genome Biology</i> , 2008, 9, R76.	9.6	54
45	Deciphering highly similar multigene family transcripts from Iso-Seq data with IsoCon. <i>Nature Communications</i> , 2018, 9, 4601.	12.8	54
46	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
47	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
48	A Massively Parallel Sequencing Approach Uncovers Ancient Origins and High Genetic Variability of Endangered Przewalski's Horses. <i>Genome Biology and Evolution</i> , 2011, 3, 1096-1106.	2.5	51
49	Artifactual mutations resulting from DNA lesions limit detection levels in ultrasensitive sequencing applications. <i>DNA Research</i> , 2016, 23, 547-559.	3.4	51
50	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
51	The (r)evolution of SINE versus LINE distributions in primate genomes: Sex chromosomes are important. <i>Genome Research</i> , 2010, 20, 600-613.	5.5	48
52	Insertions and Deletions Are Male Biased Too: A Whole-Genome Analysis in Rodents. <i>Genome Research</i> , 2004, 14, 567-573.	5.5	47
53	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
54	A Population Phylogenetic View of Mitochondrial Heteroplasmy. <i>Genetics</i> , 2018, 208, 1261-1274.	2.9	41

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55	Integration and Fixation Preferences of Human and Mouse Endogenous Retroviruses Uncovered with Functional Data Analysis. <i>PLoS Computational Biology</i> , 2016, 12, e1004956.	3.2	41
56	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
57	Child Weight Gain Trajectories Linked To Oral Microbiota Composition. <i>Scientific Reports</i> , 2018, 8, 14030.	3.3	39
58	A genome-wide view of mutation rate co-variation using multivariate analyses. <i>Genome Biology</i> , 2011, 12, R27.	9.6	37
59	Noise-cancelling repeat finder: uncovering tandem repeats in error-prone long-read sequencing data. <i>Bioinformatics</i> , 2019, 35, 4809-4811.	4.1	37
60	Strong Purifying Selection at Genes Escaping X Chromosome Inactivation. <i>Molecular Biology and Evolution</i> , 2010, 27, 2446-2450.	8.9	35
61	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
62	Rescuing Alu: Recovery of New Inserts Shows LINE-1 Preserves Alu Activity through A-Tail Expansion. <i>PLoS Genetics</i> , 2012, 8, e1002842.	3.5	33
63	Genomic Landscape of Human, Bat, and Ex Vivo DNA Transposon Integrations. <i>Molecular Biology and Evolution</i> , 2014, 31, 1816-1832.	8.9	30
64	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
65	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
66	Ride the wavelet: A multiscale analysis of genomic contexts flanking small insertions and deletions. <i>Genome Research</i> , 2009, 19, 1153-1164.	5.5	27
67	Microsatellite Interruptions Stabilize Primate Genomes and Exist as Population-Specific Single Nucleotide Polymorphisms within Individual Human Genomes. <i>PLoS Genetics</i> , 2014, 10, e1004498.	3.5	26
68	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
69	Streamlined analysis of duplex sequencing data with Du Novo. <i>Genome Biology</i> , 2016, 17, 180.	8.8	24
70	Controlling for contamination in re-sequencing studies with a reproducible web-based phylogenetic approach. <i>BioTechniques</i> , 2014, 56, 134-141.	1.8	22
71	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
72	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

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73	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
74	Segmenting the human genome based on states of neutral genetic divergence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14699-14704.	7.1	18
75	Increased Yield of Tri- and Tetranucleotide Heterospecific Microsatellites from Unenriched Small-Insert Libraries. <i>BioTechniques</i> , 1998, 24, 38-43.	1.8	16
76	Correcting palindromes in long reads after whole-genome amplification. <i>BMC Genomics</i> , 2018, 19, 798.	2.8	16
77	DiscoverY: a classifier for identifying Y chromosome sequences in male assemblies. <i>BMC Genomics</i> , 2019, 20, 641.	2.8	16
78	Reverse Transcription Errors and RNA-DNA Differences at Short Tandem Repeats. <i>Molecular Biology and Evolution</i> , 2016, 33, 2744-2758.	8.9	15
79	RecoverY: k-mer-based read classification for Y-chromosome-specific sequencing and assembly. <i>Bioinformatics</i> , 2018, 34, 1125-1131.	4.1	15
80	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
81	Functional data analysis for computational biology. <i>Bioinformatics</i> , 2019, 35, 3211-3213.	4.1	14
82	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
83	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
84	Isolation of binary species-specific PCR-based markers and their value for diagnostic applications. <i>Gene</i> , 2000, 249, 47-51.	2.2	11
85	A computational approach to candidate gene prioritization for X-linked mental retardation using annotation-based binary filtering and motif-based linear discriminatory analysis. <i>Biology Direct</i> , 2011, 6, 30.	4.6	11
86	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
87	Family reunion via error correction: an efficient analysis of duplex sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 96.	2.6	10
88	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
89	IWTomics: testing high-resolution sequence-based Omics data at multiple locations and scales. <i>Bioinformatics</i> , 2018, 34, 2289-2291.	4.1	8
90	Metabolomic profiling of stool of two-year old children from the INSIGHT study reveals links between butyrate and child weight outcomes. <i>Pediatric Obesity</i> , 2022, 17, e12833.	2.8	8

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91	Associations between stool micro-transcriptome, gut microbiota, and infant growth. Journal of Developmental Origins of Health and Disease, 2021, 12, 876-882.	1.4	4
92	Constructing a polygenic risk score for childhood obesity using functional data analysis. Econometrics and Statistics, 2023, 25, 66-86.	0.8	3
93	Human L1 Transposition Dynamics Unraveled with Functional Data Analysis. Molecular Biology and Evolution, 2020, 37, 3576-3600.	8.9	2
94	A macaque's-eye view of human insertions and deletions: differences in mechanisms. PLoS Computational Biology, 2005, preprint, e176.	3.2	2
95	Using Statistics to Shed Light on the Dynamics of the Human Genome: A Review. Contributions To Statistics, 2015, , 69-85.	0.2	2
96	Functional data analysis of "Omic" data: how does the genomic landscape influence integration and fixation of endogenous retroviruses?. Contributions To Statistics, 2017, , 87-93.	0.2	0
97	An evolutionary view of a biomedically important gene family. Peer Community in Evolutionary Biology, 0, , 100104.	0.0	0
98	Title is missing!. , 2020, 18, e3000745.		0
99	Title is missing!. , 2020, 18, e3000745.		0
100	Title is missing!. , 2020, 18, e3000745.		0
101	Title is missing!. , 2020, 18, e3000745.		0
102	Title is missing!. , 2020, 18, e3000745.		0
103	Title is missing!. , 2020, 18, e3000745.		0
104	Exploring the Effects of Mitonuclear Interactions on Mitochondrial DNA Gene Expression in Humans. Frontiers in Genetics, 0, 13, .	2.3	0