

Maxat K Zhabagin

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

371
citations

933447

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28
all docs

28
docs citations

28
times ranked

701
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic polymorphism of 27 Y-STR loci in Kazakh populations from Northern Kazakhstan. <i>Annals of Human Biology</i> , 2022, 49, 87-89.	1.0	6
2	Determining the Area of Ancestral Origin for Individuals From North Eurasia Based on 5,229 SNP Markers. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	3
3	Medieval Super-Grandfather founder of Western Kazakh Clans from Haplogroup C2a1a2-M48. <i>Journal of Human Genetics</i> , 2021, 66, 707-716.	2.3	9
4	Optimizing the genetic prediction of the eye and hair color for North Eurasian populations. <i>BMC Genomics</i> , 2020, 21, 527.	2.8	10
5	The medieval Mongolian roots of Y-chromosomal lineages from South Kazakhstan. <i>BMC Genetics</i> , 2020, 21, 87.	2.7	15
6	Phylogenetic analysis of the Y-chromosome haplogroup C2b-F1067, a dominant paternal lineage in Eastern Eurasia. <i>Journal of Human Genetics</i> , 2020, 65, 823-829.	2.3	11
7	Y-chromosome evidence confirmed the Kerei-Abakh origin of Aksay Kazakhs. <i>Journal of Human Genetics</i> , 2020, 65, 797-803.	2.3	7
8	Analysis of Clan Structure of Tuvans by Y-Chromosome Markers. <i>Russian Journal of Genetics</i> , 2020, 56, 763-768.	0.6	2
9	Genetic entangling of the Tungusic-speaking populations of the Far East: Evens, Evenks, Nanai. <i>Moscow University Anthropology Bulletin (Vestnik Moskovskogo Universiteta Seria XXIII Antropologia)</i> , 2020, , 113-125.	0.1	1
10	Development of the Kazakhstan Y-chromosome haplotype reference database: analysis of 27 Y-STR in Kazakh population. <i>International Journal of Legal Medicine</i> , 2019, 133, 1029-1032.	2.2	20
11	Molecular genealogy of Tusi Lu's family reveals their paternal relationship with Jochi, Genghis Khan's eldest son. <i>Journal of Human Genetics</i> , 2019, 64, 815-820.	2.3	11
12	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019, 3, 966-976.	7.8	135
13	Analysis of the gene pool of the south-eastern Bashkirs in the context of their clan structure (according to the y-chromosome polymorphism). <i>Moscow University Anthropology Bulletin (Vestnik Tj ETQq1 1 0.084314 rgBT /Ove</i>		
14	The gene pool of hunters-reindeer herders of Southern Siberia: Tofalars and Todzhins. <i>Moscow University Anthropology Bulletin (Vestnik Moskovskogo Universiteta Seria XXIII Antropologia)</i> , 2019, , 67-80.	0.1	1
15	Demographic and Genetic Portraits of the Ulchi Population. <i>Russian Journal of Genetics</i> , 2018, 54, 1245-1253.	0.6	2
16	Estimating the impact of the Mongol expansion upon the gene pool of Tuvans. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2018, 22, 611-619.	1.1	5
17	Reconstructing the genetic structure of the Kazakh from clan distribution data. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2018, 22, 895-904.	1.1	5
18	Phylogeography of human Y-chromosome haplogroup Q3-L275 from an academic/citizen science collaboration. <i>BMC Evolutionary Biology</i> , 2017, 17, 18.	3.2	16

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19	Genetic differentiation between upland and lowland populations shapes the Y-chromosomal landscape of West Asia. <i>Human Genetics</i> , 2017, 136, 437-450.	3.8	17
20	The Connection of the Genetic, Cultural and Geographic Landscapes of Transoxiana. <i>Scientific Reports</i> , 2017, 7, 3085.	3.3	22
21	Population biobanks: Organizational models and prospects of application in gene geography and personalized medicine. <i>Russian Journal of Genetics</i> , 2016, 52, 1227-1243.	0.6	26
22	Gene pool of Siberian Tatars: Five ways of origin for five subethnic groups. <i>Molecular Biology</i> , 2016, 50, 860-873.	1.3	4
23	Deep Phylogenetic Analysis of Haplogroup G1 Provides Estimates of SNP and STR Mutation Rates on the Human Y-Chromosome and Reveals Migrations of Iranic Speakers. <i>PLoS ONE</i> , 2015, 10, e0122968.	2.5	35
24	Draft Genome Sequences of Two Clinical Isolates of <i>Mycobacterium tuberculosis</i> from Sputum of Kazakh Patients. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
25	Vitamin D Receptor Gene Polymorphisms in Susceptibility to Tuberculosis in the Kazakh Population in Almaty and Almaty Area. <i>Central Asian Journal of Global Health</i> , 2014, 2, 102.	0.6	1
26	Whole genome sequencing of <i>M.tuberculosis</i> in Kazakhstan: preliminary data. <i>Central Asian Journal of Global Health</i> , 2013, 2, 121.	0.6	0
27	Whole-Genome Sequencing and Genomic Variant Analysis of Kazakh Individuals. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2