

# Georgi Hudjashov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6002085/publications.pdf>

Version: 2024-02-01

24  
papers

2,430  
citations

471509

17  
h-index

610901

24  
g-index

28  
all docs

28  
docs citations

28  
times ranked

3687  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	27.8	360
2	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	5.5	348
3	Most of the extant mtDNA boundaries in south and southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans. <i>BMC Genetics</i> , 2004, 5, 26.	2.7	305
4	Revealing the prehistoric settlement of Australia by Y chromosome and mtDNA analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8726-8730.	7.1	204
5	Climate Change and Postglacial Human Dispersals in Southeast Asia. <i>Molecular Biology and Evolution</i> , 2008, 25, 1209-1218.	8.9	186
6	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32.	28.9	181
7	Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia. <i>American Journal of Human Genetics</i> , 2011, 89, 731-744.	6.2	149
8	Population Genetic Structure in Indian Austroasiatic Speakers: The Role of Landscape Barriers and Sex-Specific Admixture. <i>Molecular Biology and Evolution</i> , 2011, 28, 1013-1024.	8.9	135
9	The Light Skin Allele of SLC24A5 in South Asians and Europeans Shares Identity by Descent. <i>PLoS Genetics</i> , 2013, 9, e1003912.	3.5	93
10	Selective sweep on human amylase genes postdates the split with Neanderthals. <i>Scientific Reports</i> , 2016, 6, 37198.	3.3	67
11	Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. <i>Genome Biology</i> , 2018, 19, 139.	8.8	67
12	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251-284.	0.2	66
13	Complex Patterns of Admixture across the Indonesian Archipelago. <i>Molecular Biology and Evolution</i> , 2017, 34, 2439-2452.	8.9	65
14	Genome-wide DNA methylation and gene expression patterns reflect genetic ancestry and environmental differences across the Indonesian archipelago. <i>PLoS Genetics</i> , 2020, 16, e1008749.	3.5	30
15	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. <i>Scientific Reports</i> , 2017, 7, 13042.	3.3	29
16	Widespread Denisovan ancestry in Island Southeast Asia but no evidence of substantial super-archaic hominin admixture. <i>Nature Ecology and Evolution</i> , 2021, 5, 616-624.	7.8	27
17	Differences in local population history at the finest level: the case of the Estonian population. <i>European Journal of Human Genetics</i> , 2020, 28, 1580-1591.	2.8	23
18	Investigating the origins of eastern Polynesians using genome-wide data from the Leeward Society Isles. <i>Scientific Reports</i> , 2018, 8, 1823.	3.3	22

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19	Global Patterns of Diversity and Selection in Human Tyrosinase Gene. PLoS ONE, 2013, 8, e74307.	2.5	21
20	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. Human Biology, 2013, 85, 251.	0.2	12
21	Small Traditional Human Communities Sustain Genomic Diversity over Microgeographic Scales despite Linguistic Isolation. Molecular Biology and Evolution, 2016, 33, 2273-2284.	8.9	12
22	Genetic architecture of gene regulation in Indonesian populations identifies QTLs associated with global and local ancestries. American Journal of Human Genetics, 2022, 109, 50-65.	6.2	11
23	Episodes of Diversification and Isolation in Island Southeast Asian and Near Oceanian Male Lineages. Molecular Biology and Evolution, 2022, 39, .	8.9	9
24	Chronology of natural selection in Oceanian genomes. IScience, 2022, 25, 104583.	4.1	3