

Omer Gokcumen

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

4,632
citations

218677

26
h-index

138484

58
g-index

72
all docs

72
docs citations

72
times ranked

9091
citing authors

#	ARTICLE	IF	CITATIONS
1	Similarity-Based Analysis of Allele Frequency Distribution among Multiple Populations Identifies Adaptive Genomic Structural Variants. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	6
2	Sex-specific phenotypic effects and evolutionary history of an ancient polymorphic deletion of the human growth hormone receptor. <i>Science Advances</i> , 2021, 7, eabi4476.	10.3	11
3	Protein acylation by saturated very long chain fatty acids and endocytosis are involved in necroptosis. <i>Cell Chemical Biology</i> , 2021, 28, 1298-1309.e7.	5.2	21
4	Evolutionary context of psoriatic immune skin response. <i>Evolution, Medicine and Public Health</i> , 2021, 9, 474-486.	2.5	6
5	An Evolutionary Perspective on the Impact of Genomic Copy Number Variation on Human Health. <i>Journal of Molecular Evolution</i> , 2020, 88, 104-119.	1.8	27
6	Human and Nonhuman Primate Lineage-Specific Footprints in the Salivary Proteome. <i>Molecular Biology and Evolution</i> , 2020, 37, 395-405.	8.9	19
7	Archaic hominin introgression into modern human genomes. <i>American Journal of Physical Anthropology</i> , 2020, 171, 60-73.	2.1	33
8	The Impact of Ancient Genome Studies in Archaeology. <i>Annual Review of Anthropology</i> , 2020, 49, 277-298.	1.5	13
9	Functional Specialization of Human Salivary Glands and Origins of Proteins Intrinsic to Human Saliva. <i>Cell Reports</i> , 2020, 33, 108402.	6.4	54
10	Analysis of Haplotypic Variation and Deletion Polymorphisms Point to Multiple Archaic Introgression Events, Including from Altai Neanderthal Lineage. <i>Genetics</i> , 2020, 215, 497-509.	2.9	17
11	Genome-Wide Selection Scan in an Arabian Peninsula Population Identifies a TNKS Haplotype Linked to Metabolic Traits and Hypertension. <i>Genome Biology and Evolution</i> , 2020, 12, 77-87.	2.5	11
12	Loss-of-function tolerance of enhancers in the human genome. <i>PLoS Genetics</i> , 2020, 16, e1008663.	3.5	12
13	Resolving the Insertion Sites of Polymorphic Duplications Reveals a HERC2 Haplotype under Selection. <i>Genome Biology and Evolution</i> , 2019, 11, 1679-1690.	2.5	6
14	Filamentation Regulatory Pathways Control Adhesion-Dependent Surface Responses in Yeast. <i>Genetics</i> , 2019, 212, 667-690.	2.9	20
15	Fine-Scale Characterization of Genomic Structural Variation in the Human Genome Reveals Adaptive and Biomedically Relevant Hotspots. <i>Genome Biology and Evolution</i> , 2019, 11, 1136-1151.	2.5	41
16	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. <i>American Journal of Physical Anthropology</i> , 2019, 168, 4-26.	2.1	45
17	Independent amylase gene copy number bursts correlate with dietary preferences in mammals. <i>ELife</i> , 2019, 8, .	6.0	78
18	Complex Haplotypes of <i>GSTM1</i> Gene Deletions Harbor Signatures of a Selective Sweep in East Asian Populations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2953-2966.	1.8	8

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19	The Year In Genetic Anthropology: New Lands, New Technologies, New Questions. <i>American Anthropologist</i> , 2018, 120, 266-277.	1.4	5
20	An evolutionary transcriptomics approach links CD36 to membrane remodeling in replicative senescence. <i>Molecular Omics</i> , 2018, 14, 237-246.	2.8	12
21	Structural Variants in Ancient Genomes. <i>Population Genomics</i> , 2018, , 375-391.	0.5	1
22	Complex evolution of the GSTM gene family involves sharing of GSTM1 deletion polymorphism in humans and chimpanzees. <i>BMC Genomics</i> , 2018, 19, 293.	2.8	12
23	Regulation of lipids is central to replicative senescence. <i>Molecular BioSystems</i> , 2017, 13, 498-509.	2.9	69
24	Variation and Functional Impact of Neanderthal Ancestry in Western Asia. <i>Genome Biology and Evolution</i> , 2017, 9, 3516-3524.	2.5	14
25	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. <i>Molecular Biology and Evolution</i> , 2017, 34, 2704-2715.	8.9	57
26	Segmental duplications and evolutionary acquisition of UV damage response in the SPATA31 gene family of primates and humans. <i>BMC Genomics</i> , 2017, 18, 222.	2.8	8
27	VCFtoTree: a user-friendly tool to construct locus-specific alignments and phylogenies from thousands of anthropologically relevant genome sequences. <i>BMC Bioinformatics</i> , 2017, 18, 426.	2.6	14
28	The Multiple Histories of Western Asia: Perspectives from Ancient and Modern Genomes. <i>Human Biology</i> , 2017, 89, 107.	0.2	6
29	Evolution, Function, and Deconstructing Histories: A New Generation of Anthropological Genetics. <i>Human Biology</i> , 2017, 89, 5.	0.2	2
30	Atopic Dermatitis Susceptibility Variants in Filaggrin Hitchhike Hornerin Selective Sweep. <i>Genome Biology and Evolution</i> , 2016, 8, 3240-3255.	2.5	35
31	Recent evolution of the salivary mucin MUC7. <i>Scientific Reports</i> , 2016, 6, 31791.	3.3	30
32	The psoriasis-associated deletion of late cornified envelope genes LCE3B and LCE3C has been maintained under balancing selection since Human Denisovan divergence. <i>BMC Evolutionary Biology</i> , 2016, 16, 265.	3.2	35
33	Next-generation sequencing-based detection of germline L1-mediated transductions. <i>BMC Genomics</i> , 2016, 17, 342.	2.8	7
34	The Evolution and Functional Impact of Human Deletion Variants Shared with Archaic Hominin Genomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 1008-1019.	8.9	45
35	Global Survey of Variation in a Human Olfactory Receptor Gene Reveals Signatures of Non-Neutral Evolution. <i>Chemical Senses</i> , 2015, 40, 481-488.	2.0	31
36	Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. <i>BMC Genomics</i> , 2014, 15, 963.	2.8	46

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37	Geographic Distribution and Adaptive Significance of Genomic Structural Variants: An Anthropological Genetics Perspective. <i>Human Biology</i> , 2014, 86, 260.	0.2	11
38	Impact of constitutional copy number variants on biological pathway evolution. <i>BMC Evolutionary Biology</i> , 2013, 13, 19.	3.2	25
39	Primate genome architecture influences structural variation mechanisms and functional consequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15764-15769.	7.1	80
40	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. <i>Genome Research</i> , 2013, 23, 2042-2052.	5.5	52
41	Balancing Selection on a Regulatory Region Exhibiting Ancient Variation That Predates Human-Neandertal Divergence. <i>PLoS Genetics</i> , 2013, 9, e1003404.	3.5	26
42	Vif Proteins from Diverse Primate Lentiviral Lineages Use the Same Binding Site in APOBEC3G. <i>Journal of Virology</i> , 2013, 87, 11861-11871.	3.4	36
43	Extensive genetic diversity and substructuring among zebrafish strains revealed through copy number variant analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 529-534.	7.1	102
44	Regulatory element copy number differences shape primate expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12656-12661.	7.1	37
45	Landscape of Somatic Retrotransposition in Human Cancers. <i>Science</i> , 2012, 337, 967-971.	12.6	631
46	Mitochondrial DNA and Y Chromosome Variation Provides Evidence for a Recent Common Ancestry between Native Americans and Indigenous Altaians. <i>American Journal of Human Genetics</i> , 2012, 90, 229-246.	6.2	146
47	Mitochondrial DNA and Y Chromosome Variation Provides Evidence for a Recent Common Ancestry between Native Americans and Indigenous Altaians. <i>American Journal of Human Genetics</i> , 2012, 90, 573.	6.2	6
48	Exploring the role of copy number variants in human adaptation. <i>Trends in Genetics</i> , 2012, 28, 245-257.	6.7	126
49	Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. <i>Nature Genetics</i> , 2011, 43, 745-752.	21.4	121
50	Refinement of primate copy number variation hotspots identifies candidate genomic regions evolving under positive selection. <i>Genome Biology</i> , 2011, 12, R52.	8.8	58
51	Biological Ancestries, Kinship Connections, and Projected Identities in Four Central Anatolian Settlements: Insights from Culturally Contextualized Genetic Anthropology. <i>American Anthropologist</i> , 2011, 113, 116-131.	1.4	22
52	Origins and functional impact of copy number variation in the human genome. <i>Nature</i> , 2010, 464, 704-712.	27.8	1,721
53	Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing. <i>Nature Genetics</i> , 2010, 42, 400-405.	21.4	179
54	Y-chromosome and autosomal STR diversity in four proximate settlements in Central Anatolia. <i>Forensic Science International: Genetics</i> , 2010, 4, e135-e137.	3.1	13

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55	A highly annotated whole-genome sequence of a Korean individual. <i>Nature</i> , 2009, 460, 1011-1015.	27.8	295
56	Copy number variants (CNVs) in primate species using array-based comparative genomic hybridization. <i>Methods</i> , 2009, 49, 18-25.	3.8	22
57	Genetic variation in the enigmatic Altaian Kazakhs of South-Central Russia: Insights into Turkic population history. <i>American Journal of Physical Anthropology</i> , 2008, 136, 278-293.	2.1	46
58	Russian Old Believers: Genetic Consequences of Their Persecution and Exile, as Shown by Mitochondrial DNA Evidence. <i>Human Biology</i> , 2008, 80, 203-237.	0.2	10
59	GENETİK VE KAMUSAL ALAN. <i>Ankara Üniversitesi Dil Ve Tarih-Coğrafya Fakültesi Dergisi</i> , 0, , 019-031.	0.8	1