

List of Publications by Citations

Source: <https://exaly.com/author-pdf/9476930/eran-elhaik-publications-by-citations.pdf>

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

69 papers	7,517 citations	24 h-index	78 g-index
78 ext. papers	8,717 ext. citations	10.5 avg, IF	5.88 L-index

#	Paper	IF	Citations
69	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414
68	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008 , 452, 949-55	50.4	1043
67	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
66	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
65	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , 2010 , 327, 343-8	33.3	682
64	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 12168-73	11.5	383
63	On the immortality of television sets: "function" in the human genome according to the evolution-free gospel of ENCODE. <i>Genome Biology and Evolution</i> , 2013 , 5, 578-90	3.9	340
62	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014 , 15, 86	4.5	284
61	Draft genome of the globally widespread and invasive Argentine ant (<i>Linepithema humile</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5673-8	11.5	214
60	Draft genome of the red harvester ant <i>Pogonomyrmex barbatus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5667-72	11.5	200
59	The genome sequence of the leaf-cutter ant <i>Atta cephalotes</i> reveals insights into its obligate symbiotic lifestyle. <i>PLoS Genetics</i> , 2011 , 7, e1002007	6	191
58	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , 2013 , 23, 1235-47	9.7	166
57	Geographic population structure analysis of worldwide human populations infers their biogeographical origins. <i>Nature Communications</i> , 2014 , 5, 3513	17.4	78
56	The "inverse relationship between evolutionary rate and age of mammalian genes" is an artifact of increased genetic distance with rate of evolution and time of divergence. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1-3	8.3	77
55	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020 , 26, 941-951	50.5	50
54	Targeting TMPRSS2 in SARS-CoV-2 Infection. <i>Mayo Clinic Proceedings</i> , 2020 , 95, 1989-1999	6.4	48
53	The GenoChip: a new tool for genetic anthropology. <i>Genome Biology and Evolution</i> , 2013 , 5, 1021-31	3.9	44

51	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021 , 184, 3376-3393	17.42	
50	The missing link of Jewish European ancestry: contrasting the Rhineland and the Khazarian hypotheses. <i>Genome Biology and Evolution</i> , 2013 , 5, 61-74	3.9	36
49	Empirical distributions of F(ST) from large-scale human polymorphism data. <i>PLoS ONE</i> , 2012 , 7, e49837	3.7	32
48	Can GC content at third-codon positions be used as a proxy for isochore composition?. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1829-33	8.3	32
47	Differences in genomic abnormalities among African individuals with monoclonal gammopathies using calculated ancestry. <i>Blood Cancer Journal</i> , 2018 , 8, 96	7	29
46	Localizing Ashkenazic Jews to Primeval Villages in the Ancient Iranian Lands of Ashkenaz. <i>Genome Biology and Evolution</i> , 2016 , 8, 1132-49	3.9	28
45	Dysregulation of the NF- κ B pathway as a potential inducer of bipolar disorder. <i>Journal of Psychiatric Research</i> , 2015 , 70, 18-27	5.2	24
44	The Rextremely ancientRchromosome that isnR: a forensic bioinformatic investigation of Albert PerryR X-degenerate portion of the Y chromosome. <i>European Journal of Human Genetics</i> , 2014 , 22, 1111-16	5.3	19
43	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , 2017 , 5, 132	16.6	18
42	Toward high-resolution population genomics using archaeological samples. <i>DNA Research</i> , 2016 , 23, 295-310	4.5	17
41	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe, The</i> , 2021 , 2, e135-e136	22.2	17
40	Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance		16
39	Comparative testing of DNA segmentation algorithms using benchmark simulations. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1015-24	8.3	15
38	Identifying compositionally homogeneous and nonhomogeneous domains within the human genome using a novel segmentation algorithm. <i>Nucleic Acids Research</i> , 2010 , 38, e158	20.1	13
37	Reconstructing Druze population history. <i>Scientific Reports</i> , 2016 , 6, 35837	4.9	12
36	Gene expression and nucleotide composition are associated with genic methylation level in <i>Oryza sativa</i> . <i>BMC Bioinformatics</i> , 2014 , 15, 23	3.6	12
35	Exonic DNA sequencing of ERBB4 in bipolar disorder. <i>PLoS ONE</i> , 2011 , 6, e20242	3.7	12

34	Forensic Applications of Microbiomics: A Review. <i>Frontiers in Microbiology</i> , 2020 , 11, 608101	5.7	11
33	Ancient Ancestry Informative Markers for Identifying Fine-Scale Ancient Population Structure in Eurasians. <i>Genes</i> , 2018 , 9,	4.2	10
32	The Origins of Ashkenaz, Ashkenazic Jews, and Yiddish. <i>Frontiers in Genetics</i> , 2017 , 8, 87	4.5	8
31	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis.. <i>Neuron</i> , 2022 ,	13.9	8
30	The Diversity of REcent and Ancient huMan (DREAM): A New Microarray for Genetic Anthropology and Genealogy, Forensics, and Personalized Medicine. <i>Genome Biology and Evolution</i> , 2017 , 9, 3225-3237	3.9	7
29	GC3 Biology in Eukaryotes and Prokaryotes 2012 ,		7
28	Geographic variation in plant community structure of salt marshes: species, functional and phylogenetic perspectives. <i>PLoS ONE</i> , 2015 , 10, e0127781	3.7	6
27	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. <i>Cell Reports</i> , 2020 , 33, 108456	10.6	6
26	A "Wear and Tear" Hypothesis to Explain Sudden Infant Death Syndrome. <i>Frontiers in Neurology</i> , 2016 , 7, 180	4.1	6
25	Pair Matcher (PaM): fast model-based optimization of treatment/case-control matches. <i>Bioinformatics</i> , 2019 , 35, 2243-2250	7.2	6
24	A comparative study and a phylogenetic exploration of the compositional architectures of mammalian nuclear genomes. <i>PLoS Computational Biology</i> , 2014 , 10, e1003925	5	5
23	IsoPlotter(+): A Tool for Studying the Compositional Architecture of Genomes. <i>ISRN Bioinformatics</i> , 2013 , 2013, 725434		5
22	Neonatal circumcision and prematurity are associated with sudden infant death syndrome (SIDS). <i>Journal of Clinical and Translational Research</i> , 2019 , 4, 136-151	1.1	5
21	Genome order index should not be used for defining compositional constraints in nucleotide sequences. <i>Computational Biology and Chemistry</i> , 2008 , 32, 147	3.6	4
20	Neonatal circumcision and prematurity are associated with sudden infant death syndrome (SIDS). <i>Journal of Clinical and Translational Research</i> ,	1.1	4
19	In Search of the jüdische Typus: A Proposed Benchmark to Test the Genetic Basis of Jewishness Challenges Notions of "Jewish Biomarkers". <i>Frontiers in Genetics</i> , 2016 , 7, 141	4.5	4
18	aYChr-DB: a database of ancient human Y haplogroups. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa081	3.7	3
17	Genomics and epidemiology for gastric adenocarcinomas (GE4GAC): a Brazilian initiative to study gastric cancer. <i>Applied Cancer Research</i> , 2019 , 39,	1.6	3

16	Why most Principal Component Analyses (PCA) in population genetic studies are wrong		3
15	Population genetic considerations for using biobanks as international resources in the pandemic era and beyond. <i>BMC Genomics</i> , 2021 , 22, 351	4.5	3
14	The Genetics of Sudden Infant Death Syndrome-Towards a Gene Reference Resource. <i>Genes</i> , 2021 , 12,	4.2	3
13	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
12	Reply to Mendez et al: the R extremely ancient R chromosome that still isn R. <i>European Journal of Human Genetics</i> , 2015 , 23, 567-8	5.3	2
11	R genome order index R should not be used for defining compositional constraints in nucleotide sequences--a case study of the Z-curve. <i>Biology Direct</i> , 2010 , 5, 10	7.2	2
10	Genome-wide Identification of the Genetic Basis of Amyotrophic Lateral Sclerosis		2
9	Loop-Mediated Isothermal Amplification Detection of SARS-CoV-2 and Myriad Other Applications.. <i>Journal of Biomolecular Techniques</i> , 2021 , 32, 228-275	1.1	2
8	The CCND1 c.870G risk allele is enriched in individuals of African ancestry with plasma cell dyscrasias. <i>Blood Cancer Journal</i> , 2020 , 10, 39	7	1
7	HapZipper: sharing HapMap populations just got easier. <i>Nucleic Acids Research</i> , 2012 , 40, e159	20.1	1
6	Ancient ancestry informative markers for identifying fine-scale ancient population structure in Eurasians		1
5	On the Unfounded Enthusiasm for Soft Selective Sweeps III: The Supervised Machine Learning Algorithm That Isn R. <i>Genes</i> , 2021 , 12,	4.2	1
4	The impact of cross-kingdom molecular forensics on genetic privacy. <i>Microbiome</i> , 2021 , 9, 114	16.6	0
3	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. <i>Blood</i> , 2021 , 138, 4101-4101	2.2	
2	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. <i>Blood</i> , 2018 , 132, 4458-4458	2.2	
1	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. <i>Blood</i> , 2019 , 134, 4362-4362	2.2	