

Eran Elhaik

List of Publications by Year in Descending Order

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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	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis.. <i>Neuron</i> , 2022 ,	13.9	8
68	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. <i>Blood</i> , 2021 , 138, 4101-4101	2.2	
67	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , 2021 , 2, e135-e136	2.2	17
66	On the Unfounded Enthusiasm for Soft Selective Sweeps III: The Supervised Machine Learning Algorithm That Isn't. <i>Genes</i> , 2021 , 12,	4.2	1
65	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
64	The impact of cross-kingdom molecular forensics on genetic privacy. <i>Microbiome</i> , 2021 , 9, 114	16.6	0
63	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021 , 184, 3376-3393	36.17	42
62	The Genetics of Sudden Infant Death Syndrome-Towards a Gene Reference Resource. <i>Genes</i> , 2021 , 12,	4.2	3
61	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
60	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
59	aYChr-DB: a database of ancient human Y haplogroups. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa0817	0.17	3
58	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020 , 26, 941-951	50.5	50
57	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
56	Targeting TMPRSS2 in SARS-CoV-2 Infection. <i>Mayo Clinic Proceedings</i> , 2020 , 95, 1989-1999	6.4	48
55	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. <i>Cell Reports</i> , 2020 , 33, 108456	10.6	6
54	Forensic Applications of Microbiomics: A Review. <i>Frontiers in Microbiology</i> , 2020 , 11, 608101	5.7	11
53	Genomics and epidemiology for gastric adenocarcinomas (GE4GAC): a Brazilian initiative to study gastric cancer. <i>Applied Cancer Research</i> , 2019 , 39,	1.6	3

52	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
51	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. <i>Blood</i> , 2019 , 134, 4362-4362	2.2	
50	Pair Matcher (PaM): fast model-based optimization of treatment/case-control matches. <i>Bioinformatics</i> , 2019 , 35, 2243-2250	7.2	6
49	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. <i>Blood</i> , 2018 , 132, 4458-4458	2.2	
48	Ancient Ancestry Informative Markers for Identifying Fine-Scale Ancient Population Structure in Eurasians. <i>Genes</i> , 2018 , 9,	4.2	10
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	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , 2017 , 5, 132	16.6	18
45	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
44	The Origins of Ashkenaz, Ashkenazic Jews, and Yiddish. <i>Frontiers in Genetics</i> , 2017 , 8, 87	4.5	8
43	Toward high-resolution population genomics using archaeological samples. <i>DNA Research</i> , 2016 , 23, 295-310	4.5	17
42	Reconstructing Druze population history. <i>Scientific Reports</i> , 2016 , 6, 35837	4.9	12
41	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
40	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
39	A "Wear and Tear" Hypothesis to Explain Sudden Infant Death Syndrome. <i>Frontiers in Neurology</i> , 2016 , 7, 180	4.1	6
38	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
37	Reply to Mendez et al: the Rextremely ancientRchromosome that still isnR. <i>European Journal of Human Genetics</i> , 2015 , 23, 567-8	5.3	2
36	Geographic variation in plant community structure of salt marshes: species, functional and phylogenetic perspectives. <i>PLoS ONE</i> , 2015 , 10, e0127781	3.7	6
35	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014 , 15, 86	4.5	284

34	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
33	The extremely ancient R chromosome that isn't: a forensic bioinformatic investigation of Albert Perry's X-degenerate portion of the Y chromosome. <i>European Journal of Human Genetics</i> , 2014 , 22, 1111-16	5.3	19
32	Geographic population structure analysis of worldwide human populations infers their biogeographical origins. <i>Nature Communications</i> , 2014 , 5, 3513	17.4	78
31	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
30	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
29	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
28	The GenoChip: a new tool for genetic anthropology. <i>Genome Biology and Evolution</i> , 2013 , 5, 1021-31	3.9	44
27	Cross-species analysis of genic GC3 content and DNA methylation patterns. <i>Genome Biology and Evolution</i> , 2013 , 5, 1443-56	3.9	42
26	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
25	IsoPlotter(+): A Tool for Studying the Compositional Architecture of Genomes. <i>ISRN Bioinformatics</i> , 2013 , 2013, 725434		5
24	Empirical distributions of F(ST) from large-scale human polymorphism data. <i>PLoS ONE</i> , 2012 , 7, e49837	3.7	32
23	GC3 Biology in Eukaryotes and Prokaryotes 2012 ,		7
22	HapZipper: sharing HapMap populations just got easier. <i>Nucleic Acids Research</i> , 2012 , 40, e159	20.1	1
21	Exonic DNA sequencing of ERBB4 in bipolar disorder. <i>PLoS ONE</i> , 2011 , 6, e20242	3.7	12
20	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
19	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
18	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
17	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

16	Comparative testing of DNA segmentation algorithms using benchmark simulations. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1015-24	8.3	15
15	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
14	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , 2010 , 327, 343-8	33.3	682
13	Genome order index 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
12	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
11	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
10	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008 , 452, 949-55	50.4	1043
9	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
8	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
7	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
6	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414
5	Neonatal circumcision and prematurity are associated with sudden infant death syndrome (SIDS). <i>Journal of Clinical and Translational Research</i> ,	1.1	4
4	Genome-wide Identification of the Genetic Basis of Amyotrophic Lateral Sclerosis		2
3	Ancient ancestry informative markers for identifying fine-scale ancient population structure in Eurasians		1
2	Global Genetic Cartography of Urban Metagenomes and Anti-Microbial Resistance		16
1	Why most Principal Component Analyses (PCA) in population genetic studies are wrong		3