Alon Keinan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7065976/publications.pdf

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78	39,854	76196	69108
papers	citations	40 h-index	77 g-index

96	96	96	60543
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
4	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
5	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
6	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
7	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	3.8	612
8	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	3.3	589
9	Recent Explosive Human Population Growth Has Resulted in an Excess of Rare Genetic Variants. Science, 2012, 336, 740-743.	6.0	489
10	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
11	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
12	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
13	The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology. Genome Research, 2017, 27, 1916-1929.	2.4	273
14	The landscape of human STR variation. Genome Research, 2014, 24, 1894-1904.	2.4	256
15	Deleterious- and Disease-Allele Prevalence in Healthy Individuals: Insights from Current Predictions, Mutation Databases, and Population-Scale Resequencing. American Journal of Human Genetics, 2012, 91, 1022-1032.	2.6	255
16	Measurement of the human allele frequency spectrum demonstrates greater genetic drift in East Asians than in Europeans. Nature Genetics, 2007, 39, 1251-1255.	9.4	249
17	The History of African Gene Flow into Southern Europeans, Levantines, and Jews. PLoS Genetics, 2011, 7, e1001373.	1.5	224
18	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	15.2	212

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19	Extensive pathogenicity of mitochondrial heteroplasmy in healthy human individuals. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10654-10659.	3.3	208
20	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	1.5	185
21	Accelerated genetic drift on chromosome X during the human dispersal out of Africa. Nature Genetics, 2009, 41, 66-70.	9.4	143
22	Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics, 2013, 45, 723-729.	9.4	121
23	XWAS: A Software Toolset for Genetic Data Analysis and Association Studies of the X Chromosome. Journal of Heredity, 2015, 106, 666-671.	1.0	109
24	Neutral genomic regions refine models of recent rapid human population growth. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 757-762.	3.3	106
25	Population Genetic Inference from Personal Genome Data: Impact of Ancestry and Admixture on Human Genomic Variation. American Journal of Human Genetics, 2012, 91, 660-671.	2.6	100
26	Accounting for eXentricities: Analysis of the X Chromosome in GWAS Reveals X-Linked Genes Implicated in Autoimmune Diseases. PLoS ONE, 2014, 9, e113684.	1.1	100
27	Fair Attribution of Functional Contribution in Artificial and Biological Networks. Neural Computation, 2004, 16, 1887-1915.	1.3	93
28	Gene-Based Testing of Interactions in Association Studies of Quantitative Traits. PLoS Genetics, 2013, 9, e1003321.	1.5	89
29	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. Genome Research, 2016, 26, 151-162.	2.4	89
30	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. Nature Genetics, 2011, 43, 741-743.	9.4	81
31	Human Population Differentiation Is Strongly Correlated with Local Recombination Rate. PLoS Genetics, 2010, 6, e1000886.	1.5	78
32	Positive Selection on a Regulatory Insertionâ€“Deletion Polymorphism inFADS2Influences Apparent Endogenous Synthesis of Arachidonic Acid. Molecular Biology and Evolution, 2016, 33, 1726-1739.	3.5	76
33	Population Growth Inflates the Per-Individual Number of Deleterious Mutations and Reduces Their Mean Effect. Genetics, 2013, 195, 969-978.	1.2	71
34	Combining Evidence of Natural Selection with Association Analysis Increases Power to Detect Malaria-Resistance Variants. American Journal of Human Genetics, 2007, 81, 234-242.	2.6	68
35	Knowledge-Driven Analysis Identifies a Geneâ€“Gene Interaction Affecting High-Density Lipoprotein Cholesterol Levels in Multi-Ethnic Populations. PLoS Genetics, 2012, 8, e1002714.	1.5	64
36	Dietary adaptation of FADS genes in Europe varied across time and geography. Nature Ecology and Evolution, 2017, 1, 167.	3.4	62

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37	Contrasting X-Linked and Autosomal Diversity across 14 Human Populations. American Journal of Human Genetics, 2014, 94, 827-844.	2.6	61
38	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	2.4	52
39	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. Nature Communications, 2019, 10, 4141.	5.8	48
40	Axiomatic Scalable Neurocontroller Analysis via the Shapley Value. Artificial Life, 2006, 12, 333-352.	1.0	46
41	Mitochondrial DNA variants correlate with symptoms in myalgic encephalomyelitis/chronic fatigue syndrome. Journal of Translational Medicine, 2016, 14, 19.	1.8	42
42	Selection for Translation Efficiency on Synonymous Polymorphisms in Recent Human Evolution. Genome Biology and Evolution, 2011, 3, 749-761.	1.1	41
43	Can a Sex-Biased Human Demography Account for the Reduced Effective Population Size of Chromosome X in Non-Africans?. Molecular Biology and Evolution, 2010, 27, 2312-2321.	3.5	39
44	Quantitative Analysis of Genetic and Neuronal Multi-Perturbation Experiments. PLoS Computational Biology, 2005, 1, e64.	1.5	30
45	NRE: a tool for exploring neutral loci in the human genome. BMC Bioinformatics, 2012, 13, 301.	1.2	29
46	Inference of Super-exponential Human Population Growth via Efficient Computation of the Site Frequency Spectrum for Generalized Models. Genetics, 2016, 202, 235-245.	1.2	29
47	Detecting natural selection by empirical comparison to random regions of the genome. Human Molecular Genetics, 2009, 18, 4853-4867.	1.4	27
48	Explosive genetic evidence for explosive human population growth. Current Opinion in Genetics and Development, 2016, 41, 130-139.	1.5	26
49	X-inactivation informs variance-based testing for X-linked association of a quantitative trait. BMC Genomics, 2015, 16, 241.	1.2	25
50	Neural Processing of Counting in Evolved Spiking and McCulloch-Pitts Agents. Artificial Life, 2006, 12, 1-16.	1.0	23
51	Sex-Averaged Recombination and Mutation Rates on the X Chromosome: A Comment on Labuda etÂal.. American Journal of Human Genetics, 2010, 86, 978-980.	2.6	22
52	Causal localization of neural function: the Shapley value method. Neurocomputing, 2004, 58-60, 215-222.	3.5	21
53	Strong Constraint on Human Genes Escaping X-Inactivation Is Modulated by their Expression Level and Breadth in Both Sexes. Molecular Biology and Evolution, 2016, 33, 384-393.	3.5	20
54	Principal Component Analysis Characterizes Shared Pathogenetics from Genome-Wide Association Studies. PLoS Computational Biology, 2014, 10, e1003820.	1.5	19

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55	High burden of private mutations due to explosive human population growth and purifying selection. BMC Genomics, 2014, 15, S3.	1.2	17
56	The Genetics of Bene Israel from India Reveals Both Substantial Jewish and Indian Ancestry. PLoS ONE, 2016, 11, e0152056.	1.1	17
57	Predicting Signatures of â€œSynthetic Associationsâ€•and â€œNatural Associationsâ€•from Empirical Patterns of Human Genetic Variation. PLoS Computational Biology, 2012, 8, e1002600.	1.5	14
58	Interaction between SNPs in the RXRA and near ANGPTL3 gene region inhibits apoB reduction after statin-fenofibric acid therapy in individuals with mixed dyslipidemia. Journal of Lipid Research, 2012, 53, 2425-2428.	2.0	14
59	Clustered mutations in hominid genome evolution are consistent with APOBEC3G enzymatic activity. Genome Research, 2016, 26, 579-587.	2.4	14
60	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644.	1.1	13
61	Fair Localization of Function Via Multi-Lesion Analysis. Neuroinformatics, 2004, 2, 163-168.	1.5	12
62	The utility of ancient human DNA for improving allele age estimates, with implications for demographic models and tests of natural selection. Journal of Human Evolution, 2015, 79, 64-72.	1.3	12
63	The genetic history of Cochin Jews from India. Human Genetics, 2016, 135, 1127-1143.	1.8	12
64	Biological Knowledge-Driven Analysis of Epistasis in Human GWAS with Application to Lipid Traits. Methods in Molecular Biology, 2015, 1253, 35-45.	0.4	11
65	Analysis of Multiple Association Studies Provides Evidence of an Expression QTL Hub in Gene-Gene Interaction Network Affecting HDL Cholesterol Levels. PLoS ONE, 2014, 9, e92469.	1.1	10
66	Rare LPL gene variants attenuate triglyceride reduction and HDL cholesterol increase in response to fenofibric acid therapy in individuals with mixed dyslipidemia. Atherosclerosis, 2014, 234, 249-253.	0.4	10
67	Association between rs2294020 in X-linked CCDC22 and susceptibility to autoimmune diseases with focus on systemic lupus erythematosus. Immunology Letters, 2017, 181, 58-62.	1.1	9
68	Controlled analysis of neurocontrollers with informational lesioning. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2003, 361, 2123-2144.	1.6	7
69	Reply to Just et al.: Mitochondrial DNA heteroplasmy could be reliably detected with massively parallel sequencing technologies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4548-E4550.	3.3	7
70	Combining Sparse Group Lasso and Linear Mixed Model Improves Power to Detect Genetic Variants Underlying Quantitative Traits. Frontiers in Genetics, 2019, 10, 271.	1.1	5
71	Spikes that count: rethinking spikiness in neurally embedded systems. Neurocomputing, 2004, 58-60, 303-311.	3.5	4
72	Association of mitochondrial DNA variants with myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) symptoms. Journal of Translational Medicine, 2016, 14, 342.	1.8	4

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73	Crowdsourced genealogies and genomes. Science, 2018, 360, 153-154.	6.0	4
74	Gene-Based Nonparametric Testing of Interactions Using Distance Correlation Coefficient in Case-Control Association Studies. Genes, 2018, 9, 608.	1.0	4
75	Evolutionary Network Minimization: Adaptive Implicit Pruning of Successful Agents. Lecture Notes in Computer Science, 2003, , 319-327.	1.0	3
76	Solving a Delayed Response Task with Spiking and McCulloch-Pitts Agents. Lecture Notes in Computer Science, 2003, , 199-208.	1.0	2
77	Neurocontroller Analysis via Evolutionary Network Minimization. Artificial Life, 2006, 12, 435-448.	1.0	2
78	Genome sequencing and analysis of admixed genomes of African and Mexican ancestry: implications for personal ancestry reconstruction and multi-ethnic medical genomics. Genome Biology, 2010, 11, .	3.8	1