Alon Keinan

List of Publications by Year
in descending order

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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	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. Nature Communications, 2019, 10, 4141.	5.8	48
2	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
3	Crowdsourced genealogies and genomes. Science, 2018, 360, 153-154.	6.0	4
4	Gene-Based Nonparametric Testing of Interactions Using Distance Correlation Coefficient in Case-Control Association Studies. Genes, 2018, 9, 608.	1.0	4
5	Dietary adaptation of FADS genes in Europe varied across time and geography. Nature Ecology and Evolution, 2017, 1, 167.	3.4	62
6	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
7	The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology. Genome Research, 2017, 27, 1916-1929.	2.4	273
8	The Genetics of Bene Israel from India Reveals Both Substantial Jewish and Indian Ancestry. PLoS ONE, 2016, 11, e0152056.	1.1	17
9	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
10	Association of mitochondrial DNA variants with myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) symptoms. Journal of Translational Medicine, 2016, 14, 342.	1.8	4
11	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
12	Clustered mutations in hominid genome evolution are consistent with APOBEC3G enzymatic activity. Genome Research, 2016, 26, 579-587.	2.4	14
13	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
14	Explosive genetic evidence for explosive human population growth. Current Opinion in Genetics and Development, 2016, 41, 130-139.	1.5	26
15	The genetic history of Cochin Jews from India. Human Genetics, 2016, 135, 1127-1143.	1.8	12
16	Mitochondrial DNA variants correlate with symptoms in myalgic encephalomyelitis/chronic fatigue syndrome. Journal of Translational Medicine, 2016, 14, 19.	1.8	42
17	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. Genome Research, 2016, 26, 151-162.	2.4	89
18	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

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19	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
20	X-inactivation informs variance-based testing for X-linked association of a quantitative trait. BMC Genomics, 2015, 16, 241.	1.2	25
21	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
22	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	3.8	612
23	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	15.2	212
24	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
25	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
26	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
27	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
28	Principal Component Analysis Characterizes Shared Pathogenetics from Genome-Wide Association Studies. PLoS Computational Biology, 2014, 10, e1003820.	1.5	19
29	The landscape of human STR variation. Genome Research, 2014, 24, 1894-1904.	2.4	256
30	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
31	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
32	Contrasting X-Linked and Autosomal Diversity across 14 Human Populations. American Journal of Human Genetics, 2014, 94, 827-844.	2.6	61
33	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
34	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
35	High burden of private mutations due to explosive human population growth and purifying selection. BMC Genomics, 2014, 15, S3.	1.2	17
36	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

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37	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
38	Population Growth Inflates the Per-Individual Number of Deleterious Mutations and Reduces Their Mean Effect. Genetics, 2013, 195, 969-978.	1.2	71
39	Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics, 2013, 45, 723-729.	9.4	121
40	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	2.4	52
41	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	1.5	185
42	Gene-Based Testing of Interactions in Association Studies of Quantitative Traits. PLoS Genetics, 2013, 9, e1003321.	1.5	89
43	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
44	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
45	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
46	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
47	NRE: a tool for exploring neutral loci in the human genome. BMC Bioinformatics, 2012, 13, 301.	1.2	29
48	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
49	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
50	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
51	Recent Explosive Human Population Growth Has Resulted in an Excess of Rare Genetic Variants. Science, 2012, 336, 740-743.	6.0	489
52	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
53	Selection for Translation Efficiency on Synonymous Polymorphisms in Recent Human Evolution. Genome Biology and Evolution, 2011, 3, 749-761.	1.1	41
54	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991

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55	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
56	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. Nature Genetics, 2011, 43, 741-743.	9.4	81
57	The History of African Gene Flow into Southern Europeans, Levantines, and Jews. PLoS Genetics, 2011, 7, e1001373.	1.5	224
58	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
59	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
60	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
61	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
62	Human Population Differentiation Is Strongly Correlated with Local Recombination Rate. PLoS Genetics, 2010, 6, e1000886.	1.5	78
63	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
64	Detecting natural selection by empirical comparison to random regions of the genome. Human Molecular Genetics, 2009, 18, 4853-4867.	1.4	27
65	Accelerated genetic drift on chromosome X during the human dispersal out of Africa. Nature Genetics, 2009, 41, 66-70.	9.4	143
66	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
67	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
68	Neurocontroller Analysis via Evolutionary Network Minimization. Artificial Life, 2006, 12, 435-448.	1.0	2
69	Neural Processing of Counting in Evolved Spiking and McCulloch-Pitts Agents. Artificial Life, 2006, 12, 1-16.	1.0	23
70	Axiomatic Scalable Neurocontroller Analysis via the Shapley Value. Artificial Life, 2006, 12, 333-352.	1.0	46
71	Quantitative Analysis of Genetic and Neuronal Multi-Perturbation Experiments. PLoS Computational Biology, 2005, 1, e64.	1.5	30
72	Fair Attribution of Functional Contribution in Artificial and Biological Networks. Neural Computation, 2004, 16, 1887-1915.	1.3	93

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73	Causal localization of neural function: the Shapley value method. Neurocomputing, 2004, 58-60, 215-222.	3.5	21
74	Spikes that count: rethinking spikiness in neurally embedded systems. Neurocomputing, 2004, 58-60, 303-311.	3.5	4
75	Fair Localization of Function Via Multi-Lesion Analysis. Neuroinformatics, 2004, 2, 163-168.	1.5	12
76	Solving a Delayed Response Task with Spiking and McCulloch-Pitts Agents. Lecture Notes in Computer Science, 2003, , 199-208.	1.0	2
77	Controlled analysis of neurocontrollers with informational lesioning. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2003, 361, 2123-2144.	1.6	7
78	Evolutionary Network Minimization: Adaptive Implicit Pruning of Successful Agents. Lecture Notes in Computer Science, 2003, , 319-327.	1.0	3