Alon Keinan

List of Publications by Year in Descending Order

79 papers	29,735 citations	39 h-index	96 g-index
96 ext. papers	36,220 ext. citations	12.9 avg, IF	6.36 L-index

#	Paper	IF	Citations
79	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. *Nature Communications*, **2019**, 10, 4141	17.4	23
78	Combining Sparse Group Lasso and Linear Mixed Model Improves Power to Detect Genetic Variants Underlying Quantitative Traits. *Frontiers in Genetics*, **2019**, 10, 271	4.5	4
77	Crowdsourced genealogies and genomes. *Science*, **2018**, 360, 153-154	33.3	3
76	Gene-Based Nonparametric Testing of Interactions Using Distance Correlation Coefficient in Case-Control Association Studies. *Genes*, **2018**, 9,	4.2	3
75	Dietary adaptation of FADS genes in Europe varied across time and geography. *Nature Ecology and Evolution*, **2017**, 1, 167	12.3	41
74	Association between rs2294020 in X-linked CCDC22 and susceptibility to autoimmune diseases with focus on systemic lupus erythematosus. *Immunology Letters*, **2017**, 181, 58-62	4.1	5
73	The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology. *Genome Research*, **2017**, 27, 1916-1929	9.7	156
72	The genetic history of Cochin Jews from India. *Human Genetics*, **2016**, 135, 1127-43	6.3	8
71	Mitochondrial DNA variants correlate with symptoms in myalgic encephalomyelitis/chronic fatigue syndrome. *Journal of Translational Medicine*, **2016**, 14, 19	8.5	32
70	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. *Genome Research*, **2016**, 26, 151-62	9.7	60
69	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, 384-93	8.3	12
68	The Genetics of Bene Israel from India Reveals Both Substantial Jewish and Indian Ancestry. *PLoS ONE*, **2016**, 11, e0152056	3.7	12
67	Inference of Super-exponential Human Population Growth via Efficient Computation of the Site Frequency Spectrum for Generalized Models. *Genetics*, **2016**, 202, 235-45	4	24
66	Association of mitochondrial DNA variants with myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) symptoms. *Journal of Translational Medicine*, **2016**, 14, 342	8.5	3
65	Positive Selection on a Regulatory Insertion-Deletion Polymorphism in FADS2 Influences Apparent Endogenous Synthesis of Arachidonic Acid. *Molecular Biology and Evolution*, **2016**, 33, 1726-39	8.3	57
64	Clustered mutations in hominid genome evolution are consistent with APOBEC3G enzymatic activity. *Genome Research*, **2016**, 26, 579-87	9.7	11
63	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, **2016**, 48, 593-9	36.3	204

62	Explosive genetic evidence for explosive human population growth. *Current Opinion in Genetics and Development*, **2016**, 41, 130-139	4.9	19
61	X-inactivation informs variance-based testing for X-linked association of a quantitative trait. *BMC Genomics*, **2015**, 16, 241	4.5	16
60	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
59	Host genetic variation impacts microbiome composition across human body sites. *Genome Biology*, **2015**, 16, 191	18.3	428
58	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. *Nature Medicine*, **2015**, 21, 1018-27	50.5	143
57	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	3.1	9
56	XWAS: A Software Toolset for Genetic Data Analysis and Association Studies of the X Chromosome. *Journal of Heredity*, **2015**, 106, 666-71	2.4	68
55	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. *PLoS ONE*, **2015**, 10, e0121644	3.7	12
54	Biological knowledge-driven analysis of epistasis in human GWAS with application to lipid traits. *Methods in Molecular Biology*, **2015**, 1253, 35-45	1.4	9
53	Contrasting X-linked and autosomal diversity across 14 human populations. *American Journal of Human Genetics*, **2014**, 94, 827-44	11	39
52	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, E4548-50	11.5	6
51	Extensive pathogenicity of mitochondrial heteroplasmy in healthy human individuals. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 10654-9	11.5	160
50	High burden of private mutations due to explosive human population growth and purifying selection. *BMC Genomics*, **2014**, 15 Suppl 4, S3	4.5	14
49	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	3.7	9
48	Principal component analysis characterizes shared pathogenetics from genome-wide association studies. *PLoS Computational Biology*, **2014**, 10, e1003820	5	13
47	The landscape of human STR variation. *Genome Research*, **2014**, 24, 1894-904	9.7	157
46	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, 757-62	11.5	86
45	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, 249-53	3.1	8

44	Accounting for eXentricities: analysis of the X chromosome in GWAS reveals X-linked genes implicated in autoimmune diseases. *PLoS ONE*, **2014**, 9, e113684	3.7	71
43	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
42	Population growth inflates the per-individual number of deleterious mutations and reduces their mean effect. *Genetics*, **2013**, 195, 969-78	4	50
41	Genome-wide inference of natural selection on human transcription factor binding sites. *Nature Genetics*, **2013**, 45, 723-9	36.3	95
40	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. *Genome Research*, **2013**, 23, 2042-52	9.7	41
39	Reconstructing Native American migrations from whole-genome and whole-exome data. *PLoS Genetics*, **2013**, 9, e1004023	6	137
38	Gene-based testing of interactions in association studies of quantitative traits. *PLoS Genetics*, **2013**, 9, e1003321	6	67
37	The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62	21.6	202
36	NRE: a tool for exploring neutral loci in the human genome. *BMC Bioinformatics*, **2012**, 13, 301	3.6	20
35	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
34	Population genetic inference from personal genome data: impact of ancestry and admixture on human genomic variation. *American Journal of Human Genetics*, **2012**, 91, 660-71	11	77
33	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, 1022-32	11	221
32	Recent explosive human population growth has resulted in an excess of rare genetic variants. *Science*, **2012**, 336, 740-3	33.3	387
31	A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **2012**, 335, 823-8	33.3	880
30	Knowledge-driven analysis identifies a gene-gene interaction affecting high-density lipoprotein cholesterol levels in multi-ethnic populations. *PLoS Genetics*, **2012**, 8, e1002714	6	55
29	Predicting signatures of "synthetic associations" and "natural associations" from empirical patterns of human genetic variation. *PLoS Computational Biology*, **2012**, 8, e1002600	5	13
28	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, 2425-8	6.3	11
27	Selection for translation efficiency on synonymous polymorphisms in recent human evolution. *Genome Biology and Evolution*, **2011**, 3, 749-61	3.9	37

26	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
25	Demographic history and rare allele sharing among human populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11983-8	11.5	455
24	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. *Nature Genetics*, **2011**, 43, 741-3	36.3	63
23	The history of African gene flow into Southern Europeans, Levantines, and Jews. *PLoS Genetics*, **2011**, 7, e1001373	6	175
22	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
21	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
20	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, 2312-21	8.3	29
19	Human population differentiation is strongly correlated with local recombination rate. *PLoS Genetics*, **2010**, 6, e1000886	6	62
18	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,	18.3	78
17	Sex-averaged recombination and mutation rates on the X chromosome: a comment on Labuda et al. *American Journal of Human Genetics*, **2010**, 86, 978-80; author reply 980-1	11	17
16	Detecting natural selection by empirical comparison to random regions of the genome. *Human Molecular Genetics*, **2009**, 18, 4853-67	5.6	25
15	Accelerated genetic drift on chromosome X during the human dispersal out of Africa. *Nature Genetics*, **2009**, 41, 66-70	36.3	109
14	Measurement of the human allele frequency spectrum demonstrates greater genetic drift in East Asians than in Europeans. *Nature Genetics*, **2007**, 39, 1251-5	36.3	212
13	Combining evidence of natural selection with association analysis increases power to detect malaria-resistance variants. *American Journal of Human Genetics*, **2007**, 81, 234-42	11	60
12	Axiomatic scalable neurocontroller analysis via the Shapley value. *Artificial Life*, **2006**, 12, 333-52	1.4	30
11	Neurocontroller analysis via evolutionary network minimization. *Artificial Life*, **2006**, 12, 435-48	1.4	2
10	Neural processing of counting in evolved spiking and McCulloch-Pitts agents. *Artificial Life*, **2006**, 12, 1-16	1.4	22
9	Quantitative analysis of genetic and neuronal multi-perturbation experiments. *PLoS Computational Biology*, **2005**, 1, e64	5	27

8	Fair attribution of functional contribution in artificial and biological networks. *Neural Computation*, **2004**, 16, 1887-915	2.9	75
7	Causal localization of neural function: the Shapley value method. *Neurocomputing*, **2004**, 58-60, 215-222	5.4	12
6	Spikes that count: rethinking spikiness in neurally embedded systems. *Neurocomputing*, **2004**, 58-60, 303-311	5.4	3
5	Fair localization of function via multi-lesion analysis. *Neuroinformatics*, **2004**, 2, 163-8	3.2	12
4	Solving a Delayed Response Task with Spiking and McCulloch-Pitts Agents. *Lecture Notes in Computer Science*, **2003**, 199-208	0.9	1
3	Controlled analysis of neurocontrollers with informational lesioning. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2003**, 361, 2123-44	3	6
2	Evolutionary Network Minimization: Adaptive Implicit Pruning of Successful Agents. *Lecture Notes in Computer Science*, **2003**, 319-327	0.9	1
1	Dietary adaptation of FADS genes in Europe varied across time and geography		1