Itsik Pe'er

List of Publications by Year
in descending order

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104	17,479	76326	60623
papers	citations	40 h-index	81 g-index

115	115	115	27284
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
3	Efficiency and power in genetic association studies. Nature Genetics, 2005, 37, 1217-1223.	21.4	1,597
4	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	27.8	1,063
5	HLA-B*5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. Nature Genetics, 2009, 41, 816-819.	21.4	950
6	De novo mutations in histone-modifying genes in congenital heart disease. Nature, 2013, 498, 220-223.	27.8	798
7	Estimation of the multiple testing burden for genomewide association studies of nearly all common variants. Genetic Epidemiology, 2008, 32, 381-385.	1.3	699
8	Two independent alleles at 6q23 associated with risk of rheumatoid arthritis. Nature Genetics, 2007, 39, 1477-1482.	21.4	497
9	Whole population, genome-wide mapping of hidden relatedness. Genome Research, 2009, 19, 318-326.	5.5	411
10	Web-Based, Participant-Driven Studies Yield Novel Genetic Associations for Common Traits. PLoS Genetics, 2010, 6, e1000993.	3.5	399
11	Copy Number Variants in Schizophrenia: Confirmation of Five Previous Findings and New Evidence for 3q29 Microdeletions and VIPR2 Duplications. American Journal of Psychiatry, 2011, 168, 302-316.	7.2	398
12	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641.	28.9	300
13	FEAST: fast expectation-maximization for microbial source tracking. Nature Methods, 2019, 16, 627-632.	19.0	275
14	Evaluating and improving power in whole-genome association studies using fixed marker sets. Nature Genetics, 2006, 38, 663-667.	21.4	274
15	Functional variants in the LRRK2 gene confer shared effects on risk for Crohnâ€™s disease and Parkinsonâ€™s disease. Science Translational Medicine, 2018, 10, .	12.4	273
16	Length Distributions of Identity by Descent Reveal Fine-Scale Demographic History. American Journal of Human Genetics, 2012, 91, 809-822.	6.2	240
17	Identity inference of genomic data using long-range familial searches. Science, 2018, 362, 690-694.	12.6	235
18	Abraham's Children in the Genome Era: Major Jewish Diaspora Populations Comprise Distinct Genetic Clusters with Shared Middle Eastern Ancestry. American Journal of Human Genetics, 2010, 86, 850-859.	6.2	217

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19	Caenorhabditis elegans mutant allele identification by whole-genome sequencing. Nature Methods, 2008, 5, 865-867.	19.0	214
20	Cryptic Distant Relatives Are Common in Both Isolated and Cosmopolitan Genetic Samples. PLoS ONE, 2012, 7, e34267.	2.5	184
21	Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins. Nature Communications, 2014, 5, 4835.	12.8	156
22	A Genome-Wide Scan of Ashkenazi Jewish Crohn's Disease Suggests Novel Susceptibility Loci. PLoS Genetics, 2012, 8, e1002559.	3.5	144
23	Proteomic signatures: Amino acid and oligopeptide compositions differentiate among phyla. Proteins: Structure, Function and Bioinformatics, 2003, 54, 20-40.	2.6	130
24	Common SNPs in HMGCR in Micronesians and Whites Associated With LDL-Cholesterol Levels Affect Alternative Splicing of Exon13. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 2078-2084.	2.4	120
25	arcasHLA: high-resolution HLA typing from RNAseq. Bioinformatics, 2020, 36, 33-40.	4.1	113
26	Genome-wide association study implicates NDST3 in schizophrenia and bipolar disorder. Nature Communications, 2013, 4, 2739.	12.8	101
27	Statistical correction of the Winnerâ€™s Curse explains replication variability in quantitative trait genome-wide association studies. PLoS Genetics, 2017, 13, e1006916.	3.5	101
28	Ultrafast genome-wide scan for SNPâ€“SNP interactions in common complex disease. Genome Research, 2012, 22, 2230-2240.	5.5	96
29	The Architecture of Long-Range Haplotypes Shared within and across Populations. Molecular Biology and Evolution, 2012, 29, 473-486.	8.9	93
30	Genome-Wide Association Studies in an Isolated Founder Population from the Pacific Island of Kosrae. PLoS Genetics, 2009, 5, e1000365.	3.5	89
31	DASH: A Method for Identical-by-Descent Haplotype Mapping Uncovers Association with Recent Variation. American Journal of Human Genetics, 2011, 88, 706-717.	6.2	77
32	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	6.2	77
33	Elevated GM3 plasma concentration in idiopathic Parkinsonâ€™s disease: A lipidomic analysis. PLoS ONE, 2017, 12, e0172348.	2.5	69
34	Overlapping pools for high-throughput targeted resequencing. Genome Research, 2009, 19, 1254-1261.	5.5	68
35	Inference of historical migration rates via haplotype sharing. Bioinformatics, 2013, 29, i180-i188.	4.1	68
36	Evaluating potential for whole-genome studies in Kosrae, an isolated population in Micronesia. Nature Genetics, 2006, 38, 214-217.	21.4	61

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37	Incomplete Directed Perfect Phylogeny. SIAM Journal on Computing, 2004, 33, 590-607.	1.0	54
38	A Frameshift in CSF2RB Predominant Among Ashkenazi Jews Increases Risk for Crohn's Disease and Reduces Monocyte Signaling via GM-CSF. Gastroenterology, 2016, 151, 710-723.e2.	1.3	51
39	North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13865-13870.	7.1	49
40	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Human Molecular Genetics, 2014, 23, 4693-4702.	2.9	49
41	Implications for health and disease in the genetic signature of the Ashkenazi Jewish population. Genome Biology, 2012, 13, R2.	9.6	48
42	Compositional Lotka-Volterra describes microbial dynamics in the simplex. PLoS Computational Biology, 2020, 16, e1007917.	3.2	46
43	Biases and Reconciliation in Estimates of Linkage Disequilibrium in the Human Genome. American Journal of Human Genetics, 2006, 78, 588-603.	6.2	43
44	Comparing Platforms for C. elegans Mutant Identification Using High-Throughput Whole-Genome Sequencing. PLoS ONE, 2008, 3, e4012.	2.5	40
45	The Variance of Identity-by-Descent Sharing in the Wrightâ€“Fisher Model. Genetics, 2013, 193, 911-928.	2.9	38
46	Predicting Phenotypic Polymyxin Resistance in Klebsiella pneumoniae through Machine Learning Analysis of Genomic Data. MSystems, 2020, 5, .	3.8	35
47	A renewal theory approach to IBD sharing. Theoretical Population Biology, 2014, 97, 35-48.	1.1	34
48	Expanded genetic screening panel for the Ashkenazi Jewish population. Genetics in Medicine, 2016, 18, 522-528.	2.4	33
49	Allelic Selection of Amplicons in Glioblastoma Revealed by Combining Somatic and Germline Analysis. PLoS Genetics, 2010, 6, e1001086.	3.5	27
50	Independent evidence for an association between general cognitive ability and a genetic locus for educational attainment. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 363-373.	1.7	25
51	The time and place of European admixture in Ashkenazi Jewish history. PLoS Genetics, 2017, 13, e1006644.	3.5	25
52	Increased power of mixed models facilitates association mapping of 10 loci for metabolic traits in an isolated population. Human Molecular Genetics, 2011, 20, 827-839.	2.9	24
53	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. Human Genetics, 2018, 137, 343-355.	3.8	24
54	Systematic haplotype analysis resolves a complex plasma plant sterol locus on the Micronesian Island of Kosrae. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13886-13891.	7.1	23

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55	Inference of Population Structure from Time-Series Genotype Data. American Journal of Human Genetics, 2019, 105, 317-333.	6.2	23
56	Accurate and robust inference of microbial growth dynamics from metagenomic sequencing reveals personalized growth rates. Genome Research, 2022, 32, 558-568.	5.5	23
57	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. Neuron, 2021, 109, 1465-1478.e4.	8.1	21
58	Detecting Identity by Descent and Homozygosity Mapping in Whole-Exome Sequencing Data. PLoS ONE, 2012, 7, e47618.	2.5	20
59	Excess of homozygosity in the major histocompatibility complex in schizophrenia. Human Molecular Genetics, 2014, 23, 6088-6095.	2.9	18
60	Bias Characterization in Probabilistic Genotype Data and Improved Signal Detection with Multiple Imputation. PLoS Genetics, 2016, 12, e1006091.	3.5	17
61	Realizing Interval Graphs with Size and Distance Constraints. SIAM Journal on Discrete Mathematics, 1997, 10, 662-687.	0.8	16
62	Nonlinear partial differential equations and applications: A computational method for resequencing long DNA targets by universal oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15492-15496.	7.1	14
63	HLA Type Inference via Haplotypes Identical by Descent. Journal of Computational Biology, 2011, 18, 483-493.	1.6	14
64	Inference of modules associated to eQTLs. Nucleic Acids Research, 2012, 40, e98-e98.	14.5	12
65	Efficient and Accurate Inference of Mixed Microbial Population Trajectories from Longitudinal Count Data. Cell Systems, 2020, 10, 463-469.e6.	6.2	12
66	European admixture on the Micronesian island of Kosrae: lessons from complete genetic information. European Journal of Human Genetics, 2010, 18, 309-316.	2.8	11
67	Calling amplified haplotypes in next generation tumor sequence data. Genome Research, 2012, 22, 362-374.	5.5	10
68	Power to detect selective allelic amplification in genome-wide scans of tumor data. Bioinformatics, 2010, 26, 518-528.	4.1	9
69	ABC Transporters and the Proteasome Complex Are Implicated in Susceptibility to Stevensâ€“Johnson Syndrome and Toxic Epidermal Necrolysis across Multiple Drugs. PLoS ONE, 2015, 10, e0131038.	2.5	9
70	Inference of Population Structure from Ancient DNA. Lecture Notes in Computer Science, 2018, , 90-104.	1.3	9
71	An Introduction to Whole-Metagenome Shotgun Sequencing Studies. Methods in Molecular Biology, 2021, 2243, 107-122.	0.9	8
72	Computational Problems in Perfect Phylogeny Haplotyping: Typing without Calling the Allele. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 101-109.	3.0	6

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73	On the applicability of a haplotype map to un-assayed populations. Human Genetics, 2004, 114, 214-217.	3.8	4
74	Leveraging correlations between variants in polygenic risk scores to detect heterogeneity in GWAS cohorts. PLoS Genetics, 2020, 16, e1009015.	3.5	4
75	Advanced computational techniques for re-sequencing DNA with polymerase signaling assay arrays. Nucleic Acids Research, 2003, 31, 5667-5675.	14.5	3
76	Typing without calling the allele: a strategy for inferring SNP haplotypes. European Journal of Human Genetics, 2005, 13, 898-901.	2.8	3
77	Directional Gaussian Mixture Models of the Gut Microbiome Elucidate Microbial Spatial Structure. MSystems, 2021, 6, e0081721.	3.8	3
78	Estimation of the Multiple Testing Burden for Genomewide Association Studies of Common Variants. Nature Precedings, 2007, , .	0.1	2
79	Ultra-Rare Exonic Variants Identified in a Founder Population Implicate Cadherins and Protocadherins in Schizophrenia. Biological Psychiatry, 2021, 89, S83.	1.3	2
80	2-Way k-Means as a Model for Microbiome Samples. Journal of Healthcare Engineering, 2017, 2017, 1-7.	1.9	1
81	A Recovery Algorithm and Pooling Designs for One-Stage Noisy Group Testing Under the Probabilistic Framework. Lecture Notes in Computer Science, 2021, , 42-53.	1.3	1
82	Recovering Frequencies of Known Haplotype Blocks From Single-Nucleotide Polymorphism Allele Frequencies. Genetics, 2004, 166, 2001-2006.	2.9	1
83	METASEQ: PRIVACY PRESERVING META-ANALYSIS OF SEQUENCING-BASED ASSOCIATION STUDIES. , 2012, , .		1
84	An Algorithm Combining Discrete and Continuous Methods for Optical Mapping. Journal of Computational Biology, 2000, 7, 745-760.	1.6	0
85	A parametric Bayesian method to test the association of rare variants. , 2011, , .		0
86	Workshop: Coverage tradeoffs and power estimation in the design of whole-genome sequencing experiments for detecting association. , 2011, , .		0
87	Co-regulated Transcripts Associated to Cooperating eSNPs Define Bi-fan Motifs in Human Gene Networks. PLoS Genetics, 2014, 10, e1004587.	3.5	0
88	Rapidly Registering Identity-by-Descent Across Ancestral Recombination Graphs. Journal of Computational Biology, 2016, 23, 495-507.	1.6	0
89	Autoencoding Topographic Factors. Journal of Computational Biology, 2019, 26, 546-560.	1.6	0
90	Rapidly Registering Identity-by-Descent Across Ancestral Recombination Graphs. Lecture Notes in Computer Science, 2015, , 340-353.	1.3	0

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91	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
92	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
93	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
94	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
95	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
96	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
97	Title is missing!. , 2020, 16, e1009015.		0
98	Title is missing!. , 2020, 16, e1009015.		0
99	Title is missing!. , 2020, 16, e1009015.		0
100	Title is missing!. , 2020, 16, e1009015.		0
101	Title is missing!. , 2020, 16, e1009015.		0
102	Title is missing!. , 2020, 16, e1009015.		0
103	P514. Excess of Homozygous Ultra-Rare Exonic Variants in Schizophrenia: Evidence for Recessive Effects. Biological Psychiatry, 2022, 91, S296-S297.	1.3	0
104	MiSDEED: a synthetic data engine for microbiome study power analysis and study design. Bioinformatics Advances, 0, , .	2.4	0