

# Itsik Pe'er

## List of Publications by Year in descending order

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Version: 2024-02-01

104  
papers

17,479  
citations

76326

40  
h-index

60623

81  
g-index

115  
all docs

115  
docs citations

115  
times ranked

27284  
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate and robust inference of microbial growth dynamics from metagenomic sequencing reveals personalized growth rates. <i>Genome Research</i> , 2022, 32, 558-568.	5.5	23
2	P514. Excess of Homozygous Ultra-Rare Exonic Variants in Schizophrenia: Evidence for Recessive Effects. <i>Biological Psychiatry</i> , 2022, 91, S296-S297.	1.3	0
3	An Introduction to Whole-Metagenome Shotgun Sequencing Studies. <i>Methods in Molecular Biology</i> , 2021, 2243, 107-122.	0.9	8
4	A Recovery Algorithm and Pooling Designs for One-Stage Noisy Group Testing Under the Probabilistic Framework. <i>Lecture Notes in Computer Science</i> , 2021, , 42-53.	1.3	1
5	Ultra-Rare Exonic Variants Identified in a Founder Population Implicate Cadherins and Protocadherins in Schizophrenia. <i>Biological Psychiatry</i> , 2021, 89, S83.	1.3	2
6	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. <i>Neuron</i> , 2021, 109, 1465-1478.e4.	8.1	21
7	Directional Gaussian Mixture Models of the Gut Microbiome Elucidate Microbial Spatial Structure. <i>MSystems</i> , 2021, 6, e0081721.	3.8	3
8	arcasHLA: high-resolution HLA typing from RNAseq. <i>Bioinformatics</i> , 2020, 36, 33-40.	4.1	113
9	Leveraging correlations between variants in polygenic risk scores to detect heterogeneity in GWAS cohorts. <i>PLoS Genetics</i> , 2020, 16, e1009015.	3.5	4
10	Predicting Phenotypic Polymyxin Resistance in <i>Klebsiella pneumoniae</i> through Machine Learning Analysis of Genomic Data. <i>MSystems</i> , 2020, 5, .	3.8	35
11	Efficient and Accurate Inference of Mixed Microbial Population Trajectories from Longitudinal Count Data. <i>Cell Systems</i> , 2020, 10, 463-469.e6.	6.2	12
12	Compositional Lotka-Volterra describes microbial dynamics in the simplex. <i>PLoS Computational Biology</i> , 2020, 16, e1007917.	3.2	46
13	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
14	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
15	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
16	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
17	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0
18	Compositional Lotka-Volterra describes microbial dynamics in the simplex. , 2020, 16, e1007917.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 16, e1009015.		0
20	Title is missing!. , 2020, 16, e1009015.		0
21	Title is missing!. , 2020, 16, e1009015.		0
22	Title is missing!. , 2020, 16, e1009015.		0
23	Title is missing!. , 2020, 16, e1009015.		0
24	Title is missing!. , 2020, 16, e1009015.		0
25	Inference of Population Structure from Time-Series Genotype Data. American Journal of Human Genetics, 2019, 105, 317-333.	6.2	23
26	FEAST: fast expectation-maximization for microbial source tracking. Nature Methods, 2019, 16, 627-632.	19.0	275
27	Autoencoding Topographic Factors. Journal of Computational Biology, 2019, 26, 546-560.	1.6	0
28	Inference of Population Structure from Ancient DNA. Lecture Notes in Computer Science, 2018, , 90-104.	1.3	9
29	Functional variants in the <i>LRRK2</i> gene confer shared effects on risk for Crohn's disease and Parkinson's disease. Science Translational Medicine, 2018, 10, .	12.4	273
30	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
31	Identity inference of genomic data using long-range familial searches. Science, 2018, 362, 690-694.	12.6	235
32	2-Way <i>k</i> -Means as a Model for Microbiome Samples. Journal of Healthcare Engineering, 2017, 2017, 1-7.	1.9	1
33	The time and place of European admixture in Ashkenazi Jewish history. PLoS Genetics, 2017, 13, e1006644.	3.5	25
34	Statistical correction of the Winner's Curse explains replication variability in quantitative trait genome-wide association studies. PLoS Genetics, 2017, 13, e1006916.	3.5	101
35	Elevated GM3 plasma concentration in idiopathic Parkinson's disease: A lipidomic analysis. PLoS ONE, 2017, 12, e0172348.	2.5	69
36	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

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37	Rapidly Registering Identity-by-Descent Across Ancestral Recombination Graphs. <i>Journal of Computational Biology</i> , 2016, 23, 495-507.	1.6	0
38	Expanded genetic screening panel for the Ashkenazi Jewish population. <i>Genetics in Medicine</i> , 2016, 18, 522-528.	2.4	33
39	Bias Characterization in Probabilistic Genotype Data and Improved Signal Detection with Multiple Imputation. <i>PLoS Genetics</i> , 2016, 12, e1006091.	3.5	17
40	Independent evidence for an association between general cognitive ability and a genetic locus for educational attainment. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 363-373.	1.7	25
41	ABC Transporters and the Proteasome Complex Are Implicated in Susceptibility to Stevensâ€“Johnson Syndrome and Toxic Epidermal Necrolysis across Multiple Drugs. <i>PLoS ONE</i> , 2015, 10, e0131038.	2.5	9
42	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. <i>American Journal of Human Genetics</i> , 2015, 97, 775-789.	6.2	77
43	Rapidly Registering Identity-by-Descent Across Ancestral Recombination Graphs. <i>Lecture Notes in Computer Science</i> , 2015, , 340-353.	1.3	0
44	Co-regulated Transcripts Associated to Cooperating eSNPs Define Bi-fan Motifs in Human Gene Networks. <i>PLoS Genetics</i> , 2014, 10, e1004587.	3.5	0
45	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. <i>Human Molecular Genetics</i> , 2014, 23, 4693-4702.	2.9	49
46	A renewal theory approach to IBD sharing. <i>Theoretical Population Biology</i> , 2014, 97, 35-48.	1.1	34
47	Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins. <i>Nature Communications</i> , 2014, 5, 4835.	12.8	156
48	Excess of homozygosity in the major histocompatibility complex in schizophrenia. <i>Human Molecular Genetics</i> , 2014, 23, 6088-6095.	2.9	18
49	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. <i>Cell</i> , 2013, 152, 633-641.	28.9	300
50	De novo mutations in histone-modifying genes in congenital heart disease. <i>Nature</i> , 2013, 498, 220-223.	27.8	798
51	The Variance of Identity-by-Descent Sharing in the Wrightâ€“Fisher Model. <i>Genetics</i> , 2013, 193, 911-928.	2.9	38
52	Inference of historical migration rates via haplotype sharing. <i>Bioinformatics</i> , 2013, 29, i180-i188.	4.1	68
53	Genome-wide association study implicates NDST3 in schizophrenia and bipolar disorder. <i>Nature Communications</i> , 2013, 4, 2739.	12.8	101
54	A Genome-Wide Scan of Ashkenazi Jewish Crohn's Disease Suggests Novel Susceptibility Loci. <i>PLoS Genetics</i> , 2012, 8, e1002559.	3.5	144

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55	Inference of modules associated to eQTLs. <i>Nucleic Acids Research</i> , 2012, 40, e98-e98.	14.5	12
56	Calling amplified haplotypes in next generation tumor sequence data. <i>Genome Research</i> , 2012, 22, 362-374.	5.5	10
57	The Architecture of Long-Range Haplotypes Shared within and across Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 473-486.	8.9	93
58	Ultrafast genome-wide scan for SNP-SNP interactions in common complex disease. <i>Genome Research</i> , 2012, 22, 2230-2240.	5.5	96
59	Implications for health and disease in the genetic signature of the Ashkenazi Jewish population. <i>Genome Biology</i> , 2012, 13, R2.	9.6	48
60	Length Distributions of Identity by Descent Reveal Fine-Scale Demographic History. <i>American Journal of Human Genetics</i> , 2012, 91, 809-822.	6.2	240
61	Cryptic Distant Relatives Are Common in Both Isolated and Cosmopolitan Genetic Samples. <i>PLoS ONE</i> , 2012, 7, e34267.	2.5	184
62	North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13865-13870.	7.1	49
63	Detecting Identity by Descent and Homozygosity Mapping in Whole-Exome Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e47618.	2.5	20
64	METASEQ: PRIVACY PRESERVING META-ANALYSIS OF SEQUENCING-BASED ASSOCIATION STUDIES. , 2012, , .		1
65	A parametric Bayesian method to test the association of rare variants. , 2011, , .		0
66	Workshop: Coverage tradeoffs and power estimation in the design of whole-genome sequencing experiments for detecting association. , 2011, , .		0
67	DASH: A Method for Identical-by-Descent Haplotype Mapping Uncovers Association with Recent Variation. <i>American Journal of Human Genetics</i> , 2011, 88, 706-717.	6.2	77
68	Copy Number Variants in Schizophrenia: Confirmation of Five Previous Findings and New Evidence for 3q29 Microdeletions and VIPR2 Duplications. <i>American Journal of Psychiatry</i> , 2011, 168, 302-316.	7.2	398
69	HLA Type Inference via Haplotypes Identical by Descent. <i>Journal of Computational Biology</i> , 2011, 18, 483-493.	1.6	14
70	Increased power of mixed models facilitates association mapping of 10 loci for metabolic traits in an isolated population. <i>Human Molecular Genetics</i> , 2011, 20, 827-839.	2.9	24
71	Abraham's Children in the Genome Era: Major Jewish Diaspora Populations Comprise Distinct Genetic Clusters with Shared Middle Eastern Ancestry. <i>American Journal of Human Genetics</i> , 2010, 86, 850-859.	6.2	217
72	European admixture on the Micronesian island of Kosrae: lessons from complete genetic information. <i>European Journal of Human Genetics</i> , 2010, 18, 309-316.	2.8	11

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73	Allelic Selection of Amplicons in Glioblastoma Revealed by Combining Somatic and Germline Analysis. PLoS Genetics, 2010, 6, e1001086.	3.5	27
74	Power to detect selective allelic amplification in genome-wide scans of tumor data. Bioinformatics, 2010, 26, 518-528.	4.1	9
75	Web-Based, Participant-Driven Studies Yield Novel Genetic Associations for Common Traits. PLoS Genetics, 2010, 6, e1000993.	3.5	399
76	Whole population, genome-wide mapping of hidden relatedness. Genome Research, 2009, 19, 318-326.	5.5	411
77	Overlapping pools for high-throughput targeted resequencing. Genome Research, 2009, 19, 1254-1261.	5.5	68
78	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
79	Genome-Wide Association Studies in an Isolated Founder Population from the Pacific Island of Kosrae. PLoS Genetics, 2009, 5, e1000365.	3.5	89
80	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	27.8	1,063
81	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
82	Estimation of the multiple testing burden for genomewide association studies of nearly all common variants. Genetic Epidemiology, 2008, 32, 381-385.	1.3	699
83	Caenorhabditis elegans mutant allele identification by whole-genome sequencing. Nature Methods, 2008, 5, 865-867.	19.0	214
84	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
85	Common SNPs in HMGR 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
86	Comparing Platforms for C. elegans Mutant Identification Using High-Throughput Whole-Genome Sequencing. PLoS ONE, 2008, 3, e4012.	2.5	40
87	Estimation of the Multiple Testing Burden for Genomewide Association Studies of Common Variants. Nature Precedings, 2007, , .	0.1	2
88	Two independent alleles at 6q23 associated with risk of rheumatoid arthritis. Nature Genetics, 2007, 39, 1477-1482.	21.4	497
89	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
90	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137

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91	Biases and Reconciliation in Estimates of Linkage Disequilibrium in the Human Genome. <i>American Journal of Human Genetics</i> , 2006, 78, 588-603.	6.2	43
92	Evaluating potential for whole-genome studies in Kosrae, an isolated population in Micronesia. <i>Nature Genetics</i> , 2006, 38, 214-217.	21.4	61
93	Evaluating and improving power in whole-genome association studies using fixed marker sets. <i>Nature Genetics</i> , 2006, 38, 663-667.	21.4	274
94	Efficiency and power in genetic association studies. <i>Nature Genetics</i> , 2005, 37, 1217-1223.	21.4	1,597
95	Typing without calling the allele: a strategy for inferring SNP haplotypes. <i>European Journal of Human Genetics</i> , 2005, 13, 898-901.	2.8	3
96	On the applicability of a haplotype map to un-assayed populations. <i>Human Genetics</i> , 2004, 114, 214-217.	3.8	4
97	Incomplete Directed Perfect Phylogeny. <i>SIAM Journal on Computing</i> , 2004, 33, 590-607.	1.0	54
98	Recovering Frequencies of Known Haplotype Blocks From Single-Nucleotide Polymorphism Allele Frequencies. <i>Genetics</i> , 2004, 166, 2001-2006.	2.9	1
99	Proteomic signatures: Amino acid and oligopeptide compositions differentiate among phyla. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 20-40.	2.6	130
100	Advanced computational techniques for re-sequencing DNA with polymerase signaling assay arrays. <i>Nucleic Acids Research</i> , 2003, 31, 5667-5675.	14.5	3
101	Nonlinear partial differential equations and applications: A computational method for resequencing long DNA targets by universal oligonucleotide arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15492-15496.	7.1	14
102	An Algorithm Combining Discrete and Continuous Methods for Optical Mapping. <i>Journal of Computational Biology</i> , 2000, 7, 745-760.	1.6	0
103	Realizing Interval Graphs with Size and Distance Constraints. <i>SIAM Journal on Discrete Mathematics</i> , 1997, 10, 662-687.	0.8	16
104	MiSDEED: a synthetic data engine for microbiome study power analysis and study design. <i>Bioinformatics Advances</i> , 0, , .	2.4	0