

# Shai Carmi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2484901/publications.pdf>

Version: 2024-02-01

78  
papers

5,724  
citations

186265

28  
h-index

88630

70  
g-index

94  
all docs

94  
docs citations

94  
times ranked

9635  
citing authors

#	ARTICLE	IF	CITATIONS
1	Is Bicuspid Aortic Valve Morphology Genetically Determined? A Family-Based Study. <i>American Journal of Cardiology</i> , 2022, 163, 85-90.	1.6	5
2	Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. <i>American Journal of Human Genetics</i> , 2022, 109, 12-23.	6.2	136
3	Capacities and Limitations of Using Polygenic Risk Scores for Reproductive Decision Making. <i>American Journal of Bioethics</i> , 2022, 22, 42-45.	0.9	2
4	Decomposition of Individual SNP Patterns from Mixed DNA Samples. <i>Forensic Sciences</i> , 2022, 2, 455-472.	1.5	1
5	Screening embryos for polygenic conditions and traits: ethical considerations for an emerging technology. <i>Genetics in Medicine</i> , 2021, 23, 432-434.	2.4	36
6	Expanded clinical validation of Haploseek for comprehensive preimplantation genetic testing. <i>Genetics in Medicine</i> , 2021, 23, 1334-1340.	2.4	10
7	The landscape of autosomal-recessive pathogenic variants in European populations reveals phenotype-specific effects. <i>American Journal of Human Genetics</i> , 2021, 108, 608-619.	6.2	36
8	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
9	MHC Haplotyping of SARS-CoV-2 Patients: HLA Subtypes Are Not Associated with the Presence and Severity of COVID-19 in the Israeli Population. <i>Journal of Clinical Immunology</i> , 2021, 41, 1154-1161.	3.8	25
10	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. <i>Theoretical Population Biology</i> , 2021, 139, 50-65.	1.1	7
11	LINADMIX: evaluating the effect of ancient admixture events on modern populations. <i>Bioinformatics</i> , 2021, 37, 4744-4755.	4.1	1
12	Utility of polygenic embryo screening for disease depends on the selection strategy. <i>ELife</i> , 2021, 10, .	6.0	34
13	Bicuspid Aortic Valve: Genetic and Clinical Insights. <i>Aorta</i> , 2021, 09, 139-146.	0.5	8
14	Fine-scale population structure and demographic history of British Pakistanis. <i>Nature Communications</i> , 2021, 12, 7189.	12.8	21
15	Anti-tumor necrosis factor alpha reduces the proangiogenic effects of activated macrophages derived from patients with age-related macular degeneration.. <i>Molecular Vision</i> , 2021, 27, 622-631.	1.1	1
16	Preconception carrier screening yield: effect of variants of unknown significance in partners of carriers with clinically significant variants. <i>Genetics in Medicine</i> , 2020, 22, 646-653.	2.4	18
17	The Genomic History of the Bronze Age Southern Levant. <i>Cell</i> , 2020, 181, 1146-1157.e11.	28.9	51
18	Association of a Variant in VWA3A with Response to Anti-Vascular Endothelial Growth Factor Treatment in Neovascular AMD. , 2020, 61, 48.		4

#	ARTICLE	IF	CITATIONS
19	The challenges of maintaining genetic privacy. <i>ELife</i> , 2020, 9, .	6.0	2
20	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
21	A test for deviations from expected genotype frequencies on the X chromosome for sex-biased admixed populations. <i>Heredity</i> , 2019, 123, 470-478.	2.6	5
22	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. <i>Genetics</i> , 2019, 212, 305-316.	2.9	19
23	Screening Human Embryos for Polygenic Traits Has Limited Utility. <i>Cell</i> , 2019, 179, 1424-1435.e8.	28.9	78
24	Crossover interference and sex-specific genetic maps shape identical by descent sharing in close relatives. <i>PLoS Genetics</i> , 2019, 15, e1007979.	3.5	46
25	FactorialHMM: fast and exact inference in factorial hidden Markov models. <i>Bioinformatics</i> , 2019, 35, 2162-2164.	4.1	1
26	Haploseek: a 24-hour all-in-one method for preimplantation genetic diagnosis (PGD) of monogenic disease and aneuploidy. <i>Genetics in Medicine</i> , 2019, 21, 1390-1399.	2.4	35
27	Off the street phasing (OTSP): no hassle haplotype phasing for molecular PGD applications. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 727-739.	2.5	2
28	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018, 555, 210-215.	27.8	1,958
29	Functional variants in the <i>LRRK2</i> gene confer shared effects on risk for Crohn's disease and Parkinson's disease. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	273
30	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. <i>Human Genetics</i> , 2018, 137, 343-355.	3.8	24
31	A non-zero variance of Tajima's estimator for two sequences even for infinitely many unlinked loci. <i>Theoretical Population Biology</i> , 2018, 122, 22-29.	1.1	17
32	Identity inference of genomic data using long-range familial searches. <i>Science</i> , 2018, 362, 690-694.	12.6	235
33	POLD1 and POLE Gene Mutations in Jewish Cohorts of Early-Onset Colorectal Cancer and of Multiple Colorectal Adenomas. <i>Diseases of the Colon and Rectum</i> , 2018, 61, 1073-1079.	1.3	17
34	Germline DNA replication timing shapes mammalian genome composition. <i>Nucleic Acids Research</i> , 2018, 46, 8299-8310.	14.5	27
35	A study of Kibbutzim in Israel reveals risk factors for cardiometabolic traits and subtle population structure. <i>European Journal of Human Genetics</i> , 2018, 26, 1848-1858.	2.8	12
36	Genomic insights into the population structure and history of the Irish Travellers. <i>Scientific Reports</i> , 2017, 7, 42187.	3.3	31

#	ARTICLE	IF	CITATIONS
37	Differential analysis of mutations in the Jewish population and their implications for diseases. <i>Genetical Research</i> , 2017, 99, e3.	0.9	7
38	The genetic variation in the R1a clade among the Ashkenazi Levitesâ€™™ Y chromosome. <i>Scientific Reports</i> , 2017, 7, 14969.	3.3	13
39	The time and place of European admixture in Ashkenazi Jewish history. <i>PLoS Genetics</i> , 2017, 13, e1006644.	3.5	25
40	Transcriptome and proteome analyses and the role of atypical calpain protein and autophagy in the spliced leader silencing pathway in <i>Trypanosoma brucei</i> . <i>Molecular Microbiology</i> , 2016, 102, 1-21.	2.5	4
41	A Recurrent <i>ERCC3</i> Truncating Mutation Confers Moderate Risk for Breast Cancer. <i>Cancer Discovery</i> , 2016, 6, 1267-1275.	9.4	41
42	Rapidly Registering Identity-by-Descent Across Ancestral Recombination Graphs. <i>Journal of Computational Biology</i> , 2016, 23, 495-507.	1.6	0
43	Expanding the phenotype of <i>CRB2</i> mutations—A new ciliopathy syndrome?. <i>Clinical Genetics</i> , 2016, 90, 540-544.	2.0	18
44	An Ashkenazi founder mutation in the <i>PKHD1</i> gene. <i>European Journal of Medical Genetics</i> , 2016, 59, 86-90.	1.3	6
45	Expanded genetic screening panel for the Ashkenazi Jewish population. <i>Genetics in Medicine</i> , 2016, 18, 522-528.	2.4	33
46	The SMCâ€™² Is a Highly Accurate Approximation to the Ancestral Recombination Graph. <i>Genetics</i> , 2015, 200, 343-355.	2.9	39
47	Genotyping of geographically diverse Druze trios reveals substructure and a recent bottleneck. <i>European Journal of Human Genetics</i> , 2015, 23, 1093-1099.	2.8	10
48	Rapidly Registering Identity-by-Descent Across Ancestral Recombination Graphs. <i>Lecture Notes in Computer Science</i> , 2015, , 340-353.	1.3	0
49	Two splicing factors carrying serine-arginine motifs, <i>TSR1</i> and <i>TSR1IP</i> , regulate splicing, mRNA stability, and rRNA processing in <i>Trypanosoma brucei</i> . <i>RNA Biology</i> , 2014, 11, 715-731.	3.1	36
50	A genome-wide map of hyper-edited RNA reveals numerous new sites. <i>Nature Communications</i> , 2014, 5, 4726.	12.8	193
51	A renewal theory approach to IBD sharing. <i>Theoretical Population Biology</i> , 2014, 97, 35-48.	1.1	34
52	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
53	Basal Splicing Factors Regulate the Stability of Mature mRNAs in Trypanosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 4991-5006.	3.4	33
54	The Variance of Identity-by-Descent Sharing in the Wrightâ€™Fisher Model. <i>Genetics</i> , 2013, 193, 911-928.	2.9	38

#	ARTICLE	IF	CITATIONS
55	The hnRNP F/H homologue of <i>Trypanosoma brucei</i> is differentially expressed in the two life cycle stages of the parasite and regulates splicing and mRNA stability. <i>Nucleic Acids Research</i> , 2013, 41, 6577-6594.	14.5	44
56	Random walk with priorities in communicationlike networks. <i>Physical Review E</i> , 2013, 88, 022803.	2.1	1
57	Fractional Feynman-Kac equation for weak ergodicity breaking. <i>Physical Review E</i> , 2011, 84, 061104.	2.1	48
58	Large-scale DNA editing of retrotransposons accelerates mammalian genome evolution. <i>Nature Communications</i> , 2011, 2, 519.	12.8	43
59	Identification of Widespread Ultra-Edited Human RNAs. <i>PLoS Genetics</i> , 2011, 7, e1002317.	3.5	79
60	Fractional Feynman-Kac Equation for Anomalous Diffusion Functionals. , 2011, , 185-207.		1
61	On Distributions of Functionals of Anomalous Diffusion Paths. <i>Journal of Statistical Physics</i> , 2010, 141, 1071-1092.	1.2	66
62	Epidemic Threshold for the Susceptible-Infectious-Susceptible Model on Random Networks. <i>Physical Review Letters</i> , 2010, 104, 258701.	7.8	170
63	The Transcriptome of the Human Pathogen <i>Trypanosoma brucei</i> at Single-Nucleotide Resolution. <i>PLoS Pathogens</i> , 2010, 6, e1001090.	4.7	243
64	Persistent ER Stress Induces the Spliced Leader RNA Silencing Pathway (SLS), Leading to Programmed Cell Death in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000731.	4.7	84
65	Asymptotic Behavior of the Kleinberg Model. <i>Physical Review Letters</i> , 2009, 102, 238702.	7.8	27
66	Energy-landscape network approach to the glass transition. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009, 42, 105101.	2.1	17
67	Efficiency of complex production in changing environment. <i>BMC Systems Biology</i> , 2009, 3, 3.	3.0	9
68	Fractional Feynman-Kac Equation for Non-Brownian Functionals. <i>Physical Review Letters</i> , 2009, 103, 190201.	7.8	73
69	Trapping in complex networks. <i>Europhysics Letters</i> , 2008, 84, 40008.	2.0	50
70	Transport in networks with multiple sources and sinks. <i>Europhysics Letters</i> , 2008, 84, 28005.	2.0	28
71	Partition of networks into basins of attraction. <i>Physical Review E</i> , 2008, 78, 066111.	2.1	8
72	Priority diffusion model in lattices and complex networks. <i>Physical Review E</i> , 2008, 77, 020103.	2.1	4

#	ARTICLE	IF	CITATIONS
73	Limited Path Percolation in Complex Networks. Physical Review Letters, 2007, 99, 188701.	7.8	27
74	A model of Internet topology using k-shell decomposition. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11150-11154.	7.1	612
75	Transport between multiple users in complex networks. European Physical Journal B, 2007, 57, 165-174.	1.5	17
76	Anomalous electrical and frictionless flow conductance in complex networks. Physica D: Nonlinear Phenomena, 2006, 224, 69-76.	2.8	11
77	Searching complex networks efficiently with minimal information. Europhysics Letters, 2006, 74, 1102-1108.	2.0	35
78	Connectivity and expression in protein networks: Proteins in a complex are uniformly expressed. Physical Review E, 2006, 73, 031909.	2.1	14