

# Liran Carmel

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

4,356  
citations

147801

31  
h-index

138484

58  
g-index

61  
all docs

61  
docs citations

61  
times ranked

7019  
citing authors

#	ARTICLE	IF	CITATIONS
1	LINADMIX: evaluating the effect of ancient admixture events on modern populations. <i>Bioinformatics</i> , 2021, 37, 4744-4755.	4.1	1
2	Lead in Archeological Human Bones Reflecting Historical Changes in Lead Production. <i>Environmental Science &amp; Technology</i> , 2021, 55, 14407-14413.	10.0	7
3	SRCP: a comprehensive pipeline for accurate annotation and quantification of circRNAs. <i>Genome Biology</i> , 2021, 22, 277.	8.8	8
4	Antisense oligonucleotide-based drug development for Cystic Fibrosis patients carrying the 3849+10Åkb C-to-T splicing mutation. <i>Journal of Cystic Fibrosis</i> , 2021, 20, 865-875.	0.7	30
5	The Genomic History of the Bronze Age Southern Levant. <i>Cell</i> , 2020, 181, 1146-1157.e11.	28.9	51
6	Harnessing epigenetics to study human evolution. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 23-29.	3.3	5
7	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020, 11, 1189.	12.8	69
8	Predicted Archaic 3D Genome Organization Reveals Genes Related to Head and Spinal Cord Separating Modern from Archaic Humans. <i>Cells</i> , 2020, 9, 48.	4.1	11
9	Assessing predictions of the impact of variants on splicing in CAG15. <i>Human Mutation</i> , 2019, 40, 1215-1224.	2.5	18
10	Reconstructing Denisovan Anatomy Using DNA Methylation Maps. <i>Cell</i> , 2019, 179, 180-192.e10.	28.9	51
11	Nucleotide composition affects codon usage toward the 3'-end. <i>PLoS ONE</i> , 2019, 14, e0225633.	2.5	5
12	Alu exaptation enriches the human transcriptome by introducing new gene ends. <i>RNA Biology</i> , 2018, 15, 1-11.	3.1	11
13	Evidence for convergent evolution of SINE-directed Staufen-mediated mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 968-973.	7.1	37
14	Small RNA sequences derived from pre-microRNAs in the supraspliceosome. <i>Nucleic Acids Research</i> , 2018, 46, 11014-11029.	14.5	11
15	Archaic adaptive introgression in <i>TBX15/WARS2</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw283.	8.9	101
16	Movement correlates of lizards'™ dorsal pigmentation patterns. <i>Functional Ecology</i> , 2017, 31, 370-376.	3.6	23
17	Gene ORGANizer: linking genes to the organs they affect. <i>Nucleic Acids Research</i> , 2017, 45, W138-W145.	14.5	43
18	Identification of introns harboring functional sequence elements through positional conservation. <i>Scientific Reports</i> , 2017, 7, 4201.	3.3	17

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19	Inferring Past Environments from Ancient Epigenomes. <i>Molecular Biology and Evolution</i> , 2017, 34, 2429-2438.	8.9	47
20	A deep neural network with a restricted noisy channel for identification of functional introns. , 2017, , .		0
21	The role of nucleotide composition in premature termination codon recognition. <i>BMC Bioinformatics</i> , 2016, 17, 519.	2.6	3
22	JuncDB: an exon-exon junction database. <i>Nucleic Acids Research</i> , 2016, 44, D101-D109.	14.5	7
23	Epigenetics: It's Getting Old. Past Meets Future in Paleoepigenetics. <i>Trends in Ecology and Evolution</i> , 2016, 31, 290-300.	8.7	58
24	System-wide Analysis of the T Cell Response. <i>Cell Reports</i> , 2016, 14, 2733-2744.	6.4	67
25	Combined mineralocorticoid and glucocorticoid deficiency is caused by a novel founder nicotinamide nucleotide transhydrogenase mutation that alters mitochondrial morphology and increases oxidative stress. <i>Journal of Medical Genetics</i> , 2015, 52, 636-641.	3.2	26
26	LEMONS - A Tool for the Identification of Splice Junctions in Transcriptomes of Organisms Lacking Reference Genomes. <i>PLoS ONE</i> , 2015, 10, e0143329.	2.5	5
27	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. <i>Science</i> , 2014, 344, 523-527.	12.6	188
28	Computational identification of functional introns: high positional conservation of introns that harbor RNA genes. <i>Nucleic Acids Research</i> , 2013, 41, 5604-5613.	14.5	18
29	Dependencies among Editing Sites in Serotonin 2C Receptor mRNA. <i>PLoS Computational Biology</i> , 2012, 8, e1002663.	3.2	9
30	The Role of Reverse Transcriptase in Intron Gain and Loss Mechanisms. <i>Molecular Biology and Evolution</i> , 2012, 29, 179-186.	8.9	43
31	ApoB-containing lipoproteins regulate angiogenesis by modulating expression of VEGF receptor 1. <i>Nature Medicine</i> , 2012, 18, 967-973.	30.7	105
32	The Function of Introns. <i>Frontiers in Genetics</i> , 2012, 3, 55.	2.3	280
33	Origin and evolution of spliceosomal introns. <i>Biology Direct</i> , 2012, 7, 11.	4.6	292
34	The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011, 331, 555-561.	12.6	1,086
35	XX Ovarian Dysgenesis Is Caused by a PSMC3IP/HOP2 Mutation that Abolishes Coactivation of Estrogen-Driven Transcription. <i>American Journal of Human Genetics</i> , 2011, 89, 572-579.	6.2	99
36	EREM: Parameter Estimation and Ancestral Reconstruction by Expectation-Maximization Algorithm for a Probabilistic Model of Genomic Binary Characters Evolution. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-4.	5.7	8

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37	A Universal Nonmonotonic Relationship between Gene Compactness and Expression Levels in Multicellular Eukaryotes. <i>Genome Biology and Evolution</i> , 2009, 1, 382-390.	2.5	40
38	Endothelial cells promote migration and proliferation of enteric neural crest cells via $\alpha$ 21 integrin signaling. <i>Developmental Biology</i> , 2009, 330, 263-272.	2.0	73
39	A Maximum Likelihood Method for Reconstruction of the Evolution of Eukaryotic Gene Structure. <i>Methods in Molecular Biology</i> , 2009, 541, 357-371.	0.9	6
40	Potency and Fate Specification in CNS Stem Cell Populations In Vitro. <i>Cell Stem Cell</i> , 2008, 3, 670-680.	11.1	103
41	Predicting the Receptive Range of Olfactory Receptors. <i>PLoS Computational Biology</i> , 2008, 4, e18.	3.2	16
42	Evolution of protein domain promiscuity in eukaryotes. <i>Genome Research</i> , 2008, 18, 449-461.	5.5	153
43	Superposition of Transcriptional Behaviors Determines Gene State. <i>PLoS ONE</i> , 2008, 3, e2901.	2.5	14
44	Widespread Positive Selection in Synonymous Sites of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1821-1831.	8.9	86
45	Analysis of Rare Amino Acid Replacements Supports the Coelomata Clade. <i>Molecular Biology and Evolution</i> , 2007, 24, 2594-2597.	8.9	41
46	Three distinct modes of intron dynamics in the evolution of eukaryotes. <i>Genome Research</i> , 2007, 17, 1034-1044.	5.5	159
47	Evolutionarily conserved genes preferentially accumulate introns. <i>Genome Research</i> , 2007, 17, 1045-1050.	5.5	68
48	Ecdysozoan Clade Rejected by Genome-Wide Analysis of Rare Amino Acid Replacements. <i>Molecular Biology and Evolution</i> , 2007, 24, 1080-1090.	8.9	63
49	Patterns of intron gain and conservation in eukaryotic genes. <i>BMC Evolutionary Biology</i> , 2007, 7, 192.	3.2	67
50	Mix-to-mimic odor synthesis for electronic noses. <i>Sensors and Actuators B: Chemical</i> , 2007, 125, 635-643.	7.8	9
51	Gene expression profile of empirically delineated classes of unexplained chronic fatigue. <i>Pharmacogenomics</i> , 2006, 7, 375-386.	1.3	37
52	Genome-wide Analysis of Substrate Specificities of the Escherichia coli Haloacid Dehalogenase-like Phosphatase Family. <i>Journal of Biological Chemistry</i> , 2006, 281, 36149-36161.	3.4	249
53	Unifying measures of gene function and evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1507-1515.	2.6	74
54	Electronic nose signal restoration beyond the dynamic range limit. <i>Sensors and Actuators B: Chemical</i> , 2005, 106, 95-100.	7.8	5

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55	On mappings between electronic noses. <i>Sensors and Actuators B: Chemical</i> , 2005, 106, 76-82.	7.8	25
56	On predicting responses to mixtures in quartz microbalance sensors. <i>Sensors and Actuators B: Chemical</i> , 2005, 106, 128-135.	7.8	10
57	Combining hierarchy and energy for drawing directed graphs. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2004, 10, 46-57.	4.4	28
58	Robust linear dimensionality reduction. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2004, 10, 459-470.	4.4	123
59	Drawing Huge Graphs by Algebraic Multigrid Optimization. <i>Multiscale Modeling and Simulation</i> , 2003, 1, 645-673.	1.6	49
60	Estimating the Size of the Olfactory Repertoire. <i>Bulletin of Mathematical Biology</i> , 2001, 63, 1063-1078.	1.9	6