# Liran Carmel

## List of Publications by Year
in descending order

| 60 papers | 4,356 citations | 147801<br>31 h-index | 138484<br>58 g-index |
|---|---|---|---|
| 61 all docs | 61 docs citations | 61 times ranked | 7019 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 1 | The Ecoresponsive Genome of <i>Daphnia pulex</i>. Science, 2011, 331, 555-561. | 12.6 | 1,086 |
| 2 | Origin and evolution of spliceosomal introns. Biology Direct, 2012, 7, 11. | 4.6 | 292 |
| 3 | The Function of Introns. Frontiers in Genetics, 2012, 3, 55. | 2.3 | 280 |
| 4 | Genome-wide Analysis of Substrate Specificities of the Escherichia coli Haloacid Dehalogenase-like Phosphatase Family. Journal of Biological Chemistry, 2006, 281, 36149-36161. | 3.4 | 249 |
| 5 | Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. Science, 2014, 344, 523-527. | 12.6 | 188 |
| 6 | Three distinct modes of intron dynamics in the evolution of eukaryotes. Genome Research, 2007, 17, 1034-1044. | 5.5 | 159 |
| 7 | Evolution of protein domain promiscuity in eukaryotes. Genome Research, 2008, 18, 449-461. | 5.5 | 153 |
| 8 | Robust linear dimensionality reduction. IEEE Transactions on Visualization and Computer Graphics, 2004, 10, 459-470. | 4.4 | 123 |
| 9 | ApoB-containing lipoproteins regulate angiogenesis by modulating expression of VEGF receptor 1. Nature Medicine, 2012, 18, 967-973. | 30.7 | 105 |
| 10 | Potency and Fate Specification in CNS Stem Cell Populations In Vitro. Cell Stem Cell, 2008, 3, 670-680. | 11.1 | 103 |
| 11 | Archaic adaptive introgression in <i>TBX15/WARS2</i>. Molecular Biology and Evolution, 2017, 34, msw283. | 8.9 | 101 |
| 12 | XX Ovarian Dysgenesis Is Caused by a PSMC3IP/HOP2 Mutation that Abolishes Coactivation of Estrogen-Driven Transcription. American Journal of Human Genetics, 2011, 89, 572-579. | 6.2 | 99 |
| 13 | Widespread Positive Selection in Synonymous Sites of Mammalian Genes. Molecular Biology and Evolution, 2007, 24, 1821-1831. | 8.9 | 86 |
| 14 | Unifying measures of gene function and evolution. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 1507-1515. | 2.6 | 74 |
| 15 | Endothelial cells promote migration and proliferation of enteric neural crest cells via Î²1 integrin signaling. Developmental Biology, 2009, 330, 263-272. | 2.0 | 73 |
| 16 | Differential DNA methylation of vocal and facial anatomy genes in modern humans. Nature Communications, 2020, 11, 1189. | 12.8 | 69 |
| 17 | Evolutionarily conserved genes preferentially accumulate introns. Genome Research, 2007, 17, 1045-1050. | 5.5 | 68 |
| 18 | Patterns of intron gain and conservation in eukaryotic genes. BMC Evolutionary Biology, 2007, 7, 192. | 3.2 | 67 |

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|---|---------|-----|-----------|
| 19 | System-wide Analysis of the T Cell Response. Cell Reports, 2016, 14, 2733-2744. | 6.4 | 67 |
| 20 | Ecdysozoan Clade Rejected by Genome-Wide Analysis of Rare Amino Acid Replacements. Molecular Biology and Evolution, 2007, 24, 1080-1090. | 8.9 | 63 |
| 21 | Epigenetics: It's Getting Old. Past Meets Future in Paleoepigenetics. Trends in Ecology and Evolution, 2016, 31, 290-300. | 8.7 | 58 |
| 22 | Reconstructing Denisovan Anatomy Using DNA Methylation Maps. Cell, 2019, 179, 180-192.e10. | 28.9 | 51 |
| 23 | The Genomic History of the Bronze Age Southern Levant. Cell, 2020, 181, 1146-1157.e11. | 28.9 | 51 |
| 24 | Drawing Huge Graphs by Algebraic Multigrid Optimization. Multiscale Modeling and Simulation, 2003, 1, 645-673. | 1.6 | 49 |
| 25 | Inferring Past Environments from Ancient Epigenomes. Molecular Biology and Evolution, 2017, 34, 2429-2438. | 8.9 | 47 |
| 26 | The Role of Reverse Transcriptase in Intron Gain and Loss Mechanisms. Molecular Biology and Evolution, 2012, 29, 179-186. | 8.9 | 43 |
| 27 | Gene ORGANizer: linking genes to the organs they affect. Nucleic Acids Research, 2017, 45, W138-W145. | 14.5 | 43 |
| 28 | Analysis of Rare Amino Acid Replacements Supports the Coelomata Clade. Molecular Biology and Evolution, 2007, 24, 2594-2597. | 8.9 | 41 |
| 29 | A Universal Nonmonotonic Relationship between Gene Compactness and Expression Levels in Multicellular Eukaryotes. Genome Biology and Evolution, 2009, 1, 382-390. | 2.5 | 40 |
| 30 | Gene expression profile of empirically delineated classes of unexplained chronic fatigue. Pharmacogenomics, 2006, 7, 375-386. | 1.3 | 37 |
| 31 | Evidence for convergent evolution of SINE-directed Staufen-mediated mRNA decay. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 968-973. | 7.1 | 37 |
| 32 | Antisense oligonucleotide-based drug development for Cystic Fibrosis patients carrying the 3849+10Âkb C-to-T splicing mutation. Journal of Cystic Fibrosis, 2021, 20, 865-875. | 0.7 | 30 |
| 33 | Combining hierarchy and energy for drawing directed graphs. IEEE Transactions on Visualization and Computer Graphics, 2004, 10, 46-57. | 4.4 | 28 |
| 34 | Combined mineralocorticoid and glucocorticoid deficiency is caused by a novel founder nicotinamide nucleotide transhydrogenase mutation that alters mitochondrial morphology and increases oxidative stress. Journal of Medical Genetics, 2015, 52, 636-641. | 3.2 | 26 |
| 35 | On mappings between electronic noses. Sensors and Actuators B: Chemical, 2005, 106, 76-82. | 7.8 | 25 |
| 36 | Movement correlates of lizardsâ€™ dorsal pigmentation patterns. Functional Ecology, 2017, 31, 370-376. | 3.6 | 23 |

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|---|---------|-----|-----------|
| 37 | Computational identification of functional introns: high positional conservation of introns that harbor RNA genes. Nucleic Acids Research, 2013, 41, 5604-5613. | 14.5 | 18 |
| 38 | Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224. | 2.5 | 18 |
| 39 | Identification of introns harboring functional sequence elements through positional conservation. Scientific Reports, 2017, 7, 4201. | 3.3 | 17 |
| 40 | Predicting the Receptive Range of Olfactory Receptors. PLoS Computational Biology, 2008, 4, e18. | 3.2 | 16 |
| 41 | Superposition of Transcriptional Behaviors Determines Gene State. PLoS ONE, 2008, 3, e2901. | 2.5 | 14 |
| 42 | Alu exaptation enriches the human transcriptome by introducing new gene ends. RNA Biology, 2018, 15, 1-11. | 3.1 | 11 |
| 43 | Small RNA sequences derived from pre-microRNAs in the supraspliceosome. Nucleic Acids Research, 2018, 46, 11014-11029. | 14.5 | 11 |
| 44 | Predicted Archaic 3D Genome Organization Reveals Genes Related to Head and Spinal Cord Separating Modern from Archaic Humans. Cells, 2020, 9, 48. | 4.1 | 11 |
| 45 | On predicting responses to mixtures in quartz microbalance sensors. Sensors and Actuators B: Chemical, 2005, 106, 128-135. | 7.8 | 10 |
| 46 | Mix-to-mimic odor synthesis for electronic noses. Sensors and Actuators B: Chemical, 2007, 125, 635-643. | 7.8 | 9 |
| 47 | Dependencies among Editing Sites in Serotonin 2C Receptor mRNA. PLoS Computational Biology, 2012, 8, e1002663. | 3.2 | 9 |
| 48 | EREM: Parameter Estimation and Ancestral Reconstruction by Expectation-Maximization Algorithm for a Probabilistic Model of Genomic Binary Characters Evolution. Advances in Bioinformatics, 2010, 2010, 1-4. | 5.7 | 8 |
| 49 | SRCP: a comprehensive pipeline for accurate annotation and quantification of circRNAs. Genome Biology, 2021, 22, 277. | 8.8 | 8 |
| 50 | JuncDB: an exon–exon junction database. Nucleic Acids Research, 2016, 44, D101-D109. | 14.5 | 7 |
| 51 | Lead in Archeological Human Bones Reflecting Historical Changes in Lead Production. Environmental Science &amp; Technology, 2021, 55, 14407-14413. | 10.0 | 7 |
| 52 | Estimating the Size of the Olfactory Repertoire. Bulletin of Mathematical Biology, 2001, 63, 1063-1078. | 1.9 | 6 |
| 53 | A Maximum Likelihood Method for Reconstruction of the Evolution of Eukaryotic Gene Structure. Methods in Molecular Biology, 2009, 541, 357-371. | 0.9 | 6 |
| 54 | Electronic nose signal restoration—beyond the dynamic range limit. Sensors and Actuators B: Chemical, 2005, 106, 95-100. | 7.8 | 5 |

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|---|---------|-----|-----------|
| 55 | Nucleotide composition affects codon usage toward the 3'-end. PLoS ONE, 2019, 14, e0225633. | 2.5 | 5 |
| 56 | Harnessing epigenetics to study human evolution. Current Opinion in Genetics and Development, 2020, 62, 23-29. | 3.3 | 5 |
| 57 | LEMONS â€" A Tool for the Identification of Splice Junctions in Transcriptomes of Organisms Lacking Reference Genomes. PLoS ONE, 2015, 10, e0143329. | 2.5 | 5 |
| 58 | The role of nucleotide composition in premature termination codon recognition. BMC Bioinformatics, 2016, 17, 519. | 2.6 | 3 |
| 59 | LINADMIX: evaluating the effect of ancient admixture events on modern populations. Bioinformatics, 2021, 37, 4744-4755. | 4.1 | 1 |
| 60 | A deep neural network witharestricted noisy channel for identification of functional introns. , 2017, , . | | 0 |