

# Leonardo Mariño-Ramírez

## List of Publications by Year in descending order

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99  
papers

3,201  
citations

172457

29  
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168389

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107  
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107  
docs citations

107  
times ranked

4679  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of Genetic Ancestry and Molecular Signatures with Cancer Survival Disparities: A Pan-Cancer Analysis. <i>Cancer Research</i> , 2022, 82, 1222-1233.	0.9	11
2	Epigenetics and cancer disparities: when nature might be nurture. <i>Oncoscience</i> , 2022, 9, 23-24.	2.2	1
3	Comorbidities and ethnic health disparities in the UK biobank. <i>JAMIA Open</i> , 2022, 5, .	2.0	1
4	Effects of genetic ancestry and socioeconomic deprivation on ethnic differences in serum creatinine. <i>Gene</i> , 2022, 837, 146709.	2.2	4
5	PM4NGS, a project management framework for next-generation sequencing data analysis. <i>GigaScience</i> , 2021, 10, .	6.4	0
6	Transcriptome annotation in the cloud: complexity, best practices, and cost. <i>GigaScience</i> , 2021, 10, .	6.4	9
7	Detection of high heteroplasmy in complete loggerhead and hawksbill sea turtles mitochondrial genomes using RNAseq. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 106-114.	0.7	1
8	Transcriptional Analyses of Acute Exposure to Methylmercury on Erythrocytes of Loggerhead Sea Turtle. <i>Toxics</i> , 2021, 9, 70.	3.7	2
9	Socioeconomic deprivation and genetic ancestry interact to modify type 2 diabetes ethnic disparities in the United Kingdom. <i>EClinicalMedicine</i> , 2021, 37, 100960.	7.1	25
10	The Impact of Ethnicity and Genetic Ancestry on Disease Prevalence and Risk in Colombia. <i>Frontiers in Genetics</i> , 2021, 12, 690366.	2.3	8
11	Genetic ancestry and ethnic identity in Ecuador. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100050.	1.7	4
12	Comparing Genetic and Socioenvironmental Contributions to Ethnic Differences in C-Reactive Protein. <i>Frontiers in Genetics</i> , 2021, 12, 738485.	2.3	7
13	Comparative transcriptome analysis between patient and endometrial cancer cell lines to determine common signaling pathways and markers linked to cancer progression. <i>Oncotarget</i> , 2021, 12, 2500-2513.	1.8	2
14	Data on heteroplasmic mutations in mitochondrial genomes of loggerhead and hawksbill sea turtles: First approach. <i>Data in Brief</i> , 2020, 28, 104882.	1.0	1
15	Oxidative Stress Biomarkers in Erythrocytes of Captive Pre-Juvenile Loggerhead Turtles Following Acute Exposure to Methylmercury. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 3602.	2.5	5
16	BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. <i>Epigenetics and Chromatin</i> , 2020, 13, 21.	3.9	40
17	Structural analysis of leucine, lysine and tryptophan mitochondrial tRNA of nesting turtles <i>Caretta caretta</i> (Testudines: Chelonioidea) in the Colombian Caribbean. <i>PeerJ</i> , 2020, 8, e9204.	2.0	1
18	Direct At-Sea Observations of Elephant Seals ( <i>Mirounga</i> spp.) to Help Interpret Digital Bio-logging Data. <i>The Open Biology Journal</i> , 2020, 8, 1-5.	0.5	2

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19	Machine Learning Neuroprotective Strategy Reveals a Unique Set of Parkinson Therapeutic Nicotine Analogs. <i>Open Bioinformatics Journal</i> , 2020, 13, 1-14.	1.0	1
20	Whole-Genome Sequences of <i>Salmonella enterica</i> Serovar I 4,[5],12:i:â” Isolates from Swine. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
21	Banana ( <i>Musa acuminata</i> ) transcriptome profiling in response to rhizobacteria: <i>Bacillus amyloliquefaciens</i> Bs006 and <i>Pseudomonas fluorescens</i> Ps006. <i>BMC Genomics</i> , 2019, 20, 378.	2.8	31
22	TPMCalculator: one-step software to quantify mRNA abundance of genomic features. <i>Bioinformatics</i> , 2019, 35, 1960-1962.	4.1	149
23	Genome Sequences of 15 <i>Klebsiella</i> sp. Isolates from Sugarcane Fields in Colombiaâ”™s Cauca Valley. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
24	Genetic ancestry, admixture and health determinants in Latin America. <i>BMC Genomics</i> , 2018, 19, 861.	2.8	78
25	Benchmarking computational tools for polymorphic transposable element detection. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw072.	6.5	64
26	Population and clinical genetics of human transposable elements in the (post) genomic era. <i>Mobile Genetic Elements</i> , 2017, 7, 1-20.	1.8	22
27	Complete mitochondrial genome of the nesting Colombian Caribbean Hawksbill Turtle. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 128-129.	0.4	3
28	A Comparative Analysis of Genetic Ancestry and Admixture in the Colombian Populations of ChocÃ³ and MedellÃn. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3435-3447.	1.8	39
29	Workflow and web application for annotating NCBI BioProject transcriptome data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	6
30	De novo transcriptome assembly of loggerhead sea turtle nesting of the Colombian Caribbean. <i>Genomics Data</i> , 2017, 13, 18-20.	1.3	10
31	Whole-Genome Sequence of Multidrug-Resistant <i>Campylobacter coli</i> Strain COL B1-266, Isolated from the Colombian Poultry Chain. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
32	El ChocÃ³, Colombia: un hotspot de la biodiversidad humana. <i>Revista Biodiversidad Neotropical</i> , 2016, 6, 45.	0.2	15
33	HistoneDB 2.0: a histone database with variantsâ”™an integrated resource to explore histones and their variants. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw014.	3.0	99
34	Whole-Genome Sequences of Two <i>Campylobacter coli</i> Isolates from the Antimicrobial Resistance Monitoring Program in Colombia. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
35	Genome Sequence of the Banana Plant Growth-Promoting Rhizobacterium <i>Pseudomonas fluorescens</i> PS006. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
36	Human population-specific gene expression and transcriptional network modification with polymorphic transposable elements. <i>Nucleic Acids Research</i> , 2016, 45, gkw1286.	14.5	45

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37	Whole-Genome Sequences of 26 <i>Vibrio cholerae</i> Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
38	Transcriptomic analysis of <i>Arabidopsis</i> overexpressing flowering locus T driven by a meristem-specific promoter that induces early flowering. <i>Gene</i> , 2016, 587, 120-131.	2.2	9
39	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. <i>BMC Bioinformatics</i> , 2016, 17, 479.	2.6	1
40	Dataset of <i>Arabidopsis</i> plants that overexpress FT driven by a meristem-specific KNAT1 promoter. <i>Data in Brief</i> , 2016, 8, 520-528.	1.0	1
41	Sliding Motility, Biofilm Formation, and Glycopeptidolipid Production in <i>Mycobacterium colombiense</i> Strains. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	27
42	Genetic diversity and population structure in <i>Physalis peruviana</i> and related taxa based on InDels and SNPs derived from COSII and IRG markers. <i>Plant Gene</i> , 2015, 4, 29-37.	2.3	30
43	Genome Sequence of the Banana Plant Growth-Promoting Rhizobacterium <i>Bacillus amyloliquefaciens</i> BS006. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
44	Genome Sequences of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Paratyphi B (dT+) and Heidelberg Strains from the Colombian Poultry Chain. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
45	Mammalian-wide interspersed repeat (MIR)-derived enhancers and the regulation of human gene expression. <i>Mobile DNA</i> , 2014, 5, 14.	3.6	72
46	Genome Sequences of <i>Vibrio navarrensis</i> , a Potential Human Pathogen. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
47	Searching for repeats, as an example of using the generalised Ruzzo-Tompa algorithm to find optimal subsequences with gaps. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 384.	0.2	2
48	Clonación del gen de la cápside protéica de una cepa colombiana del Virus del Mosaico del Pepino (CMV) para su expresión en plantas por transformación mediante <i>Agrobacterium</i> . <i>Ciencia Tecnología Agropecuaria</i> , 2014, 2, 58-59.	0.3	1
49	HMGN1 Modulates Nucleosome Occupancy and DNase I Hypersensitivity at the CpG Island Promoters of Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2013, 33, 3377-3389.	2.3	68
50	Virulence and Immune Response Induced by <i>Mycobacterium avium</i> Complex Strains in a Model of Progressive Pulmonary Tuberculosis and Subcutaneous Infection in BALB/c Mice. <i>Infection and Immunity</i> , 2013, 81, 4001-4012.	2.2	18
51	Identification of Immunity Related Genes to Study the <i>Physalis peruviana</i> - <i>Fusarium oxysporum</i> Pathosystem. <i>PLoS ONE</i> , 2013, 8, e68500.	2.5	30
52	Genome Sequences for Six <i>Rhodanobacter</i> Strains, Isolated from Soils and the Terrestrial Subsurface, with Variable Denitrification Capabilities. <i>Journal of Bacteriology</i> , 2012, 194, 4461-4462.	2.2	62
53	The Practical Evaluation of DNA Barcode Efficacy. <i>Methods in Molecular Biology</i> , 2012, 858, 365-377.	0.9	12
54	The ruzzo-tompa algorithm can find the maximal paths in weighted, directed graphs on a one-dimensional lattice. , 2012, , .		2

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55	Differences in local genomic context of bound and unbound motifs. <i>Gene</i> , 2012, 506, 125-134.	2.2	3
56	The <i>Physalis peruviana</i> leaf transcriptome: assembly, annotation and gene model prediction. <i>BMC Genomics</i> , 2012, 13, 151.	2.8	52
57	In silico identification and characterization of the ion transport specificity for P-type ATPases in the <i>Mycobacterium tuberculosis</i> complex. <i>BMC Structural Biology</i> , 2012, 12, 25.	2.3	26
58	Transcriptional Regulation of N-Acetylglutamate Synthase. <i>PLoS ONE</i> , 2012, 7, e29527.	2.5	26
59	Prediction of Transposable Element Derived Enhancers Using Chromatin Modification Profiles. <i>PLoS ONE</i> , 2011, 6, e27513.	2.5	25
60	Analysis of Biological Features Associated with Meiotic Recombination Hot and Cold Spots in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2011, 6, e29711.	2.5	20
61	Effect of the Transposable Element Environment of Human Genes on Gene Length and Expression. <i>Genome Biology and Evolution</i> , 2011, 3, 259-271.	2.5	40
62	Genome Sequence of the <i>Mycobacterium colombiense</i> Type Strain, CECT 3035. <i>Journal of Bacteriology</i> , 2011, 193, 5866-5867.	2.2	7
63	The Histone Database: an integrated resource for histones and histone fold-containing proteins. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar048-bar048.	3.0	40
64	Polymorphism of the Pv200L Fragment of Merozoite Surface Protein-1 of <i>Plasmodium vivax</i> in Clinical Isolates from the Pacific Coast of Colombia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 64-70.	1.4	12
65	Development and Characterization of Microsatellite Markers for the Cape Gooseberry <i>Physalis peruviana</i> . <i>PLoS ONE</i> , 2011, 6, e26719.	2.5	45
66	Epigenetic histone modifications of human transposable elements: genome defense versus exaptation. <i>Mobile DNA</i> , 2010, 1, 2.	3.6	60
67	Many sequence-specific chromatin modifying protein-binding motifs show strong positional preferences for potential regulatory regions in the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2010, 38, 1772-1779.	14.5	21
68	Repetitive DNA elements, nucleosome binding and human gene expression. <i>Gene</i> , 2009, 436, 12-22.	2.2	32
69	Identification of cis-Regulatory Elements in Gene Co-expression Networks Using A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 541, 3-22.	0.9	14
70	A c-Myc regulatory subnetwork from human transposable element sequences. <i>Molecular BioSystems</i> , 2009, 5, 1831.	2.9	22
71	Promoter Analysis: Gene Regulatory Motif Identification with A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 537, 263-276.	0.9	7
72	Finding sequence motifs with Bayesian models incorporating positional information: an application to transcription factor binding sites. <i>BMC Bioinformatics</i> , 2008, 9, 262.	2.6	25

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73	Evolutionary rates and patterns for human transcription factor binding sites derived from repetitive DNA. BMC Genomics, 2008, 9, 226.	2.8	62
74	The biological function of some human transcription factor binding motifs varies with position relative to the transcription start site. Nucleic Acids Research, 2008, 36, 2777-2786.	14.5	19
75	Expression Patterns of Protein Kinases Correlate with Gene Architecture and Evolutionary Rates. PLoS ONE, 2008, 3, e3599.	2.5	20
76	Widespread Positive Selection in Synonymous Sites of Mammalian Genes. Molecular Biology and Evolution, 2007, 24, 1821-1831.	8.9	86
77	Origin and Evolution of Human microRNAs From Transposable Elements. Genetics, 2007, 176, 1323-1337.	2.9	311
78	TLX1/HOX11-induced hematopoietic differentiation blockade. Oncogene, 2007, 26, 4115-4123.	5.9	20
79	Multiple Evolutionary Solutions to Core Histone Gene Regulation. FASEB Journal, 2007, 21, A1033.	0.5	0
80	Multiple independent evolutionary solutions to core histone gene regulation. Genome Biology, 2006, 7, R122.	9.6	47
81	Transposable element derived DNaseI-hypersensitive sites in the human genome. Biology Direct, 2006, 1, 20.	4.6	33
82	Co-Evolutionary Rates of Functionally Related Yeast Genes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	14
83	Scanning sequences after Gibbs sampling to find multiple occurrences of functional elements. BMC Bioinformatics, 2006, 7, 408.	2.6	2
84	Global similarity and local divergence in human and mouse gene co-expression networks. BMC Evolutionary Biology, 2006, 6, 70.	3.2	75
85	Co-evolutionary rates of functionally related yeast genes. Evolutionary Bioinformatics, 2006, 2, 271-6.	1.2	14
86	The histone database: A comprehensive resource for histones and histone fold-containing proteins. Proteins: Structure, Function and Bioinformatics, 2005, 62, 838-842.	2.6	51
87	Alignments anchored on genomic landmarks can aid in the identification of regulatory elements. Bioinformatics, 2005, 21, i440-i448.	4.1	30
88	Transposable elements donate lineage-specific regulatory sequences to host genomes. Cytogenetic and Genome Research, 2005, 110, 333-341.	1.1	91
89	Global Regulation by the Yeast Spt10 Protein Is Mediated through Chromatin Structure and the Histone Upstream Activating Sequence Elements. Molecular and Cellular Biology, 2005, 25, 9127-9137.	2.3	58
90	Histone structure and nucleosome stability. Expert Review of Proteomics, 2005, 2, 719-729.	3.0	237

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91	Evolutionary significance of gene expression divergence. <i>Gene</i> , 2005, 345, 119-126.	2.2	127
92	TLX1/HOX11-Mediated Disruption of Hematopoietic Differentiation Programs.. <i>Blood</i> , 2005, 106, 2997-2997.	1.4	0
93	Conservation and Coevolution in the Scale-Free Human Gene Coexpression Network. <i>Molecular Biology and Evolution</i> , 2004, 21, 2058-2070.	8.9	192
94	Identification and Mapping of Self-Assembling Protein Domains Encoded by the <i>Escherichia coli</i> K-12 Genome by Use of $\lambda$ Repressor Fusions. <i>Journal of Bacteriology</i> , 2004, 186, 1311-1319.	2.2	13
95	Statistical analysis of over-represented words in human promoter sequences. <i>Nucleic Acids Research</i> , 2004, 32, 949-958.	14.5	108
96	Statistical analysis of over-represented words in human promoter sequences. <i>Nucleic Acids Research</i> , 2004, 32, 5972-5972.	14.5	2
97	Screening Peptide/Protein Libraries Fused to the $\lambda$ Repressor DNA-Binding Domain in <i>E. coli</i> Cells. , 2003, 205, 235-250.		10
98	Isolation and mapping of self-assembling protein domains encoded by the <i>Saccharomyces cerevisiae</i> genome using $\lambda$ repressor fusions. <i>Yeast</i> , 2002, 19, 641-650.	1.7	28
99	Socioeconomic Deprivation and Genetic Ancestry Interact to Modify Type 2 Diabetes Ethnic Disparities in the United Kingdom. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0