

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

53
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107
all docs

107
docs citations

107
times ranked

4679
citing authors

#	ARTICLE	IF	CITATIONS
1	Origin and Evolution of Human microRNAs From Transposable Elements. <i>Genetics</i> , 2007, 176, 1323-1337.	2.9	311
2	Histone structure and nucleosome stability. <i>Expert Review of Proteomics</i> , 2005, 2, 719-729.	3.0	237
3	Conservation and Coevolution in the Scale-Free Human Gene Coexpression Network. <i>Molecular Biology and Evolution</i> , 2004, 21, 2058-2070.	8.9	192
4	TPMCalculator: one-step software to quantify mRNA abundance of genomic features. <i>Bioinformatics</i> , 2019, 35, 1960-1962.	4.1	149
5	Evolutionary significance of gene expression divergence. <i>Gene</i> , 2005, 345, 119-126.	2.2	127
6	Statistical analysis of over-represented words in human promoter sequences. <i>Nucleic Acids Research</i> , 2004, 32, 949-958.	14.5	108
7	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
8	Transposable elements donate lineage-specific regulatory sequences to host genomes. <i>Cytogenetic and Genome Research</i> , 2005, 110, 333-341.	1.1	91
9	Widespread Positive Selection in Synonymous Sites of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1821-1831.	8.9	86
10	Genetic ancestry, admixture and health determinants in Latin America. <i>BMC Genomics</i> , 2018, 19, 861.	2.8	78
11	Global similarity and local divergence in human and mouse gene co-expression networks. <i>BMC Evolutionary Biology</i> , 2006, 6, 70.	3.2	75
12	Mammalian-wide interspersed repeat (MIR)-derived enhancers and the regulation of human gene expression. <i>Mobile DNA</i> , 2014, 5, 14.	3.6	72
13	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
14	Benchmarking computational tools for polymorphic transposable element detection. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw072.	6.5	64
15	Evolutionary rates and patterns for human transcription factor binding sites derived from repetitive DNA. <i>BMC Genomics</i> , 2008, 9, 226.	2.8	62
16	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
17	Epigenetic histone modifications of human transposable elements: genome defense versus exaptation. <i>Mobile DNA</i> , 2010, 1, 2.	3.6	60
18	Global Regulation by the Yeast Spt10 Protein Is Mediated through Chromatin Structure and the Histone Upstream Activating Sequence Elements. <i>Molecular and Cellular Biology</i> , 2005, 25, 9127-9137.	2.3	58

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19	The <i>Physalis peruviana</i> leaf transcriptome: assembly, annotation and gene model prediction. <i>BMC Genomics</i> , 2012, 13, 151.	2.8	52
20	The histone database: A comprehensive resource for histones and histone fold-containing proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 838-842.	2.6	51
21	Multiple independent evolutionary solutions to core histone gene regulation. <i>Genome Biology</i> , 2006, 7, R122.	9.6	47
22	Human population-specific gene expression and transcriptional network modification with polymorphic transposable elements. <i>Nucleic Acids Research</i> , 2016, 45, gkw1286.	14.5	45
23	Development and Characterization of Microsatellite Markers for the Cape Gooseberry <i>Physalis peruviana</i> . <i>PLoS ONE</i> , 2011, 6, e26719.	2.5	45
24	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
25	The Histone Database: an integrated resource for histones and histone fold-containing proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar048-bar048.	3.0	40
26	BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. <i>Epigenetics and Chromatin</i> , 2020, 13, 21.	3.9	40
27	A Comparative Analysis of Genetic Ancestry and Admixture in the Colombian Populations of Chocó and Medellín. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3435-3447.	1.8	39
28	Transposable element derived DNaseI-hypersensitive sites in the human genome. <i>Biology Direct</i> , 2006, 1, 20.	4.6	33
29	Repetitive DNA elements, nucleosome binding and human gene expression. <i>Gene</i> , 2009, 436, 12-22.	2.2	32
30	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
31	Alignments anchored on genomic landmarks can aid in the identification of regulatory elements. <i>Bioinformatics</i> , 2005, 21, i440-i448.	4.1	30
32	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
33	Identification of Immunity Related Genes to Study the <i>Physalis peruviana</i> " Fusarium oxysporum Pathosystem. <i>PLoS ONE</i> , 2013, 8, e68500.	2.5	30
34	Isolation and mapping of self-assembling protein domains encoded by the <i>Saccharomyces cerevisiae</i> genome using λ repressor fusions. <i>Yeast</i> , 2002, 19, 641-650.	1.7	28
35	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
36	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

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37	Transcriptional Regulation of N-Acetylglutamate Synthase. PLoS ONE, 2012, 7, e29527.	2.5	26
38	Finding sequence motifs with Bayesian models incorporating positional information: an application to transcription factor binding sites. BMC Bioinformatics, 2008, 9, 262.	2.6	25
39	Prediction of Transposable Element Derived Enhancers Using Chromatin Modification Profiles. PLoS ONE, 2011, 6, e27513.	2.5	25
40	Socioeconomic deprivation and genetic ancestry interact to modify type 2 diabetes ethnic disparities in the United Kingdom. EClinicalMedicine, 2021, 37, 100960.	7.1	25
41	A c-Myc regulatory subnetwork from human transposable element sequences. Molecular BioSystems, 2009, 5, 1831.	2.9	22
42	Population and clinical genetics of human transposable elements in the (post) genomic era. Mobile Genetic Elements, 2017, 7, 1-20.	1.8	22
43	Many sequence-specific chromatin modifying protein-binding motifs show strong positional preferences for potential regulatory regions in the Saccharomyces cerevisiae genome. Nucleic Acids Research, 2010, 38, 1772-1779.	14.5	21
44	TLX1/HOX11-induced hematopoietic differentiation blockade. Oncogene, 2007, 26, 4115-4123.	5.9	20
45	Expression Patterns of Protein Kinases Correlate with Gene Architecture and Evolutionary Rates. PLoS ONE, 2008, 3, e3599.	2.5	20
46	Analysis of Biological Features Associated with Meiotic Recombination Hot and Cold Spots in Saccharomyces cerevisiae. PLoS ONE, 2011, 6, e29711.	2.5	20
47	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
48	Virulence and Immune Response Induced by Mycobacterium avium Complex Strains in a Model of Progressive Pulmonary Tuberculosis and Subcutaneous Infection in BALB/c Mice. Infection and Immunity, 2013, 81, 4001-4012.	2.2	18
49	El Chocó ³ , Colombia: un hotspot de la biodiversidad humana. Revista Biodiversidad Neotropical, 2016, 6, 45.	0.2	15
50	Co-Evolutionary Rates of Functionally Related Yeast Genes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	14
51	Identification of cis-Regulatory Elements in Gene Co-expression Networks Using A-GLAM. Methods in Molecular Biology, 2009, 541, 3-22.	0.9	14
52	Co-evolutionary rates of functionally related yeast genes. Evolutionary Bioinformatics, 2006, 2, 271-6.	1.2	14
53	Identification and Mapping of Self-Assembling Protein Domains Encoded by the Escherichia coli K-12 Genome by Use of λ Repressor Fusions. Journal of Bacteriology, 2004, 186, 1311-1319.	2.2	13
54	Polymorphism of the Pv200L Fragment of Merozoite Surface Protein-1 of Plasmodium vivax in Clinical Isolates from the Pacific Coast of Colombia. American Journal of Tropical Medicine and Hygiene, 2011, 84, 64-70.	1.4	12

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55	The Practical Evaluation of DNA Barcode Efficacy. <i>Methods in Molecular Biology</i> , 2012, 858, 365-377.	0.9	12
56	Genome Sequence of the Banana Plant Growth-Promoting Rhizobacterium <i>Bacillus amyloliquefaciens</i> BS006. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
57	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
58	Screening Peptide/Protein Libraries Fused to the λ Repressor DNA-Binding Domain in <i>E. coli</i> Cells. , 2003, 205, 235-250.		10
59	Genome Sequence of the Banana Plant Growth-Promoting Rhizobacterium <i>Pseudomonas fluorescens</i> PS006. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
60	De novo transcriptome assembly of loggerhead sea turtle nesting of the Colombian Caribbean. <i>Genomics Data</i> , 2017, 13, 18-20.	1.3	10
61	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
62	Transcriptome annotation in the cloud: complexity, best practices, and cost. <i>GigaScience</i> , 2021, 10, .	6.4	9
63	Whole-Genome Sequences of 26 <i>Vibrio cholerae</i> Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
64	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
65	Genome Sequence of the <i>Mycobacterium colombiense</i> Type Strain, CECT 3035. <i>Journal of Bacteriology</i> , 2011, 193, 5866-5867.	2.2	7
66	Genome Sequences of <i>Vibrio navarrensis</i> , a Potential Human Pathogen. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
67	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
68	Promoter Analysis: Gene Regulatory Motif Identification with A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 537, 263-276.	0.9	7
69	Comparing Genetic and Socioenvironmental Contributions to Ethnic Differences in C-Reactive Protein. <i>Frontiers in Genetics</i> , 2021, 12, 738485.	2.3	7
70	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
71	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
72	Genetic ancestry and ethnic identity in Ecuador. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100050.	1.7	4

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73	Effects of genetic ancestry and socioeconomic deprivation on ethnic differences in serum creatinine. <i>Gene</i> , 2022, 837, 146709.	2.2	4
74	Differences in local genomic context of bound and unbound motifs. <i>Gene</i> , 2012, 506, 125-134.	2.2	3
75	Complete mitochondrial genome of the nesting Colombian Caribbean Hawksbill Turtle. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 128-129.	0.4	3
76	Statistical analysis of over-represented words in human promoter sequences. <i>Nucleic Acids Research</i> , 2004, 32, 5972-5972.	14.5	2
77	Scanning sequences after Gibbs sampling to find multiple occurrences of functional elements. <i>BMC Bioinformatics</i> , 2006, 7, 408.	2.6	2
78	The ruzzo-tompa algorithm can find the maximal paths in weighted, directed graphs on a one-dimensional lattice. , 2012, , .		2
79	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
80	Genome Sequences of 15 <i>Klebsiella</i> sp. Isolates from Sugarcane Fields in Colombia's Cauca Valley. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
81	Whole-Genome Sequences of <i>Salmonella enterica</i> Serovar I 4,[5],12:i:~ Isolates from Swine. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
82	Transcriptional Analyses of Acute Exposure to Methylmercury on Erythrocytes of Loggerhead Sea Turtle. <i>Toxics</i> , 2021, 9, 70.	3.7	2
83	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
84	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
85	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
86	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
87	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
88	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
89	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
90	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

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91	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
92	Structural analysis of leucine, lysine and tryptophan mitochondrial tRNA of nesting turtles <i>Caretta caretta</i> (Testudines: Cheloniodea) in the Colombian Caribbean. <i>PeerJ</i> , 2020, 8, e9204.	2.0	1
93	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
94	Epigenetics and cancer disparities: when nature might be nurture. <i>Oncoscience</i> , 2022, 9, 23-24.	2.2	1
95	Comorbidities and ethnic health disparities in the UK biobank. <i>JAMIA Open</i> , 2022, 5, .	2.0	1
96	PM4NGS, a project management framework for next-generation sequencing data analysis. <i>GigaScience</i> , 2021, 10, .	6.4	0
97	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
98	TLX1/HOX11-Mediated Disruption of Hematopoietic Differentiation Programs.. <i>Blood</i> , 2005, 106, 2997-2997.	1.4	0
99	Multiple Evolutionary Solutions to Core Histone Gene Regulation. <i>FASEB Journal</i> , 2007, 21, A1033.	0.5	0