

# Ignacio MarÃ-Ã-n

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

3,329  
citations

159585

30  
h-index

149698

56  
g-index

66  
all docs

66  
docs citations

66  
times ranked

3826  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tumor Necrosis Factor Superfamily: Ancestral Functions and Remodeling in Early Vertebrate Evolution. <i>Genome Biology and Evolution</i> , 2020, 12, 2074-2092.	2.5	6
2	Origin and evolution of fungal HECT ubiquitin ligases. <i>Scientific Reports</i> , 2018, 8, 6419.	3.3	12
3	Origin and Diversification of Meprin Proteases. <i>PLoS ONE</i> , 2015, 10, e0135924.	2.5	5
4	Identification of HECT E3 ubiquitin ligase family genes involved in stem cell regulation and regeneration in planarians. <i>Developmental Biology</i> , 2015, 404, 21-34.	2.0	26
5	SurpriseMe: an integrated tool for network community structure characterization using Surprise maximization. <i>Bioinformatics</i> , 2014, 30, 1041-1042.	4.1	19
6	The ubiquitin gene family: evolutionary patterns and functional insights. <i>BMC Evolutionary Biology</i> , 2014, 14, 63.	3.2	67
7	Surprise maximization reveals the community structure of complex networks. <i>Scientific Reports</i> , 2013, 3, 1060.	3.3	66
8	Exploring the limits of community detection strategies in complex networks. <i>Scientific Reports</i> , 2013, 3, 2216.	3.3	58
9	Evolution of Plant HECT Ubiquitin Ligases. <i>PLoS ONE</i> , 2013, 8, e68536.	2.5	38
10	Closed benchmarks for network community structure characterization. <i>Physical Review E</i> , 2012, 85, 026109.	2.1	14
11	Origin and Diversification of TRIM Ubiquitin Ligases. <i>PLoS ONE</i> , 2012, 7, e50030.	2.5	53
12	Deciphering Network Community Structure by Surprise. <i>PLoS ONE</i> , 2011, 6, e24195.	2.5	81
13	Ancient origin of animal U-box ubiquitin ligases. <i>BMC Evolutionary Biology</i> , 2010, 10, 331.	3.2	23
14	Animal HECT ubiquitin ligases: evolution and functional implications. <i>BMC Evolutionary Biology</i> , 2010, 10, 56.	3.2	65
15	A sequence motif enriched in regions bound by the <i>Drosophila</i> dosage compensation complex. <i>BMC Genomics</i> , 2010, 11, 169.	2.8	8
16	Jerarca: Efficient Analysis of Complex Networks Using Hierarchical Clustering. <i>PLoS ONE</i> , 2010, 5, e11585.	2.5	37
17	GIN Transposons: Genetic Elements Linking Retrotransposons and Genes. <i>Molecular Biology and Evolution</i> , 2010, 27, 1903-1911.	8.9	13
18	Diversification and Specialization of Plant RBR Ubiquitin Ligases. <i>PLoS ONE</i> , 2010, 5, e11579.	2.5	26

#	ARTICLE	IF	CITATIONS
19	CGIN1: A Retroviral Contribution to Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2009, 26, 2167-2170.	8.9	32
20	Diversification of the cullin family. <i>BMC Evolutionary Biology</i> , 2009, 9, 267.	3.2	48
21	Interactome and Gene Ontology provide congruent yet subtly different views of a eukaryotic cell. <i>BMC Systems Biology</i> , 2009, 3, 69.	3.0	6
22	RBR Ubiquitin Ligases: Diversification and Streamlining in Animal Lineages. <i>Journal of Molecular Evolution</i> , 2009, 69, 54-64.	1.8	31
23	Basic networks: Definition and applications. <i>Journal of Theoretical Biology</i> , 2009, 258, 53-59.	1.7	1
24	Ancient Origin of the Parkinson Disease Gene LRRK2. <i>Journal of Molecular Evolution</i> , 2008, 67, 41-50.	1.8	68
25	How Athila retrotransposons survive in the Arabidopsis genome. <i>BMC Genomics</i> , 2008, 9, 219.	2.8	15
26	Fast comparison of DNA sequences by oligonucleotide profiling. <i>BMC Research Notes</i> , 2008, 1, 5.	1.4	7
27	The Roco protein family: a functional perspective. <i>FASEB Journal</i> , 2008, 22, 3103-3110.	0.5	113
28	A general strategy to determine the congruence between a hierarchical and a non-hierarchical classification. <i>BMC Bioinformatics</i> , 2007, 8, 442.	2.6	6
29	Global patterns of sequence evolution in Drosophila. <i>BMC Genomics</i> , 2007, 8, 408.	2.8	17
30	Comparative Genomics and Protein Domain Graph Analyses Link Ubiquitination and RNA Metabolism. <i>Journal of Molecular Biology</i> , 2006, 357, 9-17.	4.2	33
31	Proteasome-Related HslU and HslV Genes Typical of Eubacteria Are Widespread in Eukaryotes. <i>Journal of Molecular Evolution</i> , 2006, 63, 504-512.	1.8	17
32	LVPAR: fast detection of functional shifts in duplicate genes. <i>BMC Bioinformatics</i> , 2006, 7, 174.	2.6	5
33	The Parkinson Disease Gene LRRK2: Evolutionary and Structural Insights. <i>Molecular Biology and Evolution</i> , 2006, 23, 2423-2433.	8.9	149
34	A New Evolutionary Paradigm for the Parkinson Disease Gene DJ-1. <i>Molecular Biology and Evolution</i> , 2006, 24, 551-561.	8.9	64
35	Parkinson Disease: From Cellular and Animal Models to Genomics. <i>Current Genomics</i> , 2005, 6, 241-250.	1.6	1
36	Iterative Cluster Analysis of Protein Interaction Data. <i>Bioinformatics</i> , 2005, 21, 364-378.	4.1	199

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37	New Insights into the Evolutionary History of Type 1 Rhodopsins. <i>Journal of Molecular Evolution</i> , 2004, 58, 348-358.	1.8	67
38	Parkin and relatives: the RBR family of ubiquitin ligases. <i>Physiological Genomics</i> , 2004, 17, 253-263.	2.3	103
39	Evolution of Chromatin-Remodeling Complexes: Comparative Genomics Reveals the Ancient Origin of "Novel" Compensosome Genes. <i>Journal of Molecular Evolution</i> , 2003, 56, 527-539.	1.8	50
40	Evolutionary and Structural Analyses of GDAP1, Involved in Charcot-Marie-Tooth Disease, Characterize a Novel Class of Glutathione Transferase-Related Genes. <i>Molecular Biology and Evolution</i> , 2003, 21, 176-187.	8.9	90
41	Selection on Coding Regions Determined Hox7 Genes Evolution. <i>Molecular Biology and Evolution</i> , 2003, 20, 2104-2112.	8.9	29
42	Comparative Genomics of the RBR Family, Including the Parkinson's Disease-Related Gene Parkin and the Genes of the Ariadne Subfamily. <i>Molecular Biology and Evolution</i> , 2002, 19, 2039-2050.	8.9	101
43	The gene encoding ganglioside-induced differentiation-associated protein 1 is mutated in axonal Charcot-Marie-Tooth type 4A disease. <i>Nature Genetics</i> , 2002, 30, 22-25.	21.4	341
44	Tracing the Origin of the Compensosome: Evolutionary History of DEAH Helicase and MYST Acetyltransferase Gene Families. <i>Molecular Biology and Evolution</i> , 2001, 18, 330-343.	8.9	44
45	Detecting Changes in the Functional Constraints of Paralogous Genes. <i>Journal of Molecular Evolution</i> , 2001, 52, 17-28.	1.8	15
46	A Mammalian Gene Evolved from the Integrase Domain of an LTR Retrotransposon. <i>Molecular Biology and Evolution</i> , 2001, 18, 1597-1600.	8.9	30
47	Ty3/Gypsy Retrotransposons: Description of New <i>Arabidopsis thaliana</i> Elements and Evolutionary Perspectives Derived from Comparative Genomic Data. <i>Molecular Biology and Evolution</i> , 2000, 17, 1040-1049.	8.9	96
48	The evolution of dosage-compensation mechanisms. <i>BioEssays</i> , 2000, 22, 1106-1114.	2.5	119
49	Origin and Evolution of the Regulatory Gene male-specific lethal-3. <i>Molecular Biology and Evolution</i> , 2000, 17, 1240-1250.	8.9	45
50	The Evolutionary Dynamics of Sex Determination. <i>Science</i> , 1998, 281, 1990-1994.	12.6	286
51	Brief communication. Stable <i>Drosophila buzzatii</i> - <i>Drosophila koepferae</i> hybrids. , 1998, 89, 336-339.		6
52	Evolutionary Relationships Among the Members of an Ancient Class of Non-LTR Retrotransposons Found in the Nematode <i>Caenorhabditis elegans</i> . <i>Molecular Biology and Evolution</i> , 1998, 15, 1390-1402.	8.9	26
53	Sexual Isolation in <i>Drosophila</i> . III. Estimating Isolation Using Male-choice Experiments. <i>Journal of Theoretical Biology</i> , 1997, 188, 515-524.	1.7	7
54	Evolutionary conservation and molecular characteristics of repetitive sequences of <i>Drosophila koepferae</i> . <i>Heredity</i> , 1996, 76, 355-366.	2.6	9

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55	The dosage compensation system of <i>Drosophila</i> is co-opted by newly evolved X chromosomes. <i>Nature</i> , 1996, 383, 160-163.	27.8	131
56	Characterization of Gandalf, a new inverted-repeat transposable element of <i>Drosophila koepferae</i> . <i>Molecular Genetics and Genomics</i> , 1995, 248, 423-433.	2.4	11
57	Sexual isolation in <i>Drosophila</i> . II. Intraspecific variation in mate recognition systems. <i>Journal of Evolutionary Biology</i> , 1994, 7, 303-314.	1.7	8
58	Dosage Compensation in <i>Drosophila</i> . <i>Annual Review of Genetics</i> , 1994, 28, 491-521.	7.6	216
59	Reproductive Relationships among Ten Species of the <i>Drosophila repleta</i> Group from South America and the West Indies. <i>Evolution; International Journal of Organic Evolution</i> , 1993, 47, 1616.	2.3	11
60	REPRODUCTIVE RELATIONSHIPS AMONG TEN SPECIES OF THE <i>DROSOPHILA REPLETA</i> GROUP FROM SOUTH AMERICA AND THE WEST INDIES. <i>Evolution; International Journal of Organic Evolution</i> , 1993, 47, 1616-1624.	2.3	22
61	The evolutionary history of <i>Drosophila buzzatii</i> . XXIII. High content of nonsatellite repetitive DNA in <i>D. buzzatii</i> and in its sibling <i>D. koepferae</i> . <i>Genome</i> , 1992, 35, 967-974.	2.0	17
62	Sexual isolation in <i>Drosophila</i> I. Theoretical models for multiple-choice experiments. <i>Journal of Theoretical Biology</i> , 1991, 152, 271-284.	1.7	15
63	A fast algorithm for the exhaustive analysis of 12-nucleotide-long DNA sequences. Applications to human genomics. , 0, , .		1