

Araxi O Urrutia

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1922183/publications.pdf>

Version: 2024-02-01

42
papers

2,699
citations

394421

19
h-index

289244

40
g-index

45
all docs

45
docs citations

45
times ranked

4438
citing authors

#	ARTICLE	IF	CITATIONS
1	Sex differences in immune gene expression in the brain of a small shorebird. <i>Immunogenetics</i> , 2022, 74, 487-496.	2.4	3
2	Lack of age-related mosaic loss of W chromosome in long-lived birds. <i>Biology Letters</i> , 2022, 18, 20210553.	2.3	2
3	MeDAS: a Metazoan Developmental Alternative Splicing database. <i>Nucleic Acids Research</i> , 2021, 49, D144-D150.	14.5	13
4	Emergence of co-expression in gene regulatory networks. <i>PLoS ONE</i> , 2021, 16, e0247671.	2.5	35
5	Inferring Adaptive Codon Preference to Understand Sources of Selection Shaping Codon Usage Bias. <i>Molecular Biology and Evolution</i> , 2021, 38, 3247-3266.	8.9	14
6	Chicxulub museum, geosciences in Mexico, outreach and science communication “ built from the crater up. <i>Geoscience Communication</i> , 2021, 4, 267-280.	0.9	0
7	Contrasting gene-level signatures of selection with reproductive fitness. <i>Molecular Ecology</i> , 2021, , .	3.9	1
8	Rats exhibit age-related mosaic loss of chromosome Y. <i>Communications Biology</i> , 2021, 4, 1418.	4.4	5
9	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
10	Expression Evolution of Ancestral XY Gametologs across All Major Groups of Placental Mammals. <i>Genome Biology and Evolution</i> , 2020, 12, 2015-2028.	2.5	13
11	Sex determination systems in reptiles are related to ambient temperature but not to the level of climatic fluctuation. <i>BMC Evolutionary Biology</i> , 2020, 20, 103.	3.2	17
12	Transcriptional, Behavioral and Biochemical Profiling in the 3xTg-AD Mouse Model Reveals a Specific Signature of Amyloid Deposition and Functional Decline in Alzheimer’s Disease. <i>Frontiers in Neuroscience</i> , 2020, 14, 602642.	2.8	3
13	Viviparous Reptile Regarded to Have Temperature-Dependent Sex Determination Has Old XY Chromosomes. <i>Genome Biology and Evolution</i> , 2020, 12, 924-930.	2.5	37
14	Conditional expression explains molecular evolution of social genes in a microbe. <i>Nature Communications</i> , 2019, 10, 3284.	12.8	19
15	Demographic Histories and Genome-Wide Patterns of Divergence in Incipient Species of Shorebirds. <i>Frontiers in Genetics</i> , 2019, 10, 919.	2.3	14
16	Conserved transcriptomic profiles underpin monogamy across vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1331-1336.	7.1	75
17	Postmitotic cell longevity-associated genes: a transcriptional signature of postmitotic maintenance in neural tissues. <i>Neurobiology of Aging</i> , 2019, 74, 147-160.	3.1	4
18	Alternative splicing and the evolution of phenotypic novelty. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150474.	4.0	179

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19	Perspectives on the history of evo-devo and the contemporary research landscape in the genomics era. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150473.	4.0	14
20	Modular reorganization of the global network of gene regulatory interactions during perinatal human brain development. <i>BMC Developmental Biology</i> , 2016, 16, 13.	2.1	5
21	Neocortex expansion is linked to size variations in gene families with chemotaxis, cell signalling and immune response functions in mammals. <i>Open Biology</i> , 2016, 6, 160132.	3.6	0
22	Optimization of next-generation sequencing transcriptome annotation for species lacking sequenced genomes. <i>Molecular Ecology Resources</i> , 2016, 16, 446-458.	4.8	23
23	Lineage-specific sequence evolution and exon edge conservation partially explain the relationship between evolutionary rate and expression level in <i>A. thaliana</i> . <i>Molecular Ecology</i> , 2015, 24, 3093-3106.	3.9	11
24	Alternative Splice in Alternative Lice. <i>Molecular Biology and Evolution</i> , 2015, 32, 2749-2759.	8.9	29
25	YAP is essential for tissue tension to ensure vertebrate 3D body shape. <i>Nature</i> , 2015, 521, 217-221.	27.8	237
26	Increased brain size in mammals is associated with size variations in gene families with cell signalling, chemotaxis and immune-related functions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132428.	2.6	12
27	Correcting for Differential Transcript Coverage Reveals a Strong Relationship between Alternative Splicing and Organism Complexity. <i>Molecular Biology and Evolution</i> , 2014, 31, 1402-1413.	8.9	124
28	Presence-Absence Variation in <i>A. thaliana</i> Is Primarily Associated with Genomic Signatures Consistent with Relaxed Selective Constraints. <i>Molecular Biology and Evolution</i> , 2014, 31, 59-69.	8.9	36
29	Genes That Escape X-Inactivation in Humans Have High Intraspecific Variability in Expression, Are Associated with Mental Impairment but Are Not Slow Evolving. <i>Molecular Biology and Evolution</i> , 2013, 30, 2588-2601.	8.9	113
30	Evidence for Deep Phylogenetic Conservation of Exonic Splice-Related Constraints: Splice-Related Skews at Exonic Ends in the Brown Alga <i>Ectocarpus</i> Are Common and Resemble Those Seen in Humans. <i>Genome Biology and Evolution</i> , 2013, 5, 1731-1745.	2.5	6
31	Alternative Splicing: A Potential Source of Functional Innovation in the Eukaryotic Genome. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-10.	1.0	66
32	Protein Amino Acid Composition: A Genomic Signature of Encephalization in Mammals. <i>PLoS ONE</i> , 2011, 6, e27261.	2.5	5
33	Increased levels of noisy splicing in cancers, but not for oncogene-derived transcripts. <i>Human Molecular Genetics</i> , 2011, 20, 4422-4429.	2.9	32
34	Do Alu repeats drive the evolution of the primate transcriptome?. <i>Genome Biology</i> , 2008, 9, R25.	9.6	19
35	Splicing and the Evolution of Proteins in Mammals. <i>PLoS Biology</i> , 2007, 5, e14.	5.6	94
36	Chromatin remodelling is a major source of coexpression of linked genes in yeast. <i>Trends in Genetics</i> , 2007, 23, 480-484.	6.7	87

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37	A unification of mosaic structures in the human genome. <i>Human Molecular Genetics</i> , 2003, 12, 2411-2415.	2.9	119
38	The Signature of Selection Mediated by Expression on Human Genes. <i>Genome Research</i> , 2003, 13, 2260-2264.	5.5	227
39	Evidence That the Human X Chromosome Is Enriched for Male-Specific but not Female-Specific Genes. <i>Molecular Biology and Evolution</i> , 2003, 20, 1113-1116.	8.9	112
40	Clustering of housekeeping genes provides a unified model of gene order in the human genome. <i>Nature Genetics</i> , 2002, 31, 180-183.	21.4	496
41	Codon Usage Bias Covaries With Expression Breadth and the Rate of Synonymous Evolution in Humans, but This Is Not Evidence for Selection. <i>Genetics</i> , 2001, 159, 1191-1199.	2.9	135
42	Fast species diversification among dragonflies (Anisoptera: Odonata: Insecta) inhabiting lentic environments regardless of wing pigmentation. <i>Ecological Entomology</i> , 0, , .	2.2	2