Rute R Da Fonseca

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3738816/publications.pdf

Version: 2024-02-01

60 papers 6,058 citations

201575 27 h-index 56 g-index

69 all docs

69 docs citations

69 times ranked 9483 citing authors

#	Article	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
2	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
3	Patterns of Positive Selection in Six Mammalian Genomes. PLoS Genetics, 2008, 4, e1000144.	1.5	529
4	The adaptive evolution of the mammalian mitochondrial genome. BMC Genomics, 2008, 9, 119.	1.2	303
5	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
6	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	13.7	251
7	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. Journal of Proteome Research, 2012, 11, 917-926.	1.8	196
8	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. Marine Genomics, 2016, 30, 3-13.	0.4	164
9	Cephalopods in neuroscience: regulations, research and the 3Rs. Invertebrate Neuroscience, 2014, 14, 13-36.	1.8	142
10	Ancient genomics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130387.	1.8	142
11	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	4.7	138
12	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. Science, 2017, 358, 951-954.	6.0	105
13	Positive selection on the killer whale mitogenome. Biology Letters, 2011, 7, 116-118.	1.0	97
14	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. BMC Evolutionary Biology, 2009, 9, 95.	3.2	92
15	Molecular clocks indicate turnover and diversification of modern coleoid cephalopods during the Mesozoic Marine Revolution. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162818.	1.2	86
16	The Elusive Nature of Adaptive Mitochondrial DNA Evolution of an Arctic Lineage Prone to Frequent Introgression. Genome Biology and Evolution, 2014, 6, 886-896.	1,1	78
17	Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.	3.3	72
18	Molecular evolution and the role of oxidative stress in the expansion and functional diversification of cytosolic glutathione transferases. BMC Evolutionary Biology, 2010, 10, 281.	3.2	71

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19	Cephalopod genomics: A plan of strategies and organization. Standards in Genomic Sciences, 2012, 7, 175-188.	1.5	53
20	Comparative analysis of complete mitochondrial genomes suggests that relaxed purifying selection is driving high nonsynonymous evolutionary rate of the NADH2 gene in whitefish (Coregonus ssp.). Molecular Phylogenetics and Evolution, 2016, 95, 161-170.	1.2	53
21	Comparative genomics provides insights into the aquatic adaptations of mammals. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	43
22	Declining genetic diversity of European honeybees along the twentieth century. Scientific Reports, 2020, 10, 10520.	1.6	41
23	High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. Current Biology, 2021, 31, 1862-1871.e5.	1.8	41
24	Shotgun analysis of the marine mussel <i>Mytilus edulis</i> hemolymph proteome and mapping the innate immunity elements. Proteomics, 2015, 15, 4021-4029.	1.3	40
25	Theoretical quantitative structure–activity relationships of flavone ligands interacting with cytochrome P450 1A1 and 1A2 isozymes. Bioorganic and Medicinal Chemistry, 2005, 13, 4366-4374.	1.4	39
26	Positive selection on apoptosis related genes. FEBS Letters, 2010, 584, 469-476.	1.3	38
27	A draft genome sequence of the elusive giant squid, Architeuthis dux. GigaScience, 2020, 9, .	3.3	37
28	Identifying loci under positive selection in complex population histories. Genome Research, 2019, 29, 1506-1520.	2.4	36
29	"Out of the Can― A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, Sardina pilchardus. Genes, 2018, 9, 485.	1.0	30
30	Complete Inactivation of Sebum-Producing Genes Parallels the Loss of Sebaceous Glands in Cetacea. Molecular Biology and Evolution, 2019, 36, 1270-1280.	3.5	30
31	Proteomic Profiling of Cytosolic Glutathione Transferases from Three Bivalve Species: Corbicula fluminea, Mytilus galloprovincialis and Anodonta cygnea. International Journal of Molecular Sciences, 2014, 15, 1887-1900.	1.8	29
32	Structural divergence and adaptive evolution in mammalian cytochromes P450 2C. Gene, 2007, 387, 58-66.	1.0	28
33	Response of an Afro-Palearctic bird migrant to glaciation cycles. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
34	Combined Transcriptomic and Proteomic Analysis of the Posterior Salivary Gland from the Southern Blue-Ringed Octopus and the Southern Sand Octopus. Journal of Proteome Research, 2016, 15, 3284-3297.	1.8	22
35	Cartilaginous fishes offer unique insights into the evolution of the nuclear receptor gene repertoire in gnathostomes. General and Comparative Endocrinology, 2020, 295, 113527.	0.8	22
36	Proteomic profiling of gill GSTs in Mytilus galloprovincialis from the North of Portugal and Galicia evidences variations at protein isoform level with a possible relation with water quality. Marine Environmental Research, 2015, 110, 152-161.	1.1	19

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37	Genome sequence and effectorome of Moniliophthora perniciosa and Moniliophthora roreri subpopulations. BMC Genomics, 2018, 19, 509.	1.2	18
38	Adaptive evolution of the Retinoid X receptor in vertebrates. Genomics, 2012, 99, 81-89.	1.3	17
39	A refined model of the genomic basis for phenotypic variation in vertebrate hemostasis. BMC Evolutionary Biology, 2015, 15, 124.	3.2	16
40	Using ultraconserved elements to track the influence of seaâ€level change on leafy seadragon populations. Molecular Ecology, 2021, 30, 1364-1380.	2.0	16
41	The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758). DNA Research, 2021, 28, .	1.5	15
42	Adaptive venom evolution and toxicity in octopods is driven by extensive novel gene formation, expansion, and loss. GigaScience, 2020, 9, .	3.3	15
43	Losing Genes: The Evolutionary Remodeling of Cetacea Skin. Frontiers in Marine Science, 2020, 7, .	1.2	15
44	Conformational characterization of disulfide bonds: A tool for protein classification. Journal of Theoretical Biology, 2010, 267, 388-395.	0.8	12
45	Marine genomics: News and views. Marine Genomics, 2017, 31, 1-8.	0.4	12
46	DivA: detection of non-homologous and very divergent regions in protein sequence alignments. BMC Research Notes, 2014, 7, 806.	0.6	11
47	$31 {\hat A}^{\circ}$ South: The physiology of adaptation to arid conditions in a passerine bird. Molecular Ecology, 2019, 28, 3709-3721.	2.0	11
48	Consequences of breed formation on patterns of genomic diversity and differentiation: the case of highly diverse peripheral Iberian cattle. BMC Genomics, 2019, 20, 334.	1.2	11
49	Evolution of the extracytoplasmic function $\ddot{l}f$ factor protein family. NAR Genomics and Bioinformatics, 2020, 2, $lqz026$.	1.5	9
50	Amino Acid Patterns around Disulfide Bonds. International Journal of Molecular Sciences, 2010, 11, 4673-4686.	1.8	8
51	A resource for sustainable management: De novo assembly and annotation of the liver transcriptome of the Atlantic chub mackerel, Scomber colias. Data in Brief, 2018, 18, 276-284.	0.5	7
52	Population genomic footprints of environmental pollution pressure in natural populations of the Mediterranean mussel. Marine Genomics, 2019, 45, 11-15.	0.4	5
53	Modelling the metabolic action of human and rat CYP1A2 and its relationship with the carcinogenicity of heterocyclic amines. Molecular Physics, 2003, 101, 2731-2741.	0.8	4
54	Liver transcriptome resources of four commercially exploited teleost species. Scientific Data, 2020, 7, 214.	2.4	4

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55	Conservation genomics of the endangered Seychelles Magpieâ€Robin (Copsychus sechellarum): A unique insight into the history of a precious endemic bird. Ibis, 0, , .	1.0	4
56	A genome assembly of the Atlantic chub mackerel (Scomber colias): aÂvaluable teleost fishing resource. GigaByte, 0, 2022, 1-21.	0.0	3
57	IMPACT: Integrated Multiprogram Platform for Analyses in ConTest. Journal of Heredity, 2011, 102, 366-369.	1.0	2
58	Link Your Sites (LYS) Scripts: Automated Search of Protein Structures and Mapping of Sites Under Positive Selection Detected by PAML. Evolutionary Biology, 2020, 47, 240-245.	0.5	0
59	Computational Insight into Anti-mutagenic Properties of CYP1A Flavonoid Ligands. Medicinal Chemistry, 2005, 1, 355-360.	0.7	O
60	Molecular Interactions Between Human Cytochrome P450 1A2 and Flavone Derivatives. Medicinal Chemistry, 2006, 2, 401-406.	0.7	0