

Matthias Platzer

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

26,050
citations

236612

25
h-index

233125

45
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55
all docs

55
docs citations

55
times ranked

29553
citing authors

#	ARTICLE	IF	CITATIONS
1	A perceptually optimised bivariate visualisation scheme for high-dimensional fold-change data. <i>Advances in Data Analysis and Classification</i> , 2021, 15, 463-480.	0.9	0
2	Increased longevity due to sexual activity in mole-rats is associated with transcriptional changes in the HPA stress axis. <i>ELife</i> , 2021, 10, .	2.8	17
3	Epigenetic Modifications Associated with Maternal Anxiety during Pregnancy and Children's Behavioral Measures. <i>Cells</i> , 2021, 10, 2421.	1.8	14
4	Hematologic adaptation to the subterranean environment by the naked mole-rat, <i>Heterocephalus glaber</i> (Ctenohystrica: Heterocephalidae). <i>Journal of Mammalogy</i> , 2020, 101, 1000-1009.	0.6	2
5	C/EBP β -LIP induces cancer-type metabolic reprogramming by regulating the let-7/LIN28B circuit in mice. <i>Communications Biology</i> , 2019, 2, 208.	2.0	13
6	Comment on 'Naked mole-rat mortality rates defy Gompertzian laws by not increasing with age'. <i>ELife</i> , 2019, 8, .	2.8	16
7	Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. <i>Nature Communications</i> , 2018, 9, 327.	5.8	94
8	Haplotypes composed of minor frequency single nucleotide polymorphisms of the TNF gene protect from progression into sepsis: A study using the new sepsis classification. <i>International Journal of Infectious Diseases</i> , 2018, 67, 102-106.	1.5	11
9	The microenvironment of naked mole-rat burrows in East Africa. <i>African Journal of Ecology</i> , 2018, 56, 279-289.	0.4	75
10	Naked mole-rat transcriptome signatures of socially suppressed sexual maturation and links of reproduction to aging. <i>BMC Biology</i> , 2018, 16, 77.	1.7	26
11	Species comparison of liver proteomes reveals links to naked mole-rat longevity and human aging. <i>BMC Biology</i> , 2018, 16, 82.	1.7	55
12	The high degree of cystathionine β -synthase (CBS) activation by S-adenosylmethionine (SAM) may explain naked mole-rat's distinct methionine metabolite profile compared to mouse. <i>GeroScience</i> , 2018, 40, 359-360.	2.1	7
13	Googles DeepVariant: eine Methode für die Medizin- und Bioinformatik?. <i>BioSpektrum</i> , 2018, 24, 235-235.	0.0	1
14	Long-lived rodents reveal signatures of positive selection in genes associated with lifespan. <i>PLoS Genetics</i> , 2018, 14, e1007272.	1.5	39
15	Higher gene expression stability during aging in long-lived giant mole-rats than in short-lived rats. <i>Aging</i> , 2018, 10, 3938-3956.	1.4	16
16	PosiGene: automated and easy-to-use pipeline for genome-wide detection of positively selected genes. <i>Nucleic Acids Research</i> , 2017, 45, e100-e100.	6.5	50
17	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
18	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130

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19	Parallel evolution of genes controlling mitonuclear balance in short-lived annual fishes. <i>Aging Cell</i> , 2017, 16, 488-496.	3.0	29
20	Tissue-, sex-, and age-specific DNA methylation of rat glucocorticoid receptor gene promoter and insulin-like growth factor 2 imprinting control region. <i>Physiological Genomics</i> , 2017, 49, 690-702.	1.0	12
21	A miRNA catalogue and ncRNA annotation of the short-living fish <i>Nothobranchius furzeri</i> . <i>BMC Genomics</i> , 2017, 18, 693.	1.2	18
22	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
23	Genetic Factors of the Disease Course after Sepsis: A Genome-Wide Study for 28 Day Mortality. <i>EBioMedicine</i> , 2016, 12, 239-246.	2.7	52
24	Genetic Factors of the Disease Course After Sepsis: Rare Deleterious Variants Are Predictive. <i>EBioMedicine</i> , 2016, 12, 227-238.	2.7	34
25	Outgroups and Positive Selection: The <i>Nothobranchius furzeri</i> Case. <i>Trends in Genetics</i> , 2016, 32, 523-525.	2.9	12
26	<i>Nothobranchius furzeri</i> : A Model for Aging Research and More. <i>Trends in Genetics</i> , 2016, 32, 543-552.	2.9	72
27	Low sulfide levels and a high degree of cystathionine β -synthase (CBS) activation by S-adenosylmethionine (SAM) in the long-lived naked mole-rat. <i>Redox Biology</i> , 2016, 8, 192-198.	3.9	22
28	FRAMA: from RNA-seq data to annotated mRNA assemblies. <i>BMC Genomics</i> , 2016, 17, 54.	1.2	30
29	Longitudinal RNA-Seq Analysis of Vertebrate Aging Identifies Mitochondrial Complex I as a Small-Molecule-Sensitive Modifier of Lifespan. <i>Cell Systems</i> , 2016, 2, 122-132.	2.9	155
30	Insights into Sex Chromosome Evolution and Aging from the Genome of a Short-Lived Fish. <i>Cell</i> , 2015, 163, 1527-1538.	13.5	251
31	Analysis of Alpha-2 Macroglobulin from the Long-Lived and Cancer-Resistant Naked Mole-Rat and Human Plasma. <i>PLoS ONE</i> , 2015, 10, e0130470.	1.1	24
32	The strange case of East African annual fishes: aridification correlates with diversification for a savannah aquatic group?. <i>BMC Evolutionary Biology</i> , 2014, 14, 210.	3.2	50
33	RepARK – de novo creation of repeat libraries from whole-genome NGS reads. <i>Nucleic Acids Research</i> , 2014, 42, e80-e80.	6.5	67
34	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	2.3	77
35	The age related markers lipofuscin and apoptosis show different genetic architecture by QTL mapping in short-lived <i>Nothobranchius</i> fish. <i>Aging</i> , 2014, 6, 468-480.	1.4	13
36	The transcript catalogue of the short-lived fish <i>Nothobranchius furzeri</i> provides insights into age-dependent changes of mRNA levels. <i>BMC Genomics</i> , 2013, 14, 185.	1.2	52

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37	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
38	Mapping of quantitative trait loci controlling lifespan in the short-lived fish <i>Nothobranchius furzeri</i> – a new vertebrate model for age research. <i>Aging Cell</i> , 2012, 11, 252-261.	3.0	72
39	RNA Sequencing Reveals Differential Expression of Mitochondrial and Oxidation Reduction Genes in the Long-Lived Naked Mole-Rat When Compared to Mice. <i>PLoS ONE</i> , 2011, 6, e26729.	1.1	91
40	Mitochondrial DNA copy number and function decrease with age in the short-lived fish <i>Nothobranchius furzeri</i> . <i>Aging Cell</i> , 2011, 10, 824-831.	3.0	114
41	Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011, 4, 411.	0.6	13
42	Mapping Loci Associated With Tail Color and Sex Determination in the Short-Lived Fish <i>Nothobranchius furzeri</i> . <i>Genetics</i> , 2009, 183, 1385-1395.	1.2	67
43	Telomeres shorten while Tert expression increases during ageing of the short-lived fish <i>Nothobranchius furzeri</i> . <i>Mechanisms of Ageing and Development</i> , 2009, 130, 290-296.	2.2	115
44	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. <i>BMC Genomics</i> , 2009, 10, 547.	1.2	69
45	High tandem repeat content in the genome of the short-lived annual fish <i>Nothobranchius furzeri</i> : a new vertebrate model for aging research. <i>Genome Biology</i> , 2009, 10, R16.	13.9	87
46	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074