

Lars Geffers

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/861388/publications.pdf>

Version: 2024-02-01

20
papers

1,237
citations

687363

13
h-index

839539

18
g-index

21
all docs

21
docs citations

21
times ranked

2917
citing authors

#	ARTICLE	IF	CITATIONS
1	A High-Resolution Anatomical Atlas of the Transcriptome in the Mouse Embryo. <i>PLoS Biology</i> , 2011, 9, e1000582.	5.6	552
2	Parkinsonâ€™s disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. <i>BMC Biology</i> , 2020, 18, 62.	3.8	122
3	Organization of the pronephric kidney revealed by large-scale gene expression mapping. <i>Genome Biology</i> , 2008, 9, R84.	9.6	116
4	Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. <i>JAMA Oncology</i> , 2020, 6, 714.	7.1	84
5	Generation of Thyrotropin-Releasing Hormone Receptor 1-Deficient Mice as an Animal Model of Central Hypothyroidism. <i>Molecular Endocrinology</i> , 2004, 18, 1450-1460.	3.7	76
6	The Luxembourg Parkinsonâ€™s Study: A Comprehensive Approach for Stratification and Early Diagnosis. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 326.	3.4	57
7	Common diseases alter the physiological age-related blood microRNA profile. <i>Nature Communications</i> , 2020, 11, 5958.	12.8	46
8	CRX Is a Diagnostic Marker of Retinal and Pineal Lineage Tumors. <i>PLoS ONE</i> , 2009, 4, e7932.	2.5	43
9	A nuclear protein in <i>Schizosaccharomyces pombe</i> with homology to the human tumour suppressor Fhit has decapping activity. <i>Molecular Microbiology</i> , 2002, 46, 49-62.	2.5	29
10	Deep sequencing of sncRNAs reveals hallmarks and regulatory modules of the transcriptome during Parkinsonâ€™s disease progression. <i>Nature Aging</i> , 2021, 1, 309-322.	11.6	26
11	Web-based digital gene expression atlases for the mouse. <i>Mammalian Genome</i> , 2012, 23, 525-538.	2.2	24
12	Expression patterns of the aquaporin gene family during renal development: influence of genetic variability. <i>Pflügers Archiv European Journal of Physiology</i> , 2009, 458, 745-759.	2.8	20
13	The transcription factor HNF1Î± regulates expression of chloride-proton exchanger ClC-5 in the renal proximal tubule. <i>American Journal of Physiology - Renal Physiology</i> , 2010, 299, F1339-F1347.	2.7	14
14	Meningioma transcription factors link cell lineage with systemic metabolic cues. <i>Neuro-Oncology</i> , 2018, 20, 1331-1343.	1.2	9
15	METscout: a pathfinder exploring the landscape of metabolites, enzymes and transporters. <i>Nucleic Acids Research</i> , 2012, 41, D1047-D1054.	14.5	7
16	Large-scale validation of miRNAs by disease association, evolutionary conservation and pathway activity. <i>RNA Biology</i> , 2019, 16, 93-103.	3.1	5
17	A Computational Approach to Estimate Interorgan Metabolic Transport in a Mammal. <i>PLoS ONE</i> , 2014, 9, e100963.	2.5	3
18	A compendium of expression patterns of cholesterol biosynthetic enzymes in the mouse embryo. <i>Journal of Lipid Research</i> , 2015, 56, 1551-1559.	4.2	2

#	ARTICLE	IF	CITATIONS
19	Integrated Annotation and Analysis of In Situ Hybridization Images Using the ImAnno System: Application to the Ear and Sensory Organs of the Fetal Mouse. PLoS ONE, 2015, 10, e0118024.	2.5	0
20	High-Throughput In Situ Hybridization: Systematical Production of Gene Expression Data and Beyond. Neuromethods, 2015, , 221-245.	0.3	0