

Laurentijn Tilleman

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

536
citations

933447

10
h-index

713466

21
g-index

30
all docs

30
docs citations

30
times ranked

963
citing authors

#	ARTICLE	IF	CITATIONS
1	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	10.3	15
2	Activin A-derived human embryonic stem cells show increased competence to differentiate into primordial germ cell-like cells. <i>Stem Cells</i> , 2021, 39, 551-563.	3.2	11
3	Comparative genomics of <i>Flavobacterium columnare</i> unveils novel insights in virulence and antimicrobial resistance mechanisms. <i>Veterinary Research</i> , 2021, 52, 18.	3.0	5
4	Endogenous suppression of WNT signalling in human embryonic stem cells leads to low differentiation propensity towards definitive endoderm. <i>Scientific Reports</i> , 2021, 11, 6137.	3.3	6
5	Metallothioneins alter macrophage phenotype and represent novel therapeutic targets for acetaminophen-induced liver injury. <i>Journal of Leukocyte Biology</i> , 2021, 111, 123-133.	3.3	8
6	HES1 and HES4 have non-redundant roles downstream of Notch during early human T-cell development. <i>Haematologica</i> , 2020, 106, 130-141.	3.5	20
7	Pan-cancer pharmacogenetics: targeted sequencing panels or exome sequencing?. <i>Pharmacogenomics</i> , 2020, 21, 1073-1084.	1.3	3
8	Kinship analysis on single cells after whole genome amplification. <i>Scientific Reports</i> , 2020, 10, 14647.	3.3	6
9	Comparative study of preimplantation development following distinct assisted oocyte activation protocols in a PLC-zeta knockout mouse model. <i>Molecular Human Reproduction</i> , 2020, 26, 801-815.	2.8	11
10	The transcription factor ETS1 is an important regulator of human NK cell development and terminal differentiation. <i>Blood</i> , 2020, 136, 288-298.	1.4	33
11	Maternal Recognition of Pregnancy in the Horse: Are MicroRNAs the Secret Messengers?. <i>International Journal of Molecular Sciences</i> , 2020, 21, 419.	4.1	10
12	Myeloid-specific IRE1alpha deletion reduces tumour development in a diabetic, non-alcoholic steatohepatitis-induced hepatocellular carcinoma mouse model. <i>Metabolism: Clinical and Experimental</i> , 2020, 107, 154220.	3.4	19
13	Gain of 20q11.21 in Human Pluripotent Stem Cells Impairs TGF- β -Dependent Neuroectodermal Commitment. <i>Stem Cell Reports</i> , 2019, 13, 163-176.	4.8	39
14	Uncovering low-level mosaicism in human embryonic stem cells using high throughput single cell shallow sequencing. <i>Scientific Reports</i> , 2019, 9, 14844.	3.3	12
15	A multi-omics analysis of the grapevine pathogen <i>Lasiodiplodia theobromae</i> reveals that temperature affects the expression of virulence- and pathogenicity-related genes. <i>Scientific Reports</i> , 2019, 9, 13144.	3.3	47
16	YtrASa, a GntR-Family Transcription Factor, Represses Two Genetic Loci Encoding Membrane Proteins in <i>Sulfolobus acidocaldarius</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2084.	3.5	9
17	Marine biogenics in sea spray aerosols interact with the mTOR signaling pathway. <i>Scientific Reports</i> , 2019, 9, 675.	3.3	12
18	Contemporary pharmacogenetic assays in view of the PharmGKB database. <i>Pharmacogenomics</i> , 2019, 20, 261-272.	1.3	13

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19	WNT Inhibition and Increased FGF Signaling Promotes Derivation of Less Heterogeneous Primed Human Embryonic Stem Cells, Compatible with Differentiation. <i>Stem Cells and Development</i> , 2019, 28, 579-592.	2.1	9
20	Dual RNA Sequencing of <i>Vitis vinifera</i> during <i>Lasiodiplodia theobromae</i> Infection Unveils Host-Pathogen Interactions. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6083.	4.1	28
21	Transcriptional landscape changes during human embryonic stem cell derivation. <i>Molecular Human Reproduction</i> , 2018, 24, 543-555.	2.8	5
22	Direct comparison of distinct naive pluripotent states in human embryonic stem cells. <i>Nature Communications</i> , 2017, 8, 15055.	12.8	60
23	GATA-3 Suppresses IRF8 to promote human T-cell lineage commitment. <i>Experimental Hematology</i> , 2017, 53, S83.	0.4	0
24	STR profiling and Copy Number Variation analysis on single, preserved cells using current Whole Genome Amplification methods. <i>Scientific Reports</i> , 2017, 7, 17189.	3.3	8
25	Performance of four modern whole genome amplification methods for copy number variant detection in single cells. <i>Scientific Reports</i> , 2017, 7, 3422.	3.3	54
26	The transcriptome of <i>Mycobacterium tuberculosis</i> in a lipid-rich dormancy model through RNAseq analysis. <i>Scientific Reports</i> , 2017, 7, 17665.	3.3	88