## Carla S Möller-Levet

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/195795/publications.pdf

Version: 2024-02-01

23 papers 1,371 citations

623734 14 h-index 677142 22 g-index

28 all docs 28 docs citations

times ranked

28

2349 citing authors

#	Article	IF	Citations
1	Novel stress granules-like structures are induced via a paracrine mechanism during viral infection. Journal of Cell Science, 2022, , .	2.0	5
2	HOXB9 Overexpression Promotes Colorectal Cancer Progression and Is Associated with Worse Survival in Liver Resection Patients for Colorectal Liver Metastases. International Journal of Molecular Sciences, 2022, 23, 2281.	4.1	8
3	Vitamins D2 and D3 Have Overlapping But Different Effects on the Human Immune System Revealed Through Analysis of the Blood Transcriptome. Frontiers in Immunology, 2022, 13, 790444.	4.8	20
4	Diurnal and circadian rhythmicity of the human blood transcriptome overlaps with organ- and tissue-specific expression of a non-human primate. BMC Biology, 2022, 20, 63.	3.8	4
5	HOX and PBX gene dysregulation as a therapeutic target in glioblastoma multiforme. BMC Cancer, 2022, 22, 400.	2.6	7
6	functions as a potential novel oncopromoter in colorectal cancer: a comprehensive analysis of the gene family American Journal of Cancer Research, 2022, 12, 585-600.	1.4	0
7	REM sleep's unique associations with corticosterone regulation, apoptotic pathways, and behavior in chronic stress in mice. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2733-2742.	7.1	59
8	Universal and robust assessment of circadian time?. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5205-5205.	7.1	4
9	Genome-wide analysis of the role of the antibiotic biosynthesis regulator AbsA2 in Streptomyces coelicolor A3(2). PLoS ONE, 2019, 14, e0200673.	2.5	24
10	Circadian regulation in human white adipose tissue revealed by transcriptome and metabolic network analysis. Scientific Reports, 2019, 9, 2641.	3.3	55
11	Identifying and validating blood mRNA biomarkers for acute and chronic insufficient sleep in humans: a machine learning approach. Sleep, 2019, 42, .	1.1	35
12	Oncolytic Immunotherapy for Bladder Cancer Using Coxsackie A21 Virus. Molecular Therapy - Oncolytics, 2018, 9, 1-12.	4.4	49
13	Nuclear-cytoplasmic compartmentalization of the herpes simplex virus 1 infected cell transcriptome is co-ordinated by the viral endoribonuclease vhs and cofactors to facilitate the translation of late proteins. PLoS Pathogens, 2018, 14, e1007331.	4.7	31
14	Translational control plays an important role in the adaptive heat-shock response of Streptomyces coelicolor. Nucleic Acids Research, 2018, 46, 5692-5703.	14.5	17
15	Blood transcriptome based biomarkers for human circadian phase. ELife, 2017, 6, .	6.0	117
16	The prognostic significance of specific <i>HOX</i> gene expression patterns in ovarian cancer. International Journal of Cancer, 2016, 139, 1608-1617.	5.1	54
17	Exploiting human and mouse transcriptomic data: Identification of circadian genes and pathways influencing health. BioEssays, 2015, 37, 544-556.	2.5	28
18	Mistimed sleep disrupts circadian regulation of the human transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E682-91.	7.1	312

#	Article	IF	CITATIONS
19	Effects of insufficient sleep on circadian rhythmicity and expression amplitude of the human blood transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1132-41.	7.1	452
20	Exon Array Analysis of Head and Neck Cancers Identifies a Hypoxia Related Splice Variant of LAMA3 Associated with a Poor Prognosis. PLoS Computational Biology, 2009, 5, e1000571.	3.2	37
21	MODELING AND ANALYSIS OF GENE EXPRESSION TIME-SERIES BASED ON CO-EXPRESSION. International Journal of Neural Systems, 2005, 15, 311-322.	5.2	13
22	Microarray data clustering based on temporal variation: FCV with TSD preclustering. Applied Bioinformatics, 2003, 2, 35-45.	1.6	25
23	The Curse of Normalization. Comparative and Functional Genomics, 2002, 3, 375-379.	2.0	10