

Dominik Rl Lutter

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,980
citations

361413

20
h-index

289244

40
g-index

47
all docs

47
docs citations

47
times ranked

3334
citing authors

#	ARTICLE	IF	CITATIONS
1	Atlas of exercise metabolism reveals time-dependent signatures of metabolic homeostasis. <i>Cell Metabolism</i> , 2022, 34, 329-345.e8.	16.2	86
2	Antibiotic-induced microbiome depletion remodels daily metabolic cycles in the brain. <i>Life Sciences</i> , 2022, 303, 120601.	4.3	1
3	Untargeted and Targeted Circadian Metabolomics Using Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) and Flow Injection-Electrospray Ionization-Tandem Mass Spectrometry (FIA-ESI-MS/MS). <i>Methods in Molecular Biology</i> , 2022, , 311-327.	0.9	2
4	Correlation-guided Network Integration (CoNI), an R package for integrating numerical omics data that allows multiform graph representations to study molecular interaction networks. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	0
5	Diet triggers specific responses of hypothalamic astrocytes in time and region dependent manner. <i>Glia</i> , 2022, 70, 2062-2078.	4.9	12
6	Combination therapies induce cancer cell death through the integrated stress response and disturbed pyrimidine metabolism. <i>EMBO Molecular Medicine</i> , 2021, 13, e12461.	6.9	12
7	The glucose-dependent insulinotropic polypeptide (GIP) regulates body weight and food intake via CNS-GIPR signaling. <i>Cell Metabolism</i> , 2021, 33, 833-844.e5.	16.2	128
8	Integration of feeding behavior by the liver circadian clock reveals network dependency of metabolic rhythms. <i>Science Advances</i> , 2021, 7, eabi7828.	10.3	50
9	Correlation guided Network Integration (CoNI) reveals novel genes affecting hepatic metabolism. <i>Molecular Metabolism</i> , 2021, 53, 101295.	6.5	4
10	Identification and characterization of distinct brown adipocyte subtypes in C57BL/6J mice. <i>Life Science Alliance</i> , 2021, 4, e202000924.	2.8	14
11	Molecular classification of the placebo effect in nausea. <i>PLoS ONE</i> , 2020, 15, e0238533.	2.5	6
12	Endogenous FGF21-signaling controls paradoxical obesity resistance of UCP1-deficient mice. <i>Nature Communications</i> , 2020, 11, 624.	12.8	60
13	Intermuscular adipose tissue directly modulates skeletal muscle insulin sensitivity in humans. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 316, E866-E879.	3.5	97
14	Atlas of Circadian Metabolism Reveals System-wide Coordination and Communication between Clocks. <i>Cell</i> , 2018, 174, 1571-1585.e11.	28.9	258
15	Transcriptional programming of lipid and amino acid metabolism by the skeletal muscle circadian clock. <i>PLoS Biology</i> , 2018, 16, e2005886.	5.6	107
16	Regulation of Glucose Uptake and Enteroendocrine Function by the Intestinal Epithelial Insulin Receptor. <i>Diabetes</i> , 2017, 66, 886-896.	0.6	32
17	Molecular Integration of Incretin and Glucocorticoid Action Reverses Immunometabolic Dysfunction and Obesity. <i>Cell Metabolism</i> , 2017, 26, 620-632.e6.	16.2	66
18	Time-matched analysis of DNA adduct formation and early gene expression as predictive tool for renal carcinogenesis in methylazoxymethanol acetate treated Eker rats. <i>Archives of Toxicology</i> , 2017, 91, 3427-3438.	4.2	8

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19	Role Of Neuronal Fractalkine In Reducing Diet-induced Hypothalamic Inflammation. <i>Medicine and Science in Sports and Exercise</i> , 2017, 49, 702.	0.4	1
20	Epstein-Barr virus microRNAs reduce immune surveillance by virus-specific CD8 ⁺ T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6467-E6475.	7.1	127
21	Chemical Hybridization of Glucagon and Thyroid Hormone Optimizes Therapeutic Impact for Metabolic Disease. <i>Cell</i> , 2016, 167, 843-857.e14.	28.9	153
22	Epstein-Barr viral miRNAs inhibit antiviral CD4 ⁺ T cell responses targeting IL-12 and peptide processing. <i>Journal of Experimental Medicine</i> , 2016, 213, 2065-2080.	8.5	108
23	Pitchfork and Gprasp2 Target Smoothed to the Primary Cilium for Hedgehog Pathway Activation. <i>PLoS ONE</i> , 2016, 11, e0149477.	2.5	21
24	K1 and K15 of Kaposi's Sarcoma-Associated Herpesvirus Are Partial Functional Homologues of Latent Membrane Protein 2A of Epstein-Barr Virus. <i>Journal of Virology</i> , 2015, 89, 7248-7261.	3.4	44
25	Torpor at high ambient temperature in a neotropical didelphid, the grey short-tailed opossum (<i>Monodelphis domestica</i>). <i>Die Naturwissenschaften</i> , 2014, 101, 1003-1006.	1.6	8
26	c-Jun/c-Fos heterodimers regulate cellular genes via a newly identified class of methylated DNA sequence motifs. <i>Nucleic Acids Research</i> , 2014, 42, 3059-3072.	14.5	73
27	miR-335 promotes mesendodermal lineage segregation and shapes a transcription factor gradient in the endoderm. <i>Development (Cambridge)</i> , 2014, 141, 514-525.	2.5	20
28	Sharpening of expression domains induced by transcription and microRNA regulation within a spatio-temporal model of mid-hindbrain boundary formation. <i>BMC Systems Biology</i> , 2013, 7, 48.	3.0	16
29	The signal separation evaluation campaign (2007-2010): Achievements and remaining challenges. <i>Signal Processing</i> , 2012, 92, 1928-1936.	3.7	128
30	An Ensemble Approach for Inferring Semi-quantitative Regulatory Dynamics for the Differentiation of Mouse Embryonic Stem Cells Using Prior Knowledge. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 247-260.	1.6	4
31	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , 2011, 5, 136.	3.0	49
32	Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. <i>BMC Genomics</i> , 2010, 11, 224.	2.8	126
33	The 2010 Signal Separation Evaluation Campaign (SiSEC2010): Audio Source Separation. <i>Lecture Notes in Computer Science</i> , 2010, , 114-122.	1.3	25
34	The 2010 Signal Separation Evaluation Campaign (SiSEC2010): Biomedical Source Separation. <i>Lecture Notes in Computer Science</i> , 2010, , 123-130.	1.3	2
35	GeneSet2miRNA: finding the signature of cooperative miRNA activities in the gene lists. <i>Nucleic Acids Research</i> , 2009, 37, W323-W328.	14.5	47
36	Analyzing time-dependent microarray data using independent component analysis derived expression modes from human macrophages infected with <i>F. tularensis</i> holarctica. <i>Journal of Biomedical Informatics</i> , 2009, 42, 605-611.	4.3	11

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37	Analyzing M-CSF dependent monocyte/macrophage differentiation: Expression modes and meta-modes derived from an independent component analysis. BMC Bioinformatics, 2008, 9, 100.	2.6	20
38	Knowledge-based gene expression classification via matrix factorization. Bioinformatics, 2008, 24, 1688-1697.	4.1	36
39	Comparison of unsupervised and supervised gene selection methods. , 2008, 2008, 5212-5.		2
40	Routes to identify marker genes for microarray classification. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 4617-20.	0.5	4
41	How to extract marker genes from microarray data sets. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 4215-8.	0.5	6