

Jakub O Westholm

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

5,334
citations

279798
23
h-index

414414
32
g-index

38
all docs

38
docs citations

38
times ranked

9121
citing authors

#	ARTICLE	IF	CITATIONS
1	Acute sleep loss alters circulating fibroblast growth factor 21 levels in humans: A randomised crossover trial. <i>Journal of Sleep Research</i> , 2022, 31, e13472.	3.2	6
2	Clonal relations in the mouse brain revealed by single-cell and spatial transcriptomics. <i>Nature Neuroscience</i> , 2022, 25, 285-294.	14.8	48
3	Profiling of Extracellular Small RNAs Highlights a Strong Bias towards Non-Vesicular Secretion. <i>Cells</i> , 2021, 10, 1543.	4.1	11
4	Characterization of the nuclear and cytosolic transcriptomes in human brain tissue reveals new insights into the subcellular distribution of RNA transcripts. <i>Scientific Reports</i> , 2021, 11, 4076.	3.3	27
5	Building blocks are synthesized on demand during the yeast cell cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7575-7583.	7.1	32
6	Expression profiling and in situ screening of circular RNAs in human tissues. <i>Scientific Reports</i> , 2018, 8, 16953.	3.3	21
7	Comprehensive RNA-Sequencing Analysis in Serum and Muscle Reveals Novel Small RNA Signatures with Biomarker Potential for DMD. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 13, 1-15.	5.1	41
8	Heterogeneity and interplay of the extracellular vesicle small RNA transcriptome and proteome. <i>Scientific Reports</i> , 2018, 8, 10813.	3.3	118
9	Acute sleep loss results in tissue-specific alterations in genome-wide DNA methylation state and metabolic fuel utilization in humans. <i>Science Advances</i> , 2018, 4, eaar8590.	10.3	86
10	Genome-wide identification of Grainy head targets in <i>Drosophila</i> reveals regulatory interactions with the POU-domain transcription factor, Vvl. <i>Development (Cambridge)</i> , 2017, 144, 3145-3155.	2.5	24
11	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	12.8	44
12	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. <i>Science</i> , 2016, 353, 78-82.	12.6	1,983
13	Common and distinct DNA-binding and regulatory activities of the BEN-solo transcription factor family. <i>Genes and Development</i> , 2015, 29, 48-62.	5.9	41
14	The Histone Demethylase Activity of Rph1 is Not Essential for Its Role in the Transcriptional Response to Nutrient Signaling. <i>PLoS ONE</i> , 2014, 9, e95078.	2.5	3
15	Genome-wide Analysis of <i>Drosophila</i> Circular RNAs Reveals Their Structural and Sequence Properties and Age-Dependent Neural Accumulation. <i>Cell Reports</i> , 2014, 9, 1966-1980.	6.4	866
16	Intertwined pathways for Argonaute-mediated microRNA biogenesis in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2014, 42, 1987-2002.	14.5	23
17	Diversity of miRNAs, siRNAs, and piRNAs across 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2014, 24, 1236-1250.	5.5	66
18	The BEN domain is a novel sequence-specific DNA-binding domain conserved in neural transcriptional repressors. <i>Genes and Development</i> , 2013, 27, 602-614.	5.9	70

#	ARTICLE	IF	CITATIONS
19	Widespread and extensive lengthening of 3' UTRs in the mammalian brain. <i>Genome Research</i> , 2013, 23, 812-825.	5.5	308
20	Neurophysiological Defects and Neuronal Gene Deregulation in <i>Drosophila</i> mir-124 Mutants. <i>PLoS Genetics</i> , 2012, 8, e1002515.	3.5	48
21	Discovery of hundreds of mirtrons in mouse and human small RNA data. <i>Genome Research</i> , 2012, 22, 1634-1645.	5.5	169
22	Common and distinct patterns of terminal modifications to mirtrons and canonical microRNAs. <i>Rna</i> , 2012, 18, 177-192.	3.5	64
23	Cis1 and Rph1 Regulate Glycerol and Acetate Metabolism in Glucose Depleted Yeast Cells. <i>PLoS ONE</i> , 2012, 7, e31577.	2.5	32
24	Vive la difference: biogenesis and evolution of microRNAs in plants and animals. <i>Genome Biology</i> , 2011, 12, 221.	9.6	393
25	Mirtrons: microRNA biogenesis via splicing. <i>Biochimie</i> , 2011, 93, 1897-1904.	2.6	246
26	Computational and experimental identification of mirtrons in <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2011, 21, 286-300.	5.5	71
27	Deep annotation of <i>Drosophila melanogaster</i> microRNAs yields insights into their processing, modification, and emergence. <i>Genome Research</i> , 2011, 21, 203-215.	5.5	207
28	Histone modifications influence mediator interactions with chromatin. <i>Nucleic Acids Research</i> , 2011, 39, 8342-8354.	14.5	39
29	Nitrogen depletion in the fission yeast <i>Schizosaccharomyces pombe</i> causes nucleosome loss in both promoters and coding regions of activated genes. <i>Genome Research</i> , 2010, 20, 361-371.	5.5	16
30	Transcriptional profiling reveals a critical role for tyrosine phosphatase VEGFR2 activity and endothelial cell morphogenesis. <i>FASEB Journal</i> , 2009, 23, 1490-1502.	0.5	98
31	Genome-scale study of the importance of binding site context for transcription factor binding and gene regulation. <i>BMC Bioinformatics</i> , 2008, 9, 484.	2.6	17
32	Endocan is a VEGF-A and PI3K regulated gene with increased expression in human renal cancer. <i>Experimental Cell Research</i> , 2007, 313, 1285-1294.	2.6	112
33	Global gene expression analysis by combinatorial optimization. <i>In Silico Biology</i> , 2004, 4, 225-41.	0.9	0