Robin Andersson

List of Publications by Year
in descending order

59	9,140	136940 32	133244 59
papers	citations	h-index	g-index

74	74	74	16485
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Endogenous retroviruses co-opted as divergently transcribed regulatory elements shape the regulatory landscape of embryonic stem cells. Nucleic Acids Research, 2022, 50, 2111-2127.	14.5	12
2	Methods for fighting emerging pathogens. Nature Methods, 2022, , .	19.0	1
3	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
4	Genome-wide and sister chromatid-resolved profiling of protein occupancy in replicated chromatin with ChOR-seq and SCAR-seq. Nature Protocols, 2021, 16, 4446-4493.	12.0	11
5	Principles of mRNA targeting via the Arabidopsis m6A-binding protein ECT2. ELife, 2021, 10, .	6.0	41
6	The YTHDF proteins ECT2 and ECT3 bind largely overlapping target sets and influence target mRNA abundance, not alternative polyadenylation. ELife, 2021, 10, .	6.0	33
7	Determinants of enhancer and promoter activities of regulatory elements. Nature Reviews Genetics, 2020, 21, 71-87.	16.3	464
8	Comparative transcriptomics of primary cells in vertebrates. Genome Research, 2020, 30, 951-961.	5.5	29
9	The Transcriptional Network That Controls Growth Arrest and Macrophage Differentiation in the Human Myeloid Leukemia Cell Line THP-1. Frontiers in Cell and Developmental Biology, 2020, 8, 498.	3.7	25
10	CAGEfightR: analysis of 5â€²-end data using R/Bioconductor. BMC Bioinformatics, 2019, 20, 487.	2.6	59
11	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. ELife, 2019, 8, .	6.0	32
12	Transcriptional decomposition reveals active chromatin architectures and cell specific regulatory interactions. Nature Communications, 2018, 9, 487.	12.8	50
13	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174.	21.4	156
14	Characterization of the enhancer and promoter landscape of inflammatory bowel disease from human colon biopsies. Nature Communications, 2018, 9, 1661.	12.8	78
15	Transcription start site analysis reveals widespread divergent transcription in D. melanogaster and core promoter-encoded enhancer activities. Nucleic Acids Research, 2018, 46, 5455-5469.	14.5	40
16	The RNA exosome contributes to gene expression regulation during stem cell differentiation. Nucleic Acids Research, 2018, 46, 11502-11513.	14.5	40
17	MCM2 promotes symmetric inheritance of modified histones during DNA replication. Science, 2018, 361, 1389-1392.	12.6	207
18	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	3.2	17

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19	Identification of Gene Transcription Start Sites and Enhancers Responding to Pulmonary Carbon Nanotube Exposure in Vivo. ACS Nano, 2017, 11, 3597-3613.	14.6	23
20	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. Nucleic Acids Research, 2017, 45, D737-D743.	14.5	116
21	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. Diabetes, 2017, 66, 218-230.	0.6	27
22	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	3.0	24
23	Regulating retrotransposon activity through the use of alternative transcription start sites. EMBO Reports, 2016, 17, 753-768.	4.5	21
24	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. Nature Genetics, 2016, 48, 984-994.	21.4	75
25	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. Cancer Research, 2016, 76, 216-226.	0.9	80
26	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticityÂby HDAC inhibitors. Epigenetics and Chromatin, 2015, 8, 55.	3.9	32
27	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
28	The frequent evolutionary birth and death of functional promoters in mouse and human. Genome Research, 2015, 25, 1546-1557.	5.5	55
29	A unified architecture of transcriptional regulatory elements. Trends in Genetics, 2015, 31, 426-433.	6.7	173
30	Human Gene Promoters Are Intrinsically Bidirectional. Molecular Cell, 2015, 60, 346-347.	9.7	55
31	Promoter or enhancer, what's the difference? Deconstruction of established distinctions and presentation of a unifying model. BioEssays, 2015, 37, 314-323.	2.5	92
32	Identification of TNF-Â-Responsive Promoters and Enhancers in the Intestinal Epithelial Cell Model Caco-2. DNA Research, 2014, 21, 569-583.	3.4	12
33	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	5.5	161
34	Nucleosome regulatory dynamics in response to TGFÂ. Nucleic Acids Research, 2014, 42, 6921-6934.	14.5	6
35	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
36	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	27.8	2,269

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37	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. Blood, 2014, 123, e79-e89.	1.4	72
38	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. Nature Genetics, 2014, 46, 558-566.	21.4	271
39	Nuclear stability and transcriptional directionality separate functionally distinct RNA species. Nature Communications, 2014, 5, 5336.	12.8	165
40	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. Molecular Genetics and Metabolism, 2014, 112, 73-83.	1.1	39
41	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	2.8	10
42	Polyadenylation siteâ€“induced decay of upstream transcripts enforces promoter directionality. Nature Structural and Molecular Biology, 2013, 20, 923-928.	8.2	258
43	A strand specific high resolution normalization method for chip-sequencing data employing multiple experimental control measurements. Algorithms for Molecular Biology, 2012, 7, 2.	1.2	4
44	Cancer associated epigenetic transitions identified by genome-wide histone methylation binding profiles in human colorectal cancer samples and paired normal mucosa. BMC Cancer, 2011, 11, 450.	2.6	30
45	SICTIN: Rapid footprinting of massively parallel sequencing data. BioData Mining, 2010, 3, 4.	4.0	10
46	Frequent genetic differences between matched primary and metastatic breast cancer provide an approach to identification of biomarkers for disease progression. European Journal of Human Genetics, 2010, 18, 560-568.	2.8	42
47	Recurrent genomic alterations in benign and malignant pheochromocytomas and paragangliomas revealed by whole-genome array comparative genomic hybridization analysis. Endocrine-Related Cancer, 2010, 17, 561-579.	3.1	29
48	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. Experimental and Molecular Medicine, 2010, 42, 484.	7.7	32
49	Using multi-data hidden Markov models trained on local neighborhoods of protein structure to predict residueâ€“residue contacts. Bioinformatics, 2009, 25, 1264-1270.	4.1	39
50	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. Epigenetics, 2009, 4, 107-113.	2.7	25
51	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. Neuro-Oncology, 2009, 11, 803-818.	1.2	43
52	Genomeâ€wide highâ€resolution analysis of DNA copy number alterations in NF1â€associated malignant peripheral nerve sheath tumors using 32K BAC array. Genes Chromosomes and Cancer, 2009, 48, 897-907.	2.8	50
53	Nucleosomes are well positioned in exons and carry characteristic histone modifications. Genome Research, 2009, 19, 1732-1741.	5.5	274
54	Profiling of copy number variations (CNVs) in healthy individuals from three ethnic groups using a human genome 32â€‰K BAC-clone-based array. Human Mutation, 2008, 29, 398-408.	2.5	46

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55	Somatic mosaicism for copy number variation in differentiated human tissues. Human Mutation, 2008, 29, 1118-1124.	2.5	184
56	Phenotypically Concordant and Discordant Monozygotic Twins Display Different DNA Copy-Number-Variation Profiles. American Journal of Human Genetics, 2008, 82, 763-771.	6.2	533
57	A segmental maximum a posteriori approach to genome-wide copy number profiling. Bioinformatics, 2008, 24, 751-758.	4.1	29
58	Overlapping phenotype of Wolfâ€“Hirschhorn and Beckwithâ€“Wiedemann syndromes in a girl with der(4)t(4;11)(pter;pter). American Journal of Medical Genetics, Part A, 2007, 143A, 1760-1766.	1.2	5
59	A previously unrecognized microdeletion syndrome on chromosome 22 band q11.2 encompassing the BCR gene. American Journal of Medical Genetics, Part A, 2007, 143A, 2178-2184.	1.2	42