

PÃ¥l SÃ¡trom

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

5,812
citations

100601

38
h-index

87275

74
g-index

98
all docs

98
docs citations

98
times ranked

12062
citing authors

#	ARTICLE	IF	CITATIONS
1	MicroRNA profiling of psoriatic skin identifies 11 miRNAs associated with disease severity. <i>Experimental Dermatology</i> , 2022, 31, 535-547.	1.4	11
2	Loss of Mediator complex subunit 13 (MED13) promotes resistance to alkylation through cyclin D1 upregulation. <i>Nucleic Acids Research</i> , 2021, 49, 1470-1484.	6.5	1
3	Establishment of a Patient-Derived Xenograft Model of Colorectal Cancer in CIEA NOG Mice and Exploring Smartfish Liquid Diet as a Source of Omega-3 Fatty Acids. <i>Biomedicines</i> , 2021, 9, 282.	1.4	1
4	Epigenetic mapping of the somatotrophic axis in Nile tilapia reveals differential DNA hydroxymethylation marks associated with growth. <i>Genomics</i> , 2021, 113, 2953-2964.	1.3	12
5	Joint changes in RNA, RNA polymerase II, and promoter activity through the cell cycle identify non-coding RNAs involved in proliferation. <i>Scientific Reports</i> , 2021, 11, 18952.	1.6	7
6	Non-Coding RNAs in Human Breast Milk: A Systematic Review. <i>Frontiers in Immunology</i> , 2021, 12, 725323.	2.2	32
7	Gene expression in blood reflects smoking exposure among cancer-free women in the Norwegian Women and Cancer (NOWAC) postgenome cohort. <i>Scientific Reports</i> , 2021, 11, 680.	1.6	6
8	NEIL1 and NEIL2 DNA glycosylases modulate anxiety and learning in a cooperative manner in mice. <i>Communications Biology</i> , 2021, 4, 1354.	2.0	8
9	Liver Activation of Hepatocellular Nuclear Factor-4 $\hat{\pm}$ by Small Activating RNA Rescues Dyslipidemia and Improves Metabolic Profile. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 361-370.	2.3	47
10	sMETASeq: Combined Profiling of Microbiota and Host Small RNAs. <i>IScience</i> , 2020, 23, 101131.	1.9	7
11	MTL-CEBPA, a Small Activating RNA Therapeutic Upregulating C/EBP $\hat{\pm}$, in Patients with Advanced Liver Cancer: A First-in-Human, Multicenter, Open-Label, Phase I Trial. <i>Clinical Cancer Research</i> , 2020, 26, 3936-3946.	3.2	86
12	Major gene expression changes and epigenetic remodelling in Nile tilapia muscle after just one generation of domestication. <i>Epigenetics</i> , 2020, 15, 1052-1067.	1.3	31
13	SMUG1 Promotes Telomere Maintenance through Telomerase RNA Processing. <i>Cell Reports</i> , 2019, 28, 1690-1702.e10.	2.9	23
14	Comprehensive transcriptomic analyses of tissue, serum, and serum exosomes from hepatocellular carcinoma patients. <i>BMC Cancer</i> , 2019, 19, 1007.	1.1	40
15	In utero exposure to endocrine disrupting chemicals, micro-RNA profiles, and fetal growth: a pilot study protocol. <i>Journal of Public Health Research</i> , 2019, 8, 1550.	0.5	0
16	epic2 efficiently finds diffuse domains in ChIP-seq data. <i>Bioinformatics</i> , 2019, 35, 4392-4393.	1.8	91
17	Small RNA expression from viruses, bacteria and human miRNAs in colon cancer tissue and its association with microsatellite instability and tumor location. <i>BMC Cancer</i> , 2019, 19, 161.	1.1	27
18	Alkyladenine DNA glycosylase associates with transcription elongation to coordinate DNA repair with gene expression. <i>Nature Communications</i> , 2019, 10, 5460.	5.8	28

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19	Mechanisms involved in the activation of C/EBP β by small activating RNA in hepatocellular carcinoma. <i>Oncogene</i> , 2019, 38, 3446-3457.	2.6	24
20	Unique-region phosphorylation targets LynA for rapid degradation, tuning its expression and signaling in myeloid cells. <i>ELife</i> , 2019, 8, .	2.8	13
21	Gene activation of CEBPA using saRNA: preclinical studies of the first in human saRNA drug candidate for liver cancer. <i>Oncogene</i> , 2018, 37, 3216-3228.	2.6	60
22	MicroRNAs contribute to postnatal development of laminar differences and neuronal subtypes in the rat medial entorhinal cortex. <i>Brain Structure and Function</i> , 2017, 222, 3107-3126.	1.2	7
23	Genome-wide profiling of DNA 5-hydroxymethylcytosine during rat Sertoli cell maturation. <i>Cell Discovery</i> , 2017, 3, 17013.	3.1	8
24	Gene expression differences between PAXgene and Tempus blood RNA tubes are highly reproducible between independent samples and biobanks. <i>BMC Research Notes</i> , 2017, 10, 136.	0.6	14
25	NEIL3-Dependent Regulation of Cardiac Fibroblast Proliferation Prevents Myocardial Rupture. <i>Cell Reports</i> , 2017, 18, 82-92.	2.9	45
26	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
27	Development and Mechanism of Small Activating RNA Targeting CEBPA, a Novel Therapeutic in Clinical Trials for Liver Cancer. <i>Molecular Therapy</i> , 2017, 25, 2705-2714.	3.7	76
28	Identification of metastasis-associated microRNAs in serum from rectal cancer patients. <i>Oncotarget</i> , 2017, 8, 90077-90089.	0.8	18
29	Abstract 1508: MTL-CEBPA activates the transcription factor CEBPalpha leading to inhibition of hepatocellular cancer growth. , 2017, , .		0
30	Targeted Delivery of C/EBP β -saRNA by Pancreatic Ductal Adenocarcinoma-specific RNA Aptamers Inhibits Tumor Growth In Vivo. <i>Molecular Therapy</i> , 2016, 24, 1106-1116.	3.7	53
31	Genomic uracil " Important carcinogenic mutagen but normal intermediate in adaptive immunity. <i>Toxicology Letters</i> , 2016, 258, S19.	0.4	0
32	The importance of p53 pathway genetics in inherited and somatic cancer genomes. <i>Nature Reviews Cancer</i> , 2016, 16, 251-265.	12.8	131
33	Pathway Analysis of Skin from Psoriasis Patients after Adalimumab Treatment Reveals New Early Events in the Anti-Inflammatory Mechanism of Anti-TNF- β . <i>PLoS ONE</i> , 2016, 11, e0167437.	1.1	11
34	Human Breast Milk miRNA, Maternal Probiotic Supplementation and Atopic Dermatitis in Offspring. <i>PLoS ONE</i> , 2015, 10, e0143496.	1.1	60
35	A novel POLE mutation associated with cancers of colon, pancreas, ovaries and small intestine. <i>Familial Cancer</i> , 2015, 14, 437-448.	0.9	67
36	Cell cycle regulation of human DNA repair and chromatin remodeling genes. <i>DNA Repair</i> , 2015, 30, 53-67.	1.3	174

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37	AID expression in B-cell lymphomas causes accumulation of genomic uracil and a distinct AID mutational signature. <i>DNA Repair</i> , 2015, 25, 60-71.	1.3	59
38	RNA motif discovery: a computational overview. <i>Biology Direct</i> , 2015, 10, 61.	1.9	17
39	The eGenVar data management systemâ€”cataloguing and sharing sensitive data and metadata for the life sciences. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau027.	1.4	10
40	Exploiting Human CD34+ Stem Cellâ€”conditioned Medium for Tissue Repair. <i>Molecular Therapy</i> , 2014, 22, 149-159.	3.7	7
41	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	2.6	193
42	Circular RNAs are depleted of polymorphisms at microRNA binding sites. <i>Bioinformatics</i> , 2014, 30, 2243-2246.	1.8	161
43	Regulation of Inflammatory Phenotype in Macrophages by a Diabetes-Induced Long Noncoding RNA. <i>Diabetes</i> , 2014, 63, 4249-4261.	0.3	155
44	Error-free versus mutagenic processing of genomic uracilâ€”Relevance to cancer. <i>DNA Repair</i> , 2014, 19, 38-47.	1.3	55
45	Novel RNA oligonucleotide improves liver function and inhibits liver carcinogenesis<i>in vivo</i>. <i>Hepatology</i> , 2014, 59, 216-227.	3.6	92
46	MicroRNAs act complementarily to regulate disease-related mRNA modules in human diseases. <i>Rna</i> , 2013, 19, 1552-1562.	1.6	35
47	Multiple microRNAs may regulate the DNA repair enzyme uracil-DNA glycosylase. <i>DNA Repair</i> , 2013, 12, 80-86.	1.3	17
48	Designing Dual-Targeting siRNA Duplexes Having Two Active Strands that Combine siRNA and MicroRNA-Like Targeting. <i>Methods in Molecular Biology</i> , 2013, 942, 169-177.	0.4	5
49	Transcription profiling during the cell cycle shows that a subset of Polycomb-targeted genes is upregulated during DNA replication. <i>Nucleic Acids Research</i> , 2013, 41, 2846-2856.	6.5	48
50	A Short-activating RNA Oligonucleotide Targeting the Islet Î²-cell Transcriptional Factor MafA in CD34+ Cells. <i>Molecular Therapy - Nucleic Acids</i> , 2013, 2, e97.	2.3	13
51	Novel Long Noncoding RNAs Are Regulated by Angiotensin II in Vascular Smooth Muscle Cells. <i>Circulation Research</i> , 2013, 113, 266-278.	2.0	258
52	Gene Expression Profile Changes After Short-activating RNA-mediated Induction of Endogenous Pluripotency Factors in Human Mesenchymal Stem Cells. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e35.	2.3	28
53	MicroRNA-181a* Targets Nanog in a Subpopulation of CD34+ Cells Isolated From Peripheral Blood. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e34.	2.3	14
54	Cell-type specificity of ChIP-predicted transcription factor binding sites. <i>BMC Genomics</i> , 2012, 13, 372.	1.2	17

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55	Monozygotic twins discordant for intermittent allergic rhinitis differ in mRNA and protein levels. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2012, 67, 831-833.	2.7	10
56	Target gene expression levels and competition between transfected and endogenous microRNAs are strong confounding factors in microRNA high-throughput experiments. <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 3.	8.0	30
57	Single Nucleotide Polymorphisms Can Create Alternative Polyadenylation Signals and Affect Gene Expression through Loss of MicroRNA-Regulation. <i>PLoS Computational Biology</i> , 2012, 8, e1002621.	1.5	49
58	Clustered ChIP-Seq-defined transcription factor binding sites and histone modifications map distinct classes of regulatory elements. <i>BMC Biology</i> , 2011, 9, 80.	1.7	30
59	Inferring causative variants in microRNA target sites. <i>Nucleic Acids Research</i> , 2011, 39, e109-e109.	6.5	64
60	A manually curated ChIP-seq benchmark demonstrates room for improvement in current peak-finder programs. <i>Nucleic Acids Research</i> , 2011, 39, e25-e25.	6.5	62
61	A ChIP-Seq Benchmark Shows That Sequence Conservation Mainly Improves Detection of Strong Transcription Factor Binding Sites. <i>PLoS ONE</i> , 2011, 6, e18430.	1.1	12
62	Rational Design of Micro-RNA-like Bifunctional siRNAs Targeting HIV and the HIV Coreceptor CCR5. <i>Molecular Therapy</i> , 2010, 18, 796-802.	3.7	14
63	MicroRNAs "targeting and target prediction. <i>New Biotechnology</i> , 2010, 27, 243-249.	2.4	102
64	A two-step site and mRNA-level model for predicting microRNA targets. <i>BMC Bioinformatics</i> , 2010, 11, 612.	1.2	15
65	Dual-targeting siRNAs. <i>Rna</i> , 2010, 16, 1275-1284.	1.6	19
66	Optimization of Duplex Stability and Terminal Asymmetry for shRNA Design. <i>PLoS ONE</i> , 2010, 5, e10180.	1.1	36
67	A Risk Variant in an miR-125b Binding Site in <i>BMP1B</i> Is Associated with Breast Cancer Pathogenesis. <i>Cancer Research</i> , 2009, 69, 7459-7465.	0.4	131
68	Animal microRNA Gene Prediction. , 2009, , 21-43.		0
69	Engineering and optimization of the miR-106b cluster for ectopic expression of multiplexed anti-HIV RNAs. <i>Gene Therapy</i> , 2008, 15, 1536-1549.	2.3	107
70	Meta-analysis of breast cancer microarray studies in conjunction with conserved cis-elements suggest patterns for coordinate regulation. <i>BMC Bioinformatics</i> , 2008, 9, 63.	1.2	41
71	MicroRNA-directed transcriptional gene silencing in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16230-16235.	3.3	656
72	A role for the Dicer helicase domain in the processing of thermodynamically unstable hairpin RNAs. <i>Nucleic Acids Research</i> , 2008, 36, 6511-6522.	6.5	49

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73	Comparison of approaches for rational siRNA design leading to a new efficient and transparent method. <i>Nucleic Acids Research</i> , 2007, 35, e63-e63.	6.5	129
74	Reliable prediction of Drosha processing sites improves microRNA gene prediction. <i>Bioinformatics</i> , 2007, 23, 142-149.	1.8	118
75	Epigenetics and MicroRNAs. <i>Pediatric Research</i> , 2007, 61, 17R-23R.	1.1	94
76	Distance constraints between microRNA target sites dictate efficacy and cooperativity. <i>Nucleic Acids Research</i> , 2007, 35, 2333-2342.	6.5	308
77	Robust Machine Learning Algorithms Predict MicroRNA Genes and Targets. <i>Methods in Enzymology</i> , 2007, 427, 25-49.	0.4	2
78	MicroRNAs in Disease and Potential Therapeutic Applications. <i>Molecular Therapy</i> , 2007, 15, 2070-2079.	3.7	346
79	Machine learning predicts microRNA target sites. , 2007, , 210-220.		0
80	Motif kernel generated by genetic programming improves remote homology and fold detection. <i>BMC Bioinformatics</i> , 2007, 8, 23.	1.2	43
81	Conserved MicroRNA Characteristics in Mammals. <i>Oligonucleotides</i> , 2006, 16, 115-144.	2.7	56
82	The Petacomp Machine - A MIMD Cluster for Parallel Pattern-mining. , 2006, , .		0
83	Predicting non-coding RNA genes in <i>Escherichia coli</i> with boosted genetic programming. <i>Nucleic Acids Research</i> , 2005, 33, 3263-3270.	6.5	52
84	Evolutionary Rule Mining in Time Series Databases. <i>Machine Learning</i> , 2005, 58, 107-125.	3.4	15
85	Weighted sequence motifs as an improved seeding step in microRNA target prediction algorithms. <i>Rna</i> , 2005, 11, 995-1003.	1.6	113
86	Predicting the efficacy of short oligonucleotides in antisense and RNAi experiments with boosted genetic programming. <i>Bioinformatics</i> , 2004, 20, 3055-3063.	1.8	71
87	A recursive MISD architecture for pattern matching. <i>IEEE Transactions on Very Large Scale Integration (VLSI) Systems</i> , 2004, 12, 727-734.	2.1	27
88	A comparison of siRNA efficacy predictors. <i>Biochemical and Biophysical Research Communications</i> , 2004, 321, 247-253.	1.0	114
89	Designing effective siRNAs with off-target control. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 769-773.	1.0	23
90	Temporal Rule Discovery using Genetic Programming and Specialized Hardware. , 2004, , 87-94.		6