Pål Sätrom

List of Publications by Year
in descending order

90	5,812	38	74
papers	citations	h-index	g-index

87886

76898

98	98	98	10927
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MicroRNA profiling of psoriatic skin identifies 11 miRNAs associated with disease severity. Experimental Dermatology, 2022, 31, 535-547.	2.9	11
2	Loss of Mediator complex subunit 13 (MED13) promotes resistance to alkylation through cyclin D1 upregulation. Nucleic Acids Research, 2021, 49, 1470-1484.	14.5	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. Biomedicines, 2021, 9, 282.	3.2	1
4	Epigenetic mapping of the somatotropic axis in Nile tilapia reveals differential DNA hydroxymethylation marks associated with growth. Genomics, 2021, 113, 2953-2964.	2.9	12
5	Joint changes in RNA, RNA polymerase II, and promoter activity through the cell cycle identify non-coding RNAs involved in proliferation. Scientific Reports, 2021, 11, 18952.	3.3	7
6	Non-Coding RNAs in Human Breast Milk: A Systematic Review. Frontiers in Immunology, 2021, 12, 725323.	4.8	32
7	Gene expression in blood reflects smoking exposure among cancer-free women in the Norwegian Women and Cancer (NOWAC) postgenome cohort. Scientific Reports, 2021, 11, 680.	3.3	6
8	NEIL1 and NEIL2 DNA glycosylases modulate anxiety and learning in a cooperative manner in mice. Communications Biology, 2021, 4, 1354.	4.4	8
9	Liver Activation of Hepatocellular Nuclear Factor-4Î± by Small Activating RNA Rescues Dyslipidemia and Improves Metabolic Profile. Molecular Therapy - Nucleic Acids, 2020, 19, 361-370.	5.1	47
10	sMETASeq: Combined Profiling of Microbiota and Host Small RNAs. IScience, 2020, 23, 101131.	4.1	7
11	MTL-CEBPA, a Small Activating RNA Therapeutic Upregulating C/EBP-Î±, in Patients with Advanced Liver Cancer: A First-in-Human, Multicenter, Open-Label, Phase I Trial. Clinical Cancer Research, 2020, 26, 3936-3946.	7.0	86
12	Major gene expression changes and epigenetic remodelling in Nile tilapia muscle after just one generation of domestication. Epigenetics, 2020, 15, 1052-1067.	2.7	31
13	SMUG1 Promotes Telomere Maintenance through Telomerase RNA Processing. Cell Reports, 2019, 28, 1690-1702.e10.	6.4	23
14	Comprehensive transcriptomic analyses of tissue, serum, and serum exosomes from hepatocellular carcinoma patients. BMC Cancer, 2019, 19, 1007.	2.6	40
15	In utero exposure to endocrine disrupting chemicals, micro-RNA profiles, and fetal growth: a pilot study protocol. Journal of Public Health Research, 2019, 8, 1550.	1.2	0
16	epic2 efficiently finds diffuse domains in ChIP-seq data. Bioinformatics, 2019, 35, 4392-4393.	4.1	91
17	Small RNA expression from viruses, bacteria and human miRNAs in colon cancer tissue and its association with microsatellite instability and tumor location. BMC Cancer, 2019, 19, 161.	2.6	27
18	Alkyladenine DNA glycosylase associates with transcription elongation to coordinate DNA repair with gene expression. Nature Communications, 2019, 10, 5460.	12.8	28

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19	Mechanisms involved in the activation of C/EBPÎ± by small activating RNA in hepatocellular carcinoma. Oncogene, 2019, 38, 3446-3457.	5.9	24
20	Unique-region phosphorylation targets LynA for rapid degradation, tuning its expression and signaling in myeloid cells. ELife, 2019, 8, .	6.0	13
21	Gene activation of CEBPA using saRNA: preclinical studies of the first in human saRNA drug candidate for liver cancer. Oncogene, 2018, 37, 3216-3228.	5.9	60
22	MicroRNAs contribute to postnatal development of laminar differences and neuronal subtypes in the rat medial entorhinal cortex. Brain Structure and Function, 2017, 222, 3107-3126.	2.3	7
23	Genome-wide profiling of DNA 5-hydroxymethylcytosine during rat Sertoli cell maturation. Cell Discovery, 2017, 3, 17013.	6.7	8
24	Gene expression differences between PAXgene and Tempus blood RNA tubes are highly reproducible between independent samples and biobanks. BMC Research Notes, 2017, 10, 136.	1.4	14
25	NEIL3-Dependent Regulation of Cardiac Fibroblast Proliferation Prevents Myocardial Rupture. Cell Reports, 2017, 18, 82-92.	6.4	45
26	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
27	Development and Mechanism of Small Activating RNA Targeting CEBPA, a Novel Therapeutic in Clinical Trials for Liver Cancer. Molecular Therapy, 2017, 25, 2705-2714.	8.2	76
28	Identification of metastasis-associated microRNAs in serum from rectal cancer patients. Oncotarget, 2017, 8, 90077-90089.	1.8	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/EBPÎ± -saRNA by Pancreatic Ductal Adenocarcinoma-specific RNA Aptamers Inhibits Tumor Growth In Vivo. Molecular Therapy, 2016, 24, 1106-1116.	8.2	53
31	Genomic uracil â€" Important carcinogenic mutagen but normal intermediate in adaptive immunity. Toxicology Letters, 2016, 258, S19.	0.8	0
32	The importance of p53 pathway genetics in inherited and somatic cancer genomes. Nature Reviews Cancer, 2016, 16, 251-265.	28.4	131
33	Pathway Analysis of Skin from Psoriasis Patients after Adalimumab Treatment Reveals New Early Events in the Anti-Inflammatory Mechanism of Anti-TNF-Î±. PLoS ONE, 2016, 11, e0167437.	2.5	11
34	Human Breast Milk miRNA, Maternal Probiotic Supplementation and Atopic Dermatitis in Offspring. PLoS ONE, 2015, 10, e0143496.	2.5	60
35	A novel POLE mutation associated with cancers of colon, pancreas, ovaries and small intestine. Familial Cancer, 2015, 14, 437-448.	1.9	67
36	Cell cycle regulation of human DNA repair and chromatin remodeling genes. DNA Repair, 2015, 30, 53-67.	2.8	174

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37	AID expression in B-cell lymphomas causes accumulation of genomic uracil and a distinct AID mutational signature. DNA Repair, 2015, 25, 60-71.	2.8	59
38	RNA motif discovery: a computational overview. Biology Direct, 2015, 10, 61.	4.6	17
39	The eGenVar data management systemâ€"cataloguing and sharing sensitive data and metadata for the life sciences. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau027.	3.0	10
40	Exploiting Human CD34+ Stem Cellâ€"conditioned Medium for Tissue Repair. Molecular Therapy, 2014, 22, 149-159.	8.2	7
41	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
42	Circular RNAs are depleted of polymorphisms at microRNA binding sites. Bioinformatics, 2014, 30, 2243-2246.	4.1	161
43	Regulation of Inflammatory Phenotype in Macrophages by a Diabetes-Induced Long Noncoding RNA. Diabetes, 2014, 63, 4249-4261.	0.6	155
44	Error-free versus mutagenic processing of genomic uracilâ€"Relevance to cancer. DNA Repair, 2014, 19, 38-47.	2.8	55
45	Novel RNA oligonucleotide improves liver function and inhibits liver carcinogenesis *in vivo*. Hepatology, 2014, 59, 216-227.	7.3	92
46	MicroRNAs act complementarily to regulate disease-related mRNA modules in human diseases. Rna, 2013, 19, 1552-1562.	3.5	35
47	Multiple microRNAs may regulate the DNA repair enzyme uracil-DNA glycosylase. DNA Repair, 2013, 12, 80-86.	2.8	17
48	Designing Dual-Targeting siRNA Duplexes Having Two Active Strands that Combine siRNA and MicroRNA-Like Targeting. Methods in Molecular Biology, 2013, 942, 169-177.	0.9	5
49	Transcription profiling during the cell cycle shows that a subset of Polycomb-targeted genes is upregulated during DNA replication. Nucleic Acids Research, 2013, 41, 2846-2856.	14.5	48
50	A Short-activating RNA Oligonucleotide Targeting the Islet Î²-cell Transcriptional Factor MafA in CD34+ Cells. Molecular Therapy - Nucleic Acids, 2013, 2, e97.	5.1	13
51	Novel Long Noncoding RNAs Are Regulated by Angiotensin II in Vascular Smooth Muscle Cells. Circulation Research, 2013, 113, 266-278.	4.5	258
52	Gene Expression Profile Changes After Short-activating RNA-mediated Induction of Endogenous Pluripotency Factors in Human Mesenchymal Stem Cells. Molecular Therapy - Nucleic Acids, 2012, 1, e35.	5.1	28
53	MicroRNA-181a* Targets Nanog in a Subpopulation of CD34+ Cells Isolated From Peripheral Blood. Molecular Therapy - Nucleic Acids, 2012, 1, e34.	5.1	14
54	Cell-type specificity of ChIP-predicted transcription factor binding sites. BMC Genomics, 2012, 13, 372.	2.8	17

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55	Monozygotic twins discordant for intermittent allergic rhinitis differ in mRNA and protein levels. Allergy: European Journal of Allergy and Clinical Immunology, 2012, 67, 831-833.	5.7	10
56	Target gene expression levels and competition between transfected and endogenous microRNAs are strong confounding factors in microRNA high-throughput experiments. Silence: A Journal of RNA Regulation, 2012, 3, 3.	8.1	30
57	Single Nucleotide Polymorphisms Can Create Alternative Polyadenylation Signals and Affect Gene Expression through Loss of MicroRNA-Regulation. PLoS Computational Biology, 2012, 8, e1002621.	3.2	49
58	Clustered ChIP-Seq-defined transcription factor binding sites and histone modifications map distinct classes of regulatory elements. BMC Biology, 2011, 9, 80.	3.8	30
59	Inferring causative variants in microRNA target sites. Nucleic Acids Research, 2011, 39, e109-e109.	14.5	64
60	A manually curated ChIP-seq benchmark demonstrates room for improvement in current peak-finder programs. Nucleic Acids Research, 2011, 39, e25-e25.	14.5	62
61	A ChIP-Seq Benchmark Shows That Sequence Conservation Mainly Improves Detection of Strong Transcription Factor Binding Sites. PLoS ONE, 2011, 6, e18430.	2.5	12
62	Rational Design of Micro-RNA-like Bifunctional siRNAs Targeting HIV and the HIV Coreceptor CCR5. Molecular Therapy, 2010, 18, 796-802.	8.2	14
63	MicroRNAs â€" targeting and target prediction. New Biotechnology, 2010, 27, 243-249.	4.4	102
64	A two-step site and mRNA-level model for predicting microRNA targets. BMC Bioinformatics, 2010, 11, 612.	2.6	15
65	Dual-targeting siRNAs. Rna, 2010, 16, 1275-1284.	3.5	19
66	Optimization of Duplex Stability and Terminal Asymmetry for shRNA Design. PLoS ONE, 2010, 5, e10180.	2.5	36
67	A Risk Variant in an miR-125b Binding Site in <i>BMPR1B</i> Is Associated with Breast Cancer Pathogenesis. Cancer Research, 2009, 69, 7459-7465.	0.9	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. Gene Therapy, 2008, 15, 1536-1549.	4.5	107
70	Meta-analysis of breast cancer microarray studies in conjunction with conserved cis-elements suggest patterns for coordinate regulation. BMC Bioinformatics, 2008, 9, 63.	2.6	41
71	MicroRNA-directed transcriptional gene silencing in mammalian cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16230-16235.	7.1	656
72	A role for the Dicer helicase domain in the processing of thermodynamically unstable hairpin RNAs. Nucleic Acids Research, 2008, 36, 6511-6522.	14.5	49

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73	Comparison of approaches for rational siRNA design leading to a new efficient and transparent method. Nucleic Acids Research, 2007, 35, e63-e63.	14.5	129
74	Reliable prediction of Drosha processing sites improves microRNA gene prediction. Bioinformatics, 2007, 23, 142-149.	4.1	118
75	Epigenetics and MicroRNAs. Pediatric Research, 2007, 61, 17R-23R.	2.3	94
76	Distance constraints between microRNA target sites dictate efficacy and cooperativity. Nucleic Acids Research, 2007, 35, 2333-2342.	14.5	308
77	Robust Machine Learning Algorithms Predict MicroRNA Genes and Targets. Methods in Enzymology, 2007, 427, 25-49.	1.0	2
78	MicroRNAs in Disease and Potential Therapeutic Applications. Molecular Therapy, 2007, 15, 2070-2079.	8.2	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. BMC Bioinformatics, 2007, 8, 23.	2.6	43
81	Conserved MicroRNA Characteristics in Mammals. Oligonucleotides, 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 Escherichia coli with boosted genetic programming. Nucleic Acids Research, 2005, 33, 3263-3270.	14.5	52
84	Evolutionary Rule Mining in Time Series Databases. Machine Learning, 2005, 58, 107-125.	5.4	15
85	Weighted sequence motifs as an improved seeding step in microRNA target prediction algorithms. Rna, 2005, 11, 995-1003.	3.5	113
86	Predicting the efficacy of short oligonucleotides in antisense and RNAi experiments with boosted genetic programming. Bioinformatics, 2004, 20, 3055-3063.	4.1	71
87	A recursive MISD architecture for pattern matching. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2004, 12, 727-734.	3.1	27
88	A comparison of siRNA efficacy predictors. Biochemical and Biophysical Research Communications, 2004, 321, 247-253.	2.1	114
89	Designing effective siRNAs with off-target control. Biochemical and Biophysical Research Communications, 2004, 325, 769-773.	2.1	23
90	Temporal Rule Discovery using Genetic Programming and Specialized Hardware. , 2004, , 87-94.		6