

Joakim Lundeberg

List of Publications by Year in descending order

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Version: 2024-02-01

153
papers

23,831
citations

15504

65
h-index

9861

141
g-index

181
all docs

181
docs citations

181
times ranked

30310
citing authors

#	ARTICLE	IF	CITATIONS
1	Super-resolved spatial transcriptomics by deep data fusion. <i>Nature Biotechnology</i> , 2022, 40, 476-479.	17.5	61
2	Novel loss-of-function variant in DENND5A impedes melanosomal cargo transport and predisposes to familial cutaneous melanoma. <i>Genetics in Medicine</i> , 2022, 24, 157-169.	2.4	0
3	The discovAIR project: a roadmap towards the Human Lung Cell Atlas. <i>European Respiratory Journal</i> , 2022, 60, 2102057.	6.7	15
4	The spatial transcriptomic landscape of the healing mouse intestine following damage. <i>Nature Communications</i> , 2022, 13, 828.	12.8	43
5	Clonal relations in the mouse brain revealed by single-cell and spatial transcriptomics. <i>Nature Neuroscience</i> , 2022, 25, 285-294.	14.8	48
6	Identification of early neurodegenerative pathways in progressive multiple sclerosis. <i>Nature Neuroscience</i> , 2022, 25, 944-955.	14.8	55
7	Transcriptional output, cell-type densities, and normalization in spatial transcriptomics. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 906-908.	3.3	27
8	The impact of gastrointestinal dysmotility on the aerodigestive microbiome of pediatric lung transplant recipients. <i>Journal of Heart and Lung Transplantation</i> , 2021, 40, 210-219.	0.6	3
9	The spatial RNA integrity number assay for in situ evaluation of transcriptome quality. <i>Communications Biology</i> , 2021, 4, 57.	4.4	11
10	<i>sepal</i> : identifying transcript profiles with spatial patterns by diffusion-based modeling. <i>Bioinformatics</i> , 2021, 37, 2644-2650.	4.1	28
11	Abstract 129: An integrated multi-omic cellular atlas of human breast cancers. <i>Cancer Research</i> , 2021, 81, 129-129.	0.9	3
12	A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347.	21.4	535
13	Morphological Features Extracted by AI Associated with Spatial Transcriptomics in Prostate Cancer. <i>Cancers</i> , 2021, 13, 4837.	3.7	15
14	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	27.8	114
15	Spatially resolved transcriptomics adds a new dimension to genomics. <i>Nature Methods</i> , 2021, 18, 15-18.	19.0	180
16	Spatial deconvolution of HER2-positive breast cancer delineates tumor-associated cell type interactions. <i>Nature Communications</i> , 2021, 12, 6012.	12.8	140
17	Spatial Transcriptomics to define transcriptional patterns of zonation and structural components in the mouse liver. <i>Nature Communications</i> , 2021, 12, 7046.	12.8	71
18	Genome-wide spatial expression profiling in formalin-fixed tissues. <i>Cell Genomics</i> , 2021, 1, 100065.	6.5	45

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19	Genes and variants in hematopoiesis-related pathways are associated with gemcitabine/carboplatin-induced thrombocytopenia. <i>Pharmacogenomics Journal</i> , 2020, 20, 179-191.	2.0	7
20	Single-cell and spatial transcriptomics enables probabilistic inference of cell type topography. <i>Communications Biology</i> , 2020, 3, 565.	4.4	252
21	Spatial Transcriptomics Reveals Genes Associated with Dysregulated Mitochondrial Functions and Stress Signaling in Alzheimer Disease. <i>iScience</i> , 2020, 23, 101556.	4.1	61
22	Spatial Transcriptomics and In Situ Sequencing to Study Alzheimer's Disease. <i>Cell</i> , 2020, 182, 976-991.e19.	28.9	491
23	Seamless integration of image and molecular analysis for spatial transcriptomics workflows. <i>BMC Genomics</i> , 2020, 21, 482.	2.8	144
24	Genetic association of gemcitabine/carboplatin-induced leukopenia and neutropenia in non-small cell lung cancer patients using whole-exome sequencing. <i>Lung Cancer</i> , 2020, 147, 106-114.	2.0	5
25	Whole-genome sequencing and gene network modules predict gemcitabine/carboplatin-induced myelosuppression in non-small cell lung cancer patients. <i>Npj Systems Biology and Applications</i> , 2020, 6, 25.	3.0	9
26	Single-Stranded Oligonucleotide-Mediated Inhibition of Respiratory Syncytial Virus Infection. <i>Frontiers in Immunology</i> , 2020, 11, 580547.	4.8	7
27	Spatially Resolved Transcriptomes—Next Generation Tools for Tissue Exploration. <i>BioEssays</i> , 2020, 42, e1900221.	2.5	332
28	Integrating spatial gene expression and breast tumour morphology via deep learning. <i>Nature Biomedical Engineering</i> , 2020, 4, 827-834.	22.5	208
29	Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma. <i>Cell</i> , 2020, 182, 497-514.e22.	28.9	508
30	Molecular atlas of the adult mouse brain. <i>Science Advances</i> , 2020, 6, eabb3446.	10.3	183
31	SpatialCPie: an R/Bioconductor package for spatial transcriptomics cluster evaluation. <i>BMC Bioinformatics</i> , 2020, 21, 161.	2.6	11
32	Automation of Spatial Transcriptomics library preparation to enable rapid and robust insights into spatial organization of tissues. <i>BMC Genomics</i> , 2020, 21, 298.	2.8	19
33	A latent lineage potential in resident neural stem cells enables spinal cord repair. <i>Science</i> , 2020, 370, .	12.6	89
34	Deconstructing tumor heterogeneity: the stromal perspective. <i>Oncotarget</i> , 2020, 11, 3621-3632.	1.8	29
35	ST viewer: a tool for analysis and visualization of spatial transcriptomics datasets. <i>Bioinformatics</i> , 2019, 35, 1058-1060.	4.1	30
36	High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , 2019, 16, 987-990.	19.0	708

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37	A Single-Stranded Oligonucleotide Inhibits Toll-Like Receptor 3 Activation and Reduces Influenza A (H1N1) Infection. <i>Frontiers in Immunology</i> , 2019, 10, 2161.	4.8	18
38	Transcriptomics of cardiac biopsies reveals differences in patients with or without diagnostic parameters for heart failure with preserved ejection fraction. <i>Scientific Reports</i> , 2019, 9, 3179.	3.3	35
39	Spatiotemporal dynamics of molecular pathology in amyotrophic lateral sclerosis. <i>Science</i> , 2019, 364, 89-93.	12.6	297
40	A radical switch in clonality reveals a stem cell niche in the epiphyseal growth plate. <i>Nature</i> , 2019, 567, 234-238.	27.8	153
41	A Spatiotemporal Organ-Wide Gene Expression and Cell Atlas of the Developing Human Heart. <i>Cell</i> , 2019, 179, 1647-1660.e19.	28.9	470
42	Reducing Pericyte-Derived Scarring Promotes Recovery after Spinal Cord Injury. <i>Cell</i> , 2018, 173, 153-165.e22.	28.9	242
43	ST Spot Detector: a web-based application for automatic spot and tissue detection for spatial Transcriptomics image datasets. <i>Bioinformatics</i> , 2018, 34, 1966-1968.	4.1	30
44	Single-Stranded Nucleic Acids Regulate TLR3/4/7 Activation through Interference with Clathrin-Mediated Endocytosis. <i>Scientific Reports</i> , 2018, 8, 15841.	3.3	12
45	Barcoded solid-phase RNA capture for Spatial Transcriptomics profiling in mammalian tissue sections. <i>Nature Protocols</i> , 2018, 13, 2501-2534.	12.0	144
46	Preparation of plant tissue to enable Spatial Transcriptomics profiling using barcoded microarrays. <i>Nature Protocols</i> , 2018, 13, 2425-2446.	12.0	34
47	Spatially Resolved Transcriptomics Enables Dissection of Genetic Heterogeneity in Stage III Cutaneous Malignant Melanoma. <i>Cancer Research</i> , 2018, 78, 5970-5979.	0.9	236
48	Stationary and portable sequencing-based approaches for tracing wastewater contamination in urban stormwater systems. <i>Scientific Reports</i> , 2018, 8, 11907.	3.3	24
49	Gene expression profiling of periodontitis-affected gingival tissue by spatial transcriptomics. <i>Scientific Reports</i> , 2018, 8, 9370.	3.3	49
50	Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity. <i>Nature Communications</i> , 2018, 9, 2419.	12.8	374
51	Electrochemical Genetic Profiling of Single Cancer Cells. <i>Analytical Chemistry</i> , 2017, 89, 3378-3385.	6.5	19
52	Spatially resolved transcriptome profiling in model plant species. <i>Nature Plants</i> , 2017, 3, 17061.	9.3	135
53	ST Pipeline: an automated pipeline for spatial mapping of unique transcripts. <i>Bioinformatics</i> , 2017, 33, 2591-2593.	4.1	81
54	Spatial detection of fetal marker genes expressed at low level in adult human heart tissue. <i>Scientific Reports</i> , 2017, 7, 12941.	3.3	62

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55	SweGen: a whole-genome data resource of genetic variability in a cross-section of the Swedish population. <i>European Journal of Human Genetics</i> , 2017, 25, 1253-1260.	2.8	148
56	05.16â€¦Transcriptome visualisation of the inflamed rheumatoid arthritis joint. , 2017, , .		0
57	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
58	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of <i>Malassezia sympodialis</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkx006.	14.5	47
59	Comparison of whole genome amplification techniques for human single cell exome sequencing. <i>PLoS ONE</i> , 2017, 12, e0171566.	2.5	63
60	Genome-wide identification of Wig-1 mRNA targets by RIP-Seq analysis. <i>Oncotarget</i> , 2016, 7, 1895-1911.	1.8	14
61	Rationale and design of the <scp>PREFERS</scp> (Preserved and Reduced Ejection Fraction) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF Stockholm county of 2.1 million inhabitants. <i>European Journal of Heart Failure</i> , 2016, 18, 1287-1297.	7.1	17
62	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	12.8	44
63	An automated approach to prepare tissue-derived spatially barcoded RNA-sequencing libraries. <i>Scientific Reports</i> , 2016, 6, 37137.	3.3	52
64	Comprehensive RNA sequencing of healthy human endometrium at two time points of the menstrual cycle^{<xref ref-type="fn" rid="afn2">â€€</xref>}. <i>Biology of Reproduction</i> , 2016, 96, 24-33.	2.7	34
65	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. <i>Science</i> , 2016, 353, 78-82.	12.6	1,983
66	Using Whole-Exome Sequencing to Identify Genetic Markers for Carboplatin and Gemcitabine-Induced Toxicities. <i>Clinical Cancer Research</i> , 2016, 22, 366-373.	7.0	20
67	Transcriptome analysis reveals mucin 4 to be highly associated with periodontitis and identifies pleckstrin as a link to systemic diseases. <i>Scientific Reports</i> , 2015, 5, 18475.	3.3	48
68	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. <i>Genome Biology</i> , 2015, 16, 156.	8.8	108
69	Endonuclease Specificity and Sequence Dependence of Type IIS Restriction Enzymes. <i>PLoS ONE</i> , 2015, 10, e0117059.	2.5	9
70	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (<i>Picea abies</i>). <i>PLoS ONE</i> , 2015, 10, e0139080.	2.5	27
71	A validated liquid chromatography tandem mass spectrometry method for quantification of erlotinib, OSI-420 and didesmethyl erlotinib and semi-quantification of erlotinib metabolites in human plasma. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2015, 107, 186-195.	2.8	25
72	Toward Rare Blood Cell Preservation for RNA Sequencing. <i>Journal of Molecular Diagnostics</i> , 2015, 17, 352-359.	2.8	3

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73	Mutations in SLC12A5 in epilepsy of infancy with migrating focal seizures. <i>Nature Communications</i> , 2015, 6, 8038.	12.8	160
74	Sequencing Degraded RNA Addressed by 3' Tag Counting. <i>PLoS ONE</i> , 2014, 9, e91851.	2.5	110
75	Analysis of stranded information using an automated procedure for strand specific RNA sequencing. <i>BMC Genomics</i> , 2014, 15, 631.	2.8	27
76	The age and genomic integrity of neurons after cortical stroke in humans. <i>Nature Neuroscience</i> , 2014, 17, 801-803.	14.8	108
77	The human skeletal muscle transcriptome: sex differences, alternative splicing, and tissue homogeneity assessed with RNA sequencing. <i>FASEB Journal</i> , 2014, 28, 4571-4581.	0.5	68
78	Efficient de novo assembly of large and complex genomes by massively parallel sequencing of Fosmid pools. <i>BMC Genomics</i> , 2014, 15, 439.	2.8	6
79	Assessment of Whole Genome Amplification for Sequence Capture and Massively Parallel Sequencing. <i>PLoS ONE</i> , 2014, 9, e84785.	2.5	10
80	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
81	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013, 4, e00572-12.	4.1	118
82	Hierarchical molecular tagging to resolve long continuous sequences by massively parallel sequencing. <i>Scientific Reports</i> , 2013, 3, 1186.	3.3	12
83	TagGD: Fast and Accurate Software for DNA Tag Generation and Demultiplexing. <i>PLoS ONE</i> , 2013, 8, e57521.	2.5	43
84	Improved gap size estimation for scaffolding algorithms. <i>Bioinformatics</i> , 2012, 28, 2215-2222.	4.1	23
85	Identification of candidate SNPs for drug induced toxicity from differentially expressed genes in associated tissues. <i>Gene</i> , 2012, 506, 62-68.	2.2	15
86	Stepping stones in DNA sequencing. <i>Biotechnology Journal</i> , 2012, 7, 1063-1073.	3.5	59
87	Comparison of total and cytoplasmic mRNA reveals global regulation by nuclear retention and miRNAs. <i>BMC Genomics</i> , 2012, 13, 574.	2.8	35
88	Activated Paper Surfaces for the Rapid Hybridization of DNA through Capillary Transport. <i>Analytical Chemistry</i> , 2012, 84, 3311-3317.	6.5	78
89	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. <i>Genome Medicine</i> , 2012, 4, 86.	8.2	37
90	Gene Expression Profiles in Paired Gingival Biopsies from Periodontitis-Affected and Healthy Tissues Revealed by Massively Parallel Sequencing. <i>PLoS ONE</i> , 2012, 7, e46440.	2.5	44

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91	Large Scale Library Generation for High Throughput Sequencing. PLoS ONE, 2011, 6, e19119.	2.5	142
92	Scalable Transcriptome Preparation for Massive Parallel Sequencing. PLoS ONE, 2011, 6, e21910.	2.5	18
93	Adenosine Kinase Deficiency Disrupts the Methionine Cycle and Causes Hypermethioninemia, Encephalopathy, and Abnormal Liver Function. American Journal of Human Genetics, 2011, 89, 507-515.	6.2	104
94	Increased Throughput by Parallelization of Library Preparation for Massive Sequencing. PLoS ONE, 2010, 5, e10029.	2.5	114
95	The Gene Expression Profile in the Synovium as a Predictor of the Clinical Response to Infliximab Treatment in Rheumatoid Arthritis. PLoS ONE, 2010, 5, e11310.	2.5	96
96	Defining the transcriptome and proteome in three functionally different human cell lines. Molecular Systems Biology, 2010, 6, 450.	7.2	324
97	A hypoxic niche regulates glioblastoma stem cells through hypoxia inducible factor 2 β . Brain, 2010, 133, 983-995.	7.6	401
98	The plasticity of the mammalian transcriptome. Genomics, 2010, 95, 1-6.	2.9	64
99	Dynamics of HIV-1 Quasispecies during Antiviral Treatment Dissected Using Ultra-Deep Pyrosequencing. PLoS ONE, 2010, 5, e11345.	2.5	112
100	Inheritance of Acquired Behaviour Adaptations and Brain Gene Expression in Chickens. PLoS ONE, 2009, 4, e6405.	2.5	61
101	High-Density Microwell Chip for Culture and Analysis of Stem Cells. PLoS ONE, 2009, 4, e6997.	2.5	54
102	Transcriptional profiling enables molecular classification of adrenocortical tumours. European Journal of Endocrinology, 2009, 161, 141-152.	3.7	63
103	Automation of cDNA Synthesis and Labelling Improves Reproducibility. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-7.	3.0	13
104	Generations of sequencing technologies. Genomics, 2009, 93, 105-111.	2.9	288
105	mtDNA Data Indicate a Single Origin for Dogs South of Yangtze River, Less Than 16,300 Years Ago, from Numerous Wolves. Molecular Biology and Evolution, 2009, 26, 2849-2864.	8.9	314
106	Genome wide gene amplifications and deletions in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2007, 155, 33-44.	1.1	68
107	Transmission of Stress-Induced Learning Impairment and Associated Brain Gene Expression from Parents to Offspring in Chickens. PLoS ONE, 2007, 2, e364.	2.5	86
108	NRAS and BRAF mutations in melanoma tumours in relation to clinical characteristics: a study based on mutation screening by pyrosequencing. Melanoma Research, 2006, 16, 471-478.	1.2	305

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109	The biotin-streptavidin interaction can be reversibly broken using water at elevated temperatures. <i>Electrophoresis</i> , 2005, 26, 501-510.	2.4	378
110	Analysis of 70,000 EST sequences to study divergence between two closely related <i>Populus</i> species. <i>Tree Genetics and Genomes</i> , 2005, 1, 109-115.	1.6	11
111	A Human Protein Atlas for Normal and Cancer Tissues Based on Antibody Proteomics. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1920-1932.	3.8	1,226
112	Serum Microarrays for Large Scale Screening of Protein Levels. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1942-1947.	3.8	76
113	Competitive enzymatic reaction to control allele-specific extensions. <i>Nucleic Acids Research</i> , 2005, 33, e48-e48.	14.5	28
114	A <i>Populus</i> EST resource for plant functional genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13951-13956.	7.1	278
115	The Genome Sequence of <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC Type Strain PG1 ^T , the Causative Agent of Contagious Bovine Pleuropneumonia (CBPP). <i>Genome Research</i> , 2004, 14, 221-227.	5.5	174
116	Versatile Gene-Specific Sequence Tags for Arabidopsis Functional Genomics: Transcript Profiling and Reverse Genetics Applications. <i>Genome Research</i> , 2004, 14, 2176-2189.	5.5	282
117	Cambial meristem dormancy in trees involves extensive remodelling of the transcriptome. <i>Plant Journal</i> , 2004, 40, 173-187.	5.7	229
118	A detailed picture of the origin of the Australian dingo, obtained from the study of mitochondrial DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12387-12390.	7.1	255
119	Transcriptional Responses of <i>Paxillus involutus</i> and <i>Betula pendula</i> During Formation of Ectomycorrhizal Root Tissue. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 202-215.	2.6	97
120	Gene Expression in Autumn Leaves. <i>Plant Physiology</i> , 2003, 131, 430-442.	4.8	271
121	Affinity Proteomics for Systematic Protein Profiling of Chromosome 21 Gene Products in Human Tissues. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 405-414.	3.8	105
122	SNP typing by apyrase-mediated allele-specific primer extension on DNA microarrays. <i>Nucleic Acids Research</i> , 2002, 30, 75e-75.	14.5	48
123	Genetic Evidence for an East Asian Origin of Domestic Dogs. <i>Science</i> , 2002, 298, 1610-1613.	12.6	779
124	Extensive Linkage Disequilibrium in Small Human Populations in Eurasia. <i>American Journal of Human Genetics</i> , 2002, 70, 673-685.	6.2	66
125	Pyrosequencing as an Alternative to Single-Strand Conformation Polymorphism Analysis for Detection of N-ras Mutations in Human Melanoma Metastases. <i>Clinical Chemistry</i> , 2002, 48, 2164-2170.	3.2	39
126	Pyrosequencing as an alternative to single-strand conformation polymorphism analysis for detection of N-ras mutations in human melanoma metastases. <i>Clinical Chemistry</i> , 2002, 48, 2164-70.	3.2	13

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127	Persistent p53 Mutations in Single Cells from Normal Human Skin. <i>American Journal of Pathology</i> , 2001, 159, 1247-1253.	3.8	93
128	SCREENING AND SCANNING OF SINGLE NUCLEOTIDE POLYMORPHISMS IN THE PIG MELANOCORTIN 1 RECEPTOR GENE (MC1R) BY PYROSEQUENCING. <i>Animal Biotechnology</i> , 2001, 12, 145-153.	1.5	11
129	cDNA microarray analysis of small plant tissue samples using a cDNA tag target amplification protocol. <i>Plant Journal</i> , 2001, 25, 585-591.	5.7	61
130	Quantification of HIV-1 Using Multiple Quantitative Polymerase Chain Reaction Standards and Bioluminometric Detection. <i>Analytical Biochemistry</i> , 2001, 288, 28-38.	2.4	15
131	PATCHED and p53 gene alterations in sporadic and hereditary basal cell cancer. <i>Oncogene</i> , 2001, 20, 7770-7778.	5.9	125
132	Genotyping by apyrase-mediated allele-specific extension. <i>Nucleic Acids Research</i> , 2001, 29, 121e-121.	14.5	40
133	Microarray Analysis of the in Vivo Effects of Hypophysectomy and Growth Hormone Treatment on Gene Expression in the Rat*. <i>Endocrinology</i> , 2001, 142, 3163-3176.	2.8	97
134	Microarray Analysis of the in Vivo Effects of Hypophysectomy and Growth Hormone Treatment on Gene Expression in the Rat. <i>Endocrinology</i> , 2001, 142, 3163-3176.	2.8	27
135	Single-Nucleotide Polymorphism Analysis by Pyrosequencing. <i>Analytical Biochemistry</i> , 2000, 280, 103-110.	2.4	376
136	Mutation detection by pyrosequencing: sequencing of exons 5-8 of the p53 tumor suppressor gene. <i>Gene</i> , 2000, 253, 249-257.	2.2	89
137	Sequence analysis of genes and genomes. <i>Journal of Biotechnology</i> , 2000, 76, 1-31.	3.8	46
138	Polymorphism in the Pertussis Toxin Promoter Region Affecting the DNA-Based Diagnosis of <i>Bordetella</i> Infection. <i>Journal of Clinical Microbiology</i> , 2000, 38, 55-60.	3.9	29
139	Differential Cloning of Growth Hormone-Regulated Hepatic Transcripts in the Aged Rat. <i>Endocrinology</i> , 2000, 141, 910-921.	2.8	9
140	Analyses of Secondary Structures in DNA by Pyrosequencing. <i>Analytical Biochemistry</i> , 1999, 267, 65-71.	2.4	96
141	A High Frequency of Sequence Alterations Is Due to Formalin Fixation of Archival Specimens. <i>American Journal of Pathology</i> , 1999, 155, 1467-1471.	3.8	470
142	Forensic Evidence Based on mtDNA from Dog and Wolf Hairs. <i>Journal of Forensic Sciences</i> , 1999, 44, 77-81.	1.6	54
143	Genetic instability in the 9q22.3 region is a late event in the development of squamous cell carcinoma. <i>Oncogene</i> , 1998, 17, 1837-1843.	5.9	45
144	Quantification of <i>Bordetella pertussis</i> clinical samples by colorimetric detection of competitive PCR products. <i>Apmis</i> , 1998, 106, 1041-1048.	2.0	7

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145	Variation in the hepatitis C virus NS5a region in relation to hypervariable region 1 heterogeneity during interferon treatment. , 1998, 56, 33-38.		32
146	Assessment of sequence-based p53 gene analysis in human breast cancer: messenger RNA in comparison with genomic DNA targets. Clinical Chemistry, 1998, 44, 455-462.	3.2	41
147	Affinity Fusion Strategies for Detection, Purification, and Immobilization of Recombinant Proteins. Protein Expression and Purification, 1997, 11, 1-16.	1.3	302
148	Multiple and Ancient Origins of the Domestic Dog. Science, 1997, 276, 1687-1689.	12.6	878
149	Molecular pathology in basal cell cancer with p53 as a genetic marker. Oncogene, 1997, 15, 1059-1067.	5.9	100
150	Serum Hepatitis C Virus RNA Levels in Chronic Hepatitis C-Importance for outcome of interferon alfa-2b treatment. Scandinavian Journal of Infectious Diseases, 1994, 26, 263-270.	1.5	35
151	Microtiter Assay for Colorimetric Detection of in vitro Amplified Chlamydia trachomatis Sequences. Scandinavian Journal of Infectious Diseases, 1994, 26, 275-282.	1.5	0
152	Dynamic changes in HIV-1 quasispecies from azidothymidine (AZT)-treated patients. FASEB Journal, 1992, 6, 2843-2847.	0.5	52
153	An Organ-Wide Gene Expression Atlas of the Developing Human Heart. SSRN Electronic Journal, 0, , .	0.4	1