

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	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. <i>Science</i> , 2016, 353, 78-82.	12.6	1,983
2	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
3	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
4	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
5	Multiple and Ancient Origins of the Domestic Dog. <i>Science</i> , 1997, 276, 1687-1689.	12.6	878
6	Genetic Evidence for an East Asian Origin of Domestic Dogs. <i>Science</i> , 2002, 298, 1610-1613.	12.6	779
7	High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , 2019, 16, 987-990.	19.0	708
8	A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347.	21.4	535
9	Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma. <i>Cell</i> , 2020, 182, 497-514.e22.	28.9	508
10	Spatial Transcriptomics and In Situ Sequencing to Study Alzheimer's Disease. <i>Cell</i> , 2020, 182, 976-991.e19.	28.9	491
11	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
12	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
13	A hypoxic niche regulates glioblastoma stem cells through hypoxia inducible factor 2 β . <i>Brain</i> , 2010, 133, 983-995.	7.6	401
14	The biotin-streptavidin interaction can be reversibly broken using water at elevated temperatures. <i>Electrophoresis</i> , 2005, 26, 501-510.	2.4	378
15	Single-Nucleotide Polymorphism Analysis by Pyrosequencing. <i>Analytical Biochemistry</i> , 2000, 280, 103-110.	2.4	376
16	Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity. <i>Nature Communications</i> , 2018, 9, 2419.	12.8	374
17	Spatially Resolved Transcriptomes—Next Generation Tools for Tissue Exploration. <i>BioEssays</i> , 2020, 42, e1900221.	2.5	332
18	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010, 6, 450.	7.2	324

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19	mtDNA Data Indicate a Single Origin for Dogs South of Yangtze River, Less Than 16,300 Years Ago, from Numerous Wolves. <i>Molecular Biology and Evolution</i> , 2009, 26, 2849-2864.	8.9	314
20	NRAS and BRAF mutations in melanoma tumours in relation to clinical characteristics: a study based on mutation screening by pyrosequencing. <i>Melanoma Research</i> , 2006, 16, 471-478.	1.2	305
21	Affinity Fusion Strategies for Detection, Purification, and Immobilization of Recombinant Proteins. <i>Protein Expression and Purification</i> , 1997, 11, 1-16.	1.3	302
22	Spatiotemporal dynamics of molecular pathology in amyotrophic lateral sclerosis. <i>Science</i> , 2019, 364, 89-93.	12.6	297
23	Generations of sequencing technologies. <i>Genomics</i> , 2009, 93, 105-111.	2.9	288
24	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
25	A Populus 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
26	Gene Expression in Autumn Leaves. <i>Plant Physiology</i> , 2003, 131, 430-442.	4.8	271
27	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
28	Single-cell and spatial transcriptomics enables probabilistic inference of cell type topography. <i>Communications Biology</i> , 2020, 3, 565.	4.4	252
29	Reducing Pericyte-Derived Scarring Promotes Recovery after Spinal Cord Injury. <i>Cell</i> , 2018, 173, 153-165.e22.	28.9	242
30	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
31	Cambial meristem dormancy in trees involves extensive remodelling of the transcriptome. <i>Plant Journal</i> , 2004, 40, 173-187.	5.7	229
32	Integrating spatial gene expression and breast tumour morphology via deep learning. <i>Nature Biomedical Engineering</i> , 2020, 4, 827-834.	22.5	208
33	Molecular atlas of the adult mouse brain. <i>Science Advances</i> , 2020, 6, eabb3446.	10.3	183
34	Spatially resolved transcriptomics adds a new dimension to genomics. <i>Nature Methods</i> , 2021, 18, 15-18.	19.0	180
35	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
36	Mutations in SLC12A5 in epilepsy of infancy with migrating focal seizures. <i>Nature Communications</i> , 2015, 6, 8038.	12.8	160

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37	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
38	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
39	Barcoded solid-phase RNA capture for Spatial Transcriptomics profiling in mammalian tissue sections. <i>Nature Protocols</i> , 2018, 13, 2501-2534.	12.0	144
40	Seamless integration of image and molecular analysis for spatial transcriptomics workflows. <i>BMC Genomics</i> , 2020, 21, 482.	2.8	144
41	Large Scale Library Generation for High Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e19119.	2.5	142
42	Spatial deconvolution of HER2-positive breast cancer delineates tumor-associated cell type interactions. <i>Nature Communications</i> , 2021, 12, 6012.	12.8	140
43	Spatially resolved transcriptome profiling in model plant species. <i>Nature Plants</i> , 2017, 3, 17061.	9.3	135
44	PATCHED and p53 gene alterations in sporadic and hereditary basal cell cancer. <i>Oncogene</i> , 2001, 20, 7770-7778.	5.9	125
45	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013, 4, e00572-12.	4.1	118
46	Increased Throughput by Parallelization of Library Preparation for Massive Sequencing. <i>PLoS ONE</i> , 2010, 5, e10029.	2.5	114
47	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	27.8	114
48	Dynamics of HIV-1 Quasispecies during Antiviral Treatment Dissected Using Ultra-Deep Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e11345.	2.5	112
49	Sequencing Degraded RNA Addressed by 3' Tag Counting. <i>PLoS ONE</i> , 2014, 9, e91851.	2.5	110
50	The age and genomic integrity of neurons after cortical stroke in humans. <i>Nature Neuroscience</i> , 2014, 17, 801-803.	14.8	108
51	Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. <i>Genome Biology</i> , 2015, 16, 156.	8.8	108
52	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
53	Adenosine Kinase Deficiency Disrupts the Methionine Cycle and Causes Hypermethioninemia, Encephalopathy, and Abnormal Liver Function. <i>American Journal of Human Genetics</i> , 2011, 89, 507-515.	6.2	104
54	Molecular pathology in basal cell cancer with p53 as a genetic marker. <i>Oncogene</i> , 1997, 15, 1059-1067.	5.9	100

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55	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
56	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
57	Analyses of Secondary Structures in DNA by Pyrosequencing. <i>Analytical Biochemistry</i> , 1999, 267, 65-71.	2.4	96
58	The Gene Expression Profile in the Synovium as a Predictor of the Clinical Response to Infliximab Treatment in Rheumatoid Arthritis. <i>PLoS ONE</i> , 2010, 5, e11310.	2.5	96
59	Persistent p53 Mutations in Single Cells from Normal Human Skin. <i>American Journal of Pathology</i> , 2001, 159, 1247-1253.	3.8	93
60	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
61	A latent lineage potential in resident neural stem cells enables spinal cord repair. <i>Science</i> , 2020, 370, .	12.6	89
62	Transmission of Stress-Induced Learning Impairment and Associated Brain Gene Expression from Parents to Offspring in Chickens. <i>PLoS ONE</i> , 2007, 2, e364.	2.5	86
63	ST Pipeline: an automated pipeline for spatial mapping of unique transcripts. <i>Bioinformatics</i> , 2017, 33, 2591-2593.	4.1	81
64	Activated Paper Surfaces for the Rapid Hybridization of DNA through Capillary Transport. <i>Analytical Chemistry</i> , 2012, 84, 3311-3317.	6.5	78
65	Serum Microarrays for Large Scale Screening of Protein Levels. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1942-1947.	3.8	76
66	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
67	Genome wide gene amplifications and deletions in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 155, 33-44.	1.1	68
68	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
69	Extensive Linkage Disequilibrium in Small Human Populations in Eurasia. <i>American Journal of Human Genetics</i> , 2002, 70, 673-685.	6.2	66
70	The plasticity of the mammalian transcriptome. <i>Genomics</i> , 2010, 95, 1-6.	2.9	64
71	Transcriptional profiling enables molecular classification of adrenocortical tumours. <i>European Journal of Endocrinology</i> , 2009, 161, 141-152.	3.7	63
72	Comparison of whole genome amplification techniques for human single cell exome sequencing. <i>PLoS ONE</i> , 2017, 12, e0171566.	2.5	63

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73	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
74	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
75	Inheritance of Acquired Behaviour Adaptations and Brain Gene Expression in Chickens. <i>PLoS ONE</i> , 2009, 4, e6405.	2.5	61
76	Spatial Transcriptomics Reveals Genes Associated with Dysregulated Mitochondrial Functions and Stress Signaling in Alzheimer Disease. <i>IScience</i> , 2020, 23, 101556.	4.1	61
77	Super-resolved spatial transcriptomics by deep data fusion. <i>Nature Biotechnology</i> , 2022, 40, 476-479.	17.5	61
78	Stepping stones in DNA sequencing. <i>Biotechnology Journal</i> , 2012, 7, 1063-1073.	3.5	59
79	Identification of early neurodegenerative pathways in progressive multiple sclerosis. <i>Nature Neuroscience</i> , 2022, 25, 944-955.	14.8	55
80	High-Density Microwell Chip for Culture and Analysis of Stem Cells. <i>PLoS ONE</i> , 2009, 4, e6997.	2.5	54
81	Forensic Evidence Based on mtDNA from Dog and Wolf Hairs. <i>Journal of Forensic Sciences</i> , 1999, 44, 77-81.	1.6	54
82	Dynamic changes in HIV-1 quasispecies from azidothymidine (AZT)-treated patients. <i>FASEB Journal</i> , 1992, 6, 2843-2847.	0.5	52
83	An automated approach to prepare tissue-derived spatially barcoded RNA-sequencing libraries. <i>Scientific Reports</i> , 2016, 6, 37137.	3.3	52
84	Gene expression profiling of periodontitis-affected gingival tissue by spatial transcriptomics. <i>Scientific Reports</i> , 2018, 8, 9370.	3.3	49
85	SNP typing by apyrase-mediated allele-specific primer extension on DNA microarrays. <i>Nucleic Acids Research</i> , 2002, 30, 75e-75.	14.5	48
86	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
87	Clonal relations in the mouse brain revealed by single-cell and spatial transcriptomics. <i>Nature Neuroscience</i> , 2022, 25, 285-294.	14.8	48
88	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
89	Sequence analysis of genes and genomes. <i>Journal of Biotechnology</i> , 2000, 76, 1-31.	3.8	46
90	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

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91	Genome-wide spatial expression profiling in formalin-fixed tissues. <i>Cell Genomics</i> , 2021, 1, 100065.	6.5	45
92	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
93	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	12.8	44
94	TagGD: Fast and Accurate Software for DNA Tag Generation and Demultiplexing. <i>PLoS ONE</i> , 2013, 8, e57521.	2.5	43
95	The spatial transcriptomic landscape of the healing mouse intestine following damage. <i>Nature Communications</i> , 2022, 13, 828.	12.8	43
96	Assessment of sequence-based p53 gene analysis in human breast cancer: messenger RNA in comparison with genomic DNA targets. <i>Clinical Chemistry</i> , 1998, 44, 455-462.	3.2	41
97	Genotyping by apyrase-mediated allele-specific extension. <i>Nucleic Acids Research</i> , 2001, 29, 121e-121.	14.5	40
98	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
99	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. <i>Genome Medicine</i> , 2012, 4, 86.	8.2	37
100	Serum Hepatitis C Virus RNA Levels in Chronic Hepatitis C-Importance for outcome of interferon alfa-2b treatment. <i>Scandinavian Journal of Infectious Diseases</i> , 1994, 26, 263-270.	1.5	35
101	Comparison of total and cytoplasmic mRNA reveals global regulation by nuclear retention and miRNAs. <i>BMC Genomics</i> , 2012, 13, 574.	2.8	35
102	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
103	Comprehensive RNA sequencing of healthy human endometrium at two time points of the menstrual cycle. <i>Biology of Reproduction</i> , 2016, 96, 24-33.	2.7	34
104	Preparation of plant tissue to enable Spatial Transcriptomics profiling using barcoded microarrays. <i>Nature Protocols</i> , 2018, 13, 2425-2446.	12.0	34
105	Variation in the hepatitis C virus NS5a region in relation to hypervariable region 1 heterogeneity during interferon treatment. <i>Journal of Virology</i> , 1998, 56, 33-38.		32
106	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
107	ST viewer: a tool for analysis and visualization of spatial transcriptomics datasets. <i>Bioinformatics</i> , 2019, 35, 1058-1060.	4.1	30
108	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

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109	Deconstructing tumor heterogeneity: the stromal perspective. <i>Oncotarget</i> , 2020, 11, 3621-3632.	1.8	29
110	Competitive enzymatic reaction to control allele-specific extensions. <i>Nucleic Acids Research</i> , 2005, 33, e48-e48.	14.5	28
111	<i>scater</i> : identifying transcript profiles with spatial patterns by diffusion-based modeling. <i>Bioinformatics</i> , 2021, 37, 2644-2650.	4.1	28
112	Analysis of stranded information using an automated procedure for strand specific RNA sequencing. <i>BMC Genomics</i> , 2014, 15, 631.	2.8	27
113	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (<i>Picea abies</i>). <i>PLoS ONE</i> , 2015, 10, e0139080.	2.5	27
114	Transcriptional output, cell-type densities, and normalization in spatial transcriptomics. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 906-908.	3.3	27
115	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
116	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
117	Stationary and portable sequencing-based approaches for tracing wastewater contamination in urban stormwater systems. <i>Scientific Reports</i> , 2018, 8, 11907.	3.3	24
118	Improved gap size estimation for scaffolding algorithms. <i>Bioinformatics</i> , 2012, 28, 2215-2222.	4.1	23
119	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
120	Electrochemical Genetic Profiling of Single Cancer Cells. <i>Analytical Chemistry</i> , 2017, 89, 3378-3385.	6.5	19
121	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
122	Scalable Transcriptome Preparation for Massive Parallel Sequencing. <i>PLoS ONE</i> , 2011, 6, e21910.	2.5	18
123	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
124	Rationale and design of the <i>PREFERS</i> (Preserved and Reduced Ejection Fraction) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 147 T Stockholm county of 2.1 million inhabitants. <i>European Journal of Heart Failure</i> , 2016, 18, 1287-1297.	7.1	17
125	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
126	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

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127	Morphological Features Extracted by AI Associated with Spatial Transcriptomics in Prostate Cancer. <i>Cancers</i> , 2021, 13, 4837.	3.7	15
128	The discovAIR project: a roadmap towards the Human Lung Cell Atlas. <i>European Respiratory Journal</i> , 2022, 60, 2102057.	6.7	15
129	Genome-wide identification of Wig-1 mRNA targets by RIP-Seq analysis. <i>Oncotarget</i> , 2016, 7, 1895-1911.	1.8	14
130	Automation of cDNA Synthesis and Labelling Improves Reproducibility. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-7.	3.0	13
131	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
132	Hierarchical molecular tagging to resolve long continuous sequences by massively parallel sequencing. <i>Scientific Reports</i> , 2013, 3, 1186.	3.3	12
133	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
134	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
135	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
136	SpatialCPie: an R/Bioconductor package for spatial transcriptomics cluster evaluation. <i>BMC Bioinformatics</i> , 2020, 21, 161.	2.6	11
137	The spatial RNA integrity number assay for in situ evaluation of transcriptome quality. <i>Communications Biology</i> , 2021, 4, 57.	4.4	11
138	Assessment of Whole Genome Amplification for Sequence Capture and Massively Parallel Sequencing. <i>PLoS ONE</i> , 2014, 9, e84785.	2.5	10
139	Endonuclease Specificity and Sequence Dependence of Type IIS Restriction Enzymes. <i>PLoS ONE</i> , 2015, 10, e0117059.	2.5	9
140	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
141	Differential Cloning of Growth Hormone-Regulated Hepatic Transcripts in the Aged Rat. <i>Endocrinology</i> , 2000, 141, 910-921.	2.8	9
142	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
143	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
144	Single-Stranded Oligonucleotide-Mediated Inhibition of Respiratory Syncytial Virus Infection. <i>Frontiers in Immunology</i> , 2020, 11, 580547.	4.8	7

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145	Efficient de novo assembly of large and complex genomes by massively parallel sequencing of Fosmid pools. BMC Genomics, 2014, 15, 439.	2.8	6
146	Genetic association of gemcitabine/carboplatin-induced leukopenia and neutropenia in non-small cell lung cancer patients using whole-exome sequencing. Lung Cancer, 2020, 147, 106-114.	2.0	5
147	Toward Rare Blood Cell Preservation for RNA Sequencing. Journal of Molecular Diagnostics, 2015, 17, 352-359.	2.8	3
148	The impact of gastrointestinal dysmotility on the aerodigestive microbiome of pediatric lung transplant recipients. Journal of Heart and Lung Transplantation, 2021, 40, 210-219.	0.6	3
149	Abstract 129: An integrated multi-omic cellular atlas of human breast cancers. Cancer Research, 2021, 81, 129-129.	0.9	3
150	An Organ-Wide Gene Expression Atlas of the Developing Human Heart. SSRN Electronic Journal, 0, , .	0.4	1
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	05.16â€¦Transcriptome visualisation of the inflamed rheumatoid arthritis joint. , 2017, , .		0
153	Novel loss-of-function variant in DENND5A impedes melanosomal cargo transport and predisposes to familial cutaneous melanoma. Genetics in Medicine, 2022, 24, 157-169.	2.4	0