List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	17.5	662
3	SeqMap: mapping massive amount of oligonucleotides to the genome. Bioinformatics, 2008, 24, 2395-2396.	4.1	459
4	Statistical inferences for isoform expression in RNA-Seq. Bioinformatics, 2009, 25, 1026-1032.	4.1	405
5	A Potent and Selective Small-Molecule Degrader of STAT3 Achieves Complete Tumor Regression InÂVivo. Cancer Cell, 2019, 36, 498-511.e17.	16.8	364
6	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	14.5	300
7	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. Reproductive Sciences, 2014, 21, 32-40.	2.5	259
8	Analysis of the androgen receptor–regulated IncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. Nature Genetics, 2018, 50, 814-824.	21.4	196
9	Expansion of CTCs from early stage lung cancer patients using a microfluidic co-culture model. Oncotarget, 2014, 5, 12383-12397.	1.8	175
10	Comparative analysis of circulating tumor DNA stability In K3EDTA, Streck, and CellSave blood collection tubes. Clinical Biochemistry, 2016, 49, 1354-1360.	1.9	175
11	Targeted Degradation of BET Proteins in Triple-Negative Breast Cancer. Cancer Research, 2017, 77, 2476-2487.	0.9	173
12	Modeling non-uniformity in short-read rates in RNA-Seq data. Genome Biology, 2010, 11, R50.	9.6	165
13	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. Nature Biotechnology, 2018, 36, 746-757.	17.5	134
14	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. Journal of Assisted Reproduction and Genetics, 2012, 29, 105-115.	2.5	124
15	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	7.1	122
16	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	12.8	114
17	The in vivo endothelial cell translatome is highly heterogeneous across vascular beds. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23618-23624.	7.1	89
18	Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq. Nature Cell Biology, 2013, 15, 1244-1252.	10.3	88

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19	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. Rna, 2008, 14, 1470-1479.	3.5	86
20	Development of Peptidomimetic Inhibitors of the ERG Gene Fusion Product in Prostate Cancer. Cancer Cell, 2017, 31, 532-548.e7.	16.8	85
21	A Novel RNA In Situ Hybridization Assay for the Long Noncoding RNA SChLAP1 Predicts Poor Clinical Outcome After Radical Prostatectomy in Clinically Localized Prostate Cancer. Neoplasia, 2014, 16, 1121-1127.	5.3	81
22	Statistical Modeling of RNA-Seq Data. Statistical Science, 2011, 26, .	2.8	64
23	Label-free absolute protein quantification with data-independent acquisition. Journal of Proteomics, 2019, 200, 51-59.	2.4	60
24	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. Bioinformatics, 2009, 25, 3056-3059.	4.1	54
25	Trastuzumab resistance induces EMT to transform HER2+ PTENâ^ to a triple negative breast cancer that requires unique treatment options. Scientific Reports, 2015, 5, 15821.	3.3	50
26	Genome-wide pQTL analysis of protein expression regulatory networks in the human liver. BMC Biology, 2020, 18, 97.	3.8	49
27	Fast and accurate read alignment for resequencing. Bioinformatics, 2012, 28, 2366-2373.	4.1	48
28	Expression of PDL1 (B7-H1) Before and After Neoadjuvant Chemotherapy in Urothelial Carcinoma. European Urology Focus, 2016, 1, 265-268.	3.1	45
29	Comparison of protein expression between human livers and the hepatic cell lines HepG2, Hep3B, and Huh7 using SWATH and MRM-HR proteomics: Focusing on drug-metabolizing enzymes. Drug Metabolism and Pharmacokinetics, 2018, 33, 133-140.	2.2	42
30	Multivariate Density Estimation by Bayesian Sequential Partitioning. Journal of the American Statistical Association, 2013, 108, 1402-1410.	3.1	39
31	CisGenome Browser: a flexible tool for genomic data visualization. Bioinformatics, 2010, 26, 1781-1782.	4.1	37
32	RNA-Seq Accurately Identifies Cancer Biomarker Signatures to Distinguish Tissue of Origin. Neoplasia, 2014, 16, 918-927.	5.3	37
33	Novel cancer stem cell targets during epithelial to mesenchymal transition in PTEN-deficient trastuzumab-resistant breast cancer. Oncotarget, 2016, 7, 51408-51422.	1.8	37
34	Cross-hybridization modeling on Affymetrix exon arrays. Bioinformatics, 2008, 24, 2887-2893.	4.1	35
35	Using CisGenome to Analyze ChIP hip and ChIPâ€seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
36	Frequent discordance between <i>ERG</i> gene rearrangement and ERG protein expression in a rapid autopsy cohort of patients with lethal, metastatic, castration-resistant prostate cancer. Prostate, 2014, 74, 1199-1208.	2.3	33

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37	Gestalt-based feature similarity measure in trademark database. Pattern Recognition, 2006, 39, 988-1001.	8.1	32
38	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. PLoS ONE, 2013, 8, e79448.	2.5	29
39	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. Cancer Letters, 2018, 438, 165-173.	7.2	28
40	The genomic landscape of UM-SCC oral cavity squamous cell carcinoma cell lines. Oral Oncology, 2018, 87, 144-151.	1.5	27
41	Performance of lateral flow device and galactomannan for the detection of <i>Aspergillus</i> species in bronchoalveolar fluid of patients at risk for invasive pulmonary aspergillosis. Mycoses, 2015, 58, 368-374.	4.0	26
42	Programmed Death-ligand 1 Expression in Upper Tract Urothelial Carcinoma. European Urology Focus, 2017, 3, 502-509.	3.1	25
43	Single-Cell Transcriptomics Analysis Identifies Nuclear Protein 1 as a Regulator of Docetaxel Resistance in Prostate Cancer Cells. Molecular Cancer Research, 2020, 18, 1290-1301.	3.4	25
44	The molecular landscape of the University of Michigan laryngeal squamous cell carcinoma cell line panel. Head and Neck, 2019, 41, 3114-3124.	2.0	23
45	Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Based Proteomics Method. Journal of Proteome Research, 2018, 17, 3606-3612.	3.7	20
46	Differential regulation of the c-Myc/Lin28 axis discriminates subclasses of rearranged MLL leukemia. Oncotarget, 2016, 7, 25208-25223.	1.8	19
47	Statistical properties of an early stopping rule for resampling-based multiple testing. Biometrika, 2012, 99, 973-980.	2.4	17
48	Rationale for Using Irreversible Epidermal Growth Factor Receptor Inhibitors in Combination with Phosphatidylinositol 3-Kinase Inhibitors for Advanced Head and Neck Squamous Cell Carcinoma. Molecular Pharmacology, 2019, 95, 528-536.	2.3	17
49	Minimizing Sum of Truncated Convex Functions and Its Applications. Journal of Computational and Graphical Statistics, 2019, 28, 1-10.	1.7	17
50	Combined p53- and PTEN-deficiency activates expression of mesenchyme homeobox 1 (MEOX1) required for growth of triple-negative breast cancer. Journal of Biological Chemistry, 2020, 295, 12188-12202.	3.4	16
51	Testing the performance of a prototype lateral flow device using bronchoalveolar lavage fluid for the diagnosis of invasive pulmonary aspergillosis in highâ€risk patients. Mycoses, 2018, 61, 4-10.	4.0	15
52	Fast Approximation of Small P-values in Permutation Tests by Partitioning the Permutations. Biometrics, 2018, 74, 196-206.	1.4	15
53	Variability in protein cargo detection in technical and biological replicates of exosome-enriched extracellular vesicles. PLoS ONE, 2020, 15, e0228871.	2.5	14
54	rSeqNP: a non-parametric approach for detecting differential expression and splicing from RNA-Seq data. Bioinformatics, 2015, 31, 2222-2224.	4.1	13

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55	Identifying Interaction Clusters for MiRNA and MRNA Pairs in TCGA Network. Genes, 2019, 10, 702.	2.4	13
56	A Unified Model for Joint Normalization and Differential Gene Expression Detection in RNA-Seq Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 442-454.	3.0	13
57	False Discovery Rate Control in Cancer Biomarker Selection Using Knockoffs. Cancers, 2019, 11, 744.	3.7	12
58	A penalized likelihood approach for robust estimation of isoform expression. Statistics and Its Interface, 2015, 8, 437-445.	0.3	11
59	Clinicopathologic characteristics of anterior prostate cancer (APC), including correlation with previous biopsy pathology. Medical Oncology, 2015, 32, 249.	2.5	10
60	Dissecting the biological relationship between TCGA miRNA and mRNA sequencing data using MMiRNA-Viewer. BMC Bioinformatics, 2016, 17, 336.	2.6	10
61	A direct comparison of the KBâ"¢ Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. BMC Research Notes, 2010, 3, 257.	1.4	9
62	Concurrent nuclear ERG and MYC protein overexpression defines a subset of locally advanced prostate cancer: Potential opportunities for synergistic targeted therapeutics. Prostate, 2016, 76, 845-853.	2.3	9
63	Genetic analysis of sinonasal undifferentiated carcinoma discovers recurrent SWI/SNF alterations and a novel PGAP3-SRPK1 fusion gene. BMC Cancer, 2021, 21, 636.	2.6	9
64	Correlating Bladder Cancer Risk Genes with Their Targeting MicroRNAs Using MMiRNA-Tar. Genomics, Proteomics and Bioinformatics, 2015, 13, 177-182.	6.9	8
65	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	2.5	7
66	An optimization algorithm for designing phase I cancer clinical trials. Contemporary Clinical Trials, 2008, 29, 102-108.	1.8	6
67	Accurate and efficient estimation of small <i>P</i> -values with the cross-entropy method: applications in genomic data analysis. Bioinformatics, 2019, 35, 2441-2448.	4.1	6
68	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. Bayesian Analysis, 2018, 13, 411-436.	3.0	5
69	Small molecule profiling to define synergistic <scp>EGFR</scp> inhibitor combinations in head and neck squamous cell carcinoma. Head and Neck, 2022, 44, 1192-1205.	2.0	5
70	Computational Aspects of Optional Pólya Tree. Journal of Computational and Graphical Statistics, 2016, 25, 301-320.	1.7	4
71	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. Statistics in Biosciences, 2017, 9, 178-199.	1.2	4
72	Microbe-Mediated Activation of Toll-like Receptor 2 Drives PDL1 Expression in HNSCC. Cancers, 2021, 13, 4782.	3.7	4

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73	Advancement of PI3 Kinase Inhibitor Combination Therapies for PI3K-Aberrant Chordoma. Journal of Neurological Surgery, Part B: Skull Base, 2022, 83, 087-098.	0.8	3
74	False discovery control for penalized variable selections with high-dimensional covariates. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	1
75	Joint between-sample normalization and differential expression detection through â,,"O-regularized regression. BMC Bioinformatics, 2019, 20, 593.	2.6	1
76	Graph based image matching. , 2004, , .		0
77	A Unified Model for Robust Differential Expression Analysis of RNA-Seq Data. , 2018, , .		0
78	Response to the Comments on "Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Proteomics Method― Journal of Proteome Research, 2019, 18, 1458-1459.	3.7	0
79	Differential Regulation of c-Myc/Lin28 Discriminates Subclasses of Rearranged MLL Leukemia. Blood, 2015, 126, 163-163.	1.4	0