Ana Conesa

List of Publications by Year
in descending order

148 papers	32,166 citations	31976 53 h-index	8630 146 g-index
170 all docs	170 docs citations	170 times ranked	48135 citing authors

#	Article	IF	Citations
1	Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics, 2005, 21, 3674-3676.	4.1	10,566
2	High-throughput functional annotation and data mining with the Blast2GO suite. Nucleic Acids Research, 2008, 36, 3420-3435.	14.5	3,905
3	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	8.8	1,898
4	Blast2GO: A Comprehensive Suite for Functional Analysis in Plant Genomics. International Journal of Plant Genomics, 2008, 2008, 1-12.	2.2	1,866
5	Differential expression in RNA-seq: A matter of depth. Genome Research, 2011, 21, 2213-2223.	5.5	1,456
6	Qualimap 2: advanced multi-sample quality control for high-throughput sequencing data. Bioinformatics, 2016, 32, 292-294.	4.1	1,362
7	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
8	Qualimap: evaluating next-generation sequencing alignment data. Bioinformatics, 2012, 28, 2678-2679.	4.1	799
9	Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. Nucleic Acids Research, 2015, 43, gkv711.	14.5	605
10	maSigPro: a method to identify significantly differential expression profiles in time-course microarray experiments. Bioinformatics, 2006, 22, 1096-1102.	4.1	448
11	Filamentous fungi as cell factories for heterologous protein production. Trends in Biotechnology, 2002, 20, 200-206.	9.3	387
12	Initial Genomics of the Human Nucleolus. PLoS Genetics, 2010, 6, e1000889.	3.5	324
13	Next maSigPro: updating maSigPro bioconductor package for RNA-seq time series. Bioinformatics, 2014, 30, 2598-2602.	4.1	315
14	Data integration in the era of omics: current and future challenges. BMC Systems Biology, 2014, 8, I1.	3.0	300
15	SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. Genome Research, 2018, 28, 396-411.	5.5	299
16	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Nucleic Acids Research, 2010, 38, W210-W213.	14.5	283
17	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. Nature Methods, 2015, 12, 623-630.	19.0	282
18	The Secretion Pathway in Filamentous Fungi: A Biotechnological View. Fungal Genetics and Biology, 2001, 33, 155-171.	2.1	230

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19	Paintomics: a web based tool for the joint visualization of transcriptomics and metabolomics data. Bioinformatics, 2011, 27, 137-139.	4.1	211
20	Histone modifications and expression of *DAM6* gene in peach are modulated during bud dormancy release in a cultivar‐dependent manner. New Phytologist, 2012, 193, 67-80.	7.3	195
21	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	8.2	190
22	Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth. Nature Communications, 2018, 9, 4680.	12.8	189
23	Fungal peroxidases: molecular aspects and applications. Journal of Biotechnology, 2002, 93, 143-158.	3.8	185
24	PaintOmics 3: a web resource for the pathway analysis and visualization of multi-omics data. Nucleic Acids Research, 2018, 46, W503-W509.	14.5	143
25	B2G-FAR, a species-centered GO annotation repository. Bioinformatics, 2011, 27, 919-924.	4.1	137
26	NOIseq: a RNA-seq differential expression method robust for sequencing depth biases. EMBnet Journal, 2012, 17, 18.	0.6	134
27	Studies on the Production of Fungal Peroxidases in *Aspergillus niger*. Applied and Environmental Microbiology, 2000, 66, 3016-3023.	3.1	133
28	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
29	Making multi-omics data accessible to researchers. Scientific Data, 2019, 6, 251.	5.3	107
30	Spatial Differentiation in the Vegetative Mycelium of *Aspergillus niger*. Eukaryotic Cell, 2007, 6, 2311-2322.	3.4	106
31	Sequencing and functional analysis of the genome of a nematode egg-parasitic fungus, Pochonia chlamydosporia. Fungal Genetics and Biology, 2014, 65, 69-80.	2.1	105
32	Dynamic Gene Regulatory Networks of Human Myeloid Differentiation. Cell Systems, 2017, 4, 416-429.e3.	6.2	105
33	GRAM-CNN: a deep learning approach with local context for named entity recognition in biomedical text. Bioinformatics, 2018, 34, 1547-1554.	4.1	105
34	Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies. Plant Molecular Biology, 2005, 57, 375-391.	3.9	104
35	Single-cell RNAseq for the study of isoforms—how is that possible?. Genome Biology, 2018, 19, 110.	8.8	100
36	Profiling the venom gland transcriptomes of Costa Rican snakes by 454 pyrosequencing. BMC Genomics, 2011, 12, 259.	2.8	96

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37	Transcriptional Profiling of mRNA Expression in the Mouse Distal Colon. Gastroenterology, 2008, 135, 2019-2029.	1.3	95
38	Hypoxia Promotes Efficient Differentiation of Human Embryonic Stem Cells to Functional Endothelium. Stem Cells, 2010, 28, 407-418.	3.2	92
39	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. Nucleic Acids Research, 2016, 44, W176-W180.	14.5	92
40	A network approach to elucidate and prioritize microbial dark matter in microbial communities. ISME Journal, 2021, 15, 228-244.	9.8	91
41	Plasma profile of pro‐inflammatory cytokines and chemokines in cocaine users under outpatient treatment: influence of cocaine symptom severity and psychiatric co‐morbidity. Addiction Biology, 2015, 20, 756-772.	2.6	85
42	Development of the GENIPOL European Flounder (Platichthys flesus) Microarray and Determination of Temporal Transcriptional Responses to Cadmium at Low Dose.. Environmental Science & Technology, 2006, 40, 6479-6488.	10.0	81
43	Discovering gene expression patterns in time course microarray experiments by ANOVA‐SCA. Bioinformatics, 2007, 23, 1792-1800.	4.1	80
44	Membrane transporters and carbon metabolism implicated in chloride homeostasis differentiate salt stress responses in tolerant and sensitive Citrus rootstocks. Functional and Integrative Genomics, 2009, 9, 293-309.	3.5	80
45	Calnexin Overexpression Increases Manganese Peroxidase Production in <i>Aspergillus niger</i>. Applied and Environmental Microbiology, 2002, 68, 846-851.	3.1	78
46	ARSyN: a method for the identification and removal of systematic noise in multifactorial time course microarray experiments. Biostatistics, 2012, 13, 553-566.	1.5	74
47	Time course profiling of the retinal transcriptome after optic nerve transection and optic nerve crush. Molecular Vision, 2008, 14, 1050-63.	1.1	74
48	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. Nucleic Acids Research, 2008, 36, W341-W346.	14.5	73
49	GEPAS, a web-based tool for microarray data analysis and interpretation. Nucleic Acids Research, 2008, 36, W308-W314.	14.5	67
50	Transcriptional response of Citrus aurantifolia to infection by Citrus tristeza virus. Virology, 2007, 367, 298-306.	2.4	65
51	Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. BMC Genomics, 2007, 8, 31.	2.8	64
52	Transcriptome Profiling of the Intoxication Response of Tenebrio molitor Larvae to Bacillus thuringiensis Cry3Aa Protoxin. PLoS ONE, 2012, 7, e34624.	2.5	60
53	Genome-wide changes in histone H3 lysine 27 trimethylation associated with bud dormancy release in peach. Tree Genetics and Genomes, 2015, 11, 1.	1.6	59
54	Undisclosed, unmet and neglected challenges in multi-omics studies. Nature Computational Science, 2021, 1, 395-402.	8.0	59

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55	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. PLoS Computational Biology, 2019, 15, e1006555.	3.2	56
56	Modeling Human Endometrial Decidualization from the Interaction between Proteome and Secretome. Journal of Clinical Endocrinology and Metabolism, 2011, 96, 706-716.	3.6	53
57	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. PLoS Computational Biology, 2015, 11, e1004143.	3.2	52
58	Tumor microenvironment-targeted poly-L-glutamic acid-based combination conjugate for enhanced triple negative breast cancer treatment. Biomaterials, 2018, 186, 8-21.	11.4	52
59	Identification of yeast genes that confer resistance to chitosan oligosaccharide (COS) using chemogenomics. BMC Genomics, 2012, 13, 267.	2.8	50
60	Expression of the Caldariomyces fumagoChloroperoxidase in Aspergillus niger and Characterization of the Recombinant Enzyme. Journal of Biological Chemistry, 2001, 276, 17635-17640.	3.4	45
61	Examining the Role of Glutamic Acid 183 in Chloroperoxidase Catalysis. Journal of Biological Chemistry, 2003, 278, 13855-13859.	3.4	45
62	Expression profiling shows differential molecular pathways and provides potential new diagnostic biomarkers for colorectal serrated adenocarcinoma. International Journal of Cancer, 2013, 132, 297-307.	5.1	43
63	Harmonization of quality metrics and power calculation in multi-omic studies. Nature Communications, 2020, 11, 3092.	12.8	43
64	Understanding disease mechanisms with models of signaling pathway activities. BMC Systems Biology, 2014, 8, 121.	3.0	42
65	SIMAPâ€"a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. Nucleic Acids Research, 2010, 38, D223-D226.	14.5	40
66	Transcriptome modulation during host shift is driven by secondary metabolites in desert <i><scp>D</scp>rosophila</i>. Molecular Ecology, 2016, 25, 4534-4550.	3.9	40
67	tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. Genome Biology, 2020, 21, 119.	8.8	40
68	Parallel changes in gene expression in peripheral blood mononuclear cells and the brain after maternal separation in the mouse. BMC Research Notes, 2009, 2, 195.	1.4	36
69	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. Genome Biology, 2022, 23, .	8.8	35
70	Early gene expression events in the laminar abscission zone of abscission-promoted citrus leaves after a cycle of water stress/rehydration: involvement of CitbHLH1. Journal of Experimental Botany, 2012, 63, 6079-6091.	4.8	34
71	Comparative Metagenomics Provides Insight Into the Ecosystem Functioning of the Shark Bay Stromatolites, Western Australia. Frontiers in Microbiology, 2018, 9, 1359.	3.5	34
72	Transcriptome analysis reveals novel insights into the response of low-dose benzo(a)pyrene exposure in male tilapia. Aquatic Toxicology, 2018, 201, 162-173.	4.0	33

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73	Enhanced protein isoform characterization through long-read proteogenomics. Genome Biology, 2022, 23, 69.	8.8	33
74	Comparative transcriptomics reveals striking similarities between the bovine and feline isolates of Tritrichomonas foetus: consequences for in silico drug-target identification. BMC Genomics, 2014, 15, 955.	2.8	31
75	A benchmarking of workflows for detecting differential splicing and differential expression at isoform level in human RNA-seq studies. Briefings in Bioinformatics, 2019, 20, 471-481.	6.5	31
76	PaintOmics 4: new tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases. Nucleic Acids Research, 2022, 50, W551-W559.	14.5	31
77	A multiway approach to data integration in systems biology based on Tucker3 and N-PLS. Chemometrics and Intelligent Laboratory Systems, 2010, 104, 101-111.	3.5	30
78	Pathway network inference from gene expression data. BMC Systems Biology, 2014, 8, S7.	3.0	30
79	Disease-specific biases in alternative splicing and tissue-specific dysregulation revealed by multitissue profiling of lymphocyte gene expression in type 1 diabetes. Genome Research, 2017, 27, 1807-1815.	5.5	29
80	Microarray analysis of Etrog citron (*Citrus medica* L.) reveals changes in chloroplast, cell wall, peroxidase and symporter activities in response to viroid infection. Molecular Plant Pathology, 2012, 13, 852-864.	4.2	28
81	Development, Characterization and Experimental Validation of a Cultivated Sunflower (Helianthus) Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	28
82	Defining the Genomic Signature of Totipotency and Pluripotency during Early Human Development. PLoS ONE, 2013, 8, e62135.	2.5	27
83	Two independent epigenetic biomarkers predict survival in neuroblastoma. Clinical Epigenetics, 2015, 7, 16.	4.1	26
84	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific Data, 2019, 6, 256.	5.3	26
85	RNAseq analysis of Aspergillus fumigatus in blood reveals a just wait and see resting stage behavior. BMC Genomics, 2015, 16, 640.	2.8	25
86	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	2.8	24
87	STATegra: Multi-Omics Data Integration â€" A Conceptual Scheme With a Bioinformatics Pipeline. Frontiers in Genetics, 2021, 12, 620453.	2.3	24
88	Mining of miRNAs and potential targets from gene oriented clusters of transcripts sequences of the anti-malarial plant, Artemisia annua. Biotechnology Letters, 2012, 34, 737-745.	2.2	23
89	Large-scale Gene Ontology analysis of plant transcriptome-derived sequences retrieved by AFLP technology. BMC Genomics, 2008, 9, 347.	2.8	22
90	The common ground of genomics and systems biology. BMC Systems Biology, 2014, 8, S1.	3.0	22

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91	Integrative analyses of TEDDY Omics data reveal lipid metabolism abnormalities, increased intracellular ROS and heightened inflammation prior to autoimmunity for type 1 diabetes. Genome Biology, 2021, 22, 39.	8.8	22
92	Fortunella margarita Transcriptional Reprogramming Triggered by Xanthomonas citri subsp. citri. BMC Plant Biology, 2011, 11, 159.	3.6	21
93	Methylome profiling reveals functions and genes which are differentially methylated in serrated compared to conventional colorectal carcinoma. Clinical Epigenetics, 2015, 7, 101.	4.1	21
94	Changes in the uterine metabolome of the cow during the first 7 days after estrus. Molecular Reproduction and Development, 2019, 86, 75-87.	2.0	21
95	Functional assessment of time course microarray data. BMC Bioinformatics, 2009, 10, S9.	2.6	19
96	STATegra EMS: an Experiment Management System for complex next-generation omics experiments. BMC Systems Biology, 2014, 8, S9.	3.0	19
97	The SAGA/TREX-2 subunit Sus1 binds widely to transcribed genes and affects mRNA turnover globally. Epigenetics and Chromatin, 2018, 11, 13.	3.9	19
98	Multiomics Data Integration in Time Series Experiments. Comprehensive Analytical Chemistry, 2018, 82, 505-532.	1.3	19
99	Transcriptome analysis provides new insights into liver changes induced in the rat upon dietary administration of the food additives butylated hydroxytoluene, curcumin, propyl gallate and thiabendazole. Food and Chemical Toxicology, 2008, 46, 2616-2628.	3.6	18
100	Separating common from distinctive variation. BMC Bioinformatics, 2016, 17, 195.	2.6	18
101	Growth of Chlamydia pneumoniae Is Enhanced in Cells with Impaired Mitochondrial Function. Frontiers in Cellular and Infection Microbiology, 2017, 7, 499.	3.9	18
102	Identification and visualization of differential isoform expression in RNA-seq time series. Bioinformatics, 2018, 34, 524-526.	4.1	18
103	Comparative RNA-seq analysis of the Tritrichomonas foetus PIG30/1 isolate from pigs reveals close association with Tritrichomonas foetus BP-4 isolate â€˜bovine genotypeâ€™. Veterinary Parasitology, 2015, 212, 111-117.	1.8	17
104	Assessment of unconventional antimicrobial compounds for the control of â€˜Candidatus Liberibacter asiaticusâ€™, the causative agent of citrus greening disease. Scientific Reports, 2020, 10, 5395.	3.3	17
105	C-terminal propeptide of theCaldariomyces fumagochloroperoxidase: an intramolecular chaperone?. FEBS Letters, 2001, 503, 117-120.	2.8	16
106	Large-scale transcriptional profiling and functional assays reveal important roles for Rho-GTPase signalling and SCL during haematopoietic differentiation of human embryonic stem cells. Human Molecular Genetics, 2011, 20, 4932-4946.	2.9	16
107	Transcriptional profiling of the mutualistic bacterium Vibrio fischeri and an hfq mutant under modeled microgravity. Npj Microgravity, 2018, 4, 25.	3.7	16
108	Transcriptional Differences for COVID-19 Disease Map Genes between Males and Females Indicate a Different Basal Immunophenotype Relevant to the Disease. Genes, 2020, 11, 1447.	2.4	16

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109	RGmatch: matching genomic regions to proximal genes in omics data integration. BMC Bioinformatics, 2016, 17, 427.	2.6	13
110	Serial Expression Analysis: a web tool for the analysis of serial gene expression data. Nucleic Acids Research, 2010, 38, W239-W245.	14.5	12
111	Two histologically colorectal carcinomas subsets from the serrated pathway show different methylome signatures and diagnostic biomarkers. Clinical Epigenetics, 2018, 10, 141.	4.1	12
112	Differential Modulation of Quorum Sensing Signaling through QslA in Pseudomonas aeruginosa Strains PAO1 and PA14. Journal of Bacteriology, 2019, 201, .	2.2	12
113	Event Analysis: Using Transcript Events To Improve Estimates of Abundance in RNA-seq Data. G3: Genes, Genomes, Genetics, 2018, 8, 2923-2940.	1.8	11
114	Sequencing and analysis of gerbera daisy leaf transcriptomes reveal disease resistance and susceptibility genes differentially expressed and associated with powdery mildew resistance. BMC Plant Biology, 2020, 20, 539.	3.6	11
115	Precise transcriptional control of cellular quiescence by BRAVO/WOX5 complex in *Arabidopsis* roots. Molecular Systems Biology, 2021, 17, e9864.	7.2	11
116	Molecular interactions between sugar beet and *Polymyxa betae* during its life cycle. Annals of Applied Biology, 2014, 164, 244-256.	2.5	10
117	Elucidating the Role of Chromatin State and Transcription Factors on the Regulation of the Yeast Metabolic Cycle: A Multi-Omic Integrative Approach. Frontiers in Genetics, 2018, 9, 578.	2.3	10
118	The eBioKit, a stand-alone educational platform for bioinformatics. PLoS Computational Biology, 2017, 13, e1005616.	3.2	10
119	acorde unravels functionally interpretable networks of isoform co-usage from single cell data. Nature Communications, 2022, 13, 1828.	12.8	10
120	Direct functional assessment of the composite phenotype through multivariate projection strategies. Genomics, 2008, 92, 373-383.	2.9	9
121	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in Pneumocystis. Genome Biology and Evolution, 2018, 10, 1596-1606.	2.5	9
122	MultiBaC: A strategy to remove batch effects between different omic data types. Statistical Methods in Medical Research, 2020, 29, 2851-2864.	1.5	9
123	Multi-omic analysis unveils biological pathways in peripheral immune system associated to minimal hepatic encephalopathy appearance in cirrhotic patients. Scientific Reports, 2021, 11, 1907.	3.3	9
124	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. PLoS Biology, 2019, 17, e2006506.	5.6	8
125	Variable selection for multifactorial genomic data. Chemometrics and Intelligent Laboratory Systems, 2012, 110, 113-122.	3.5	7
126	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. Cell Systems, 2017, 5, 168-175.	6.2	7

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127	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. Progress in Preventive Medicine (New York, N Y), 2017, 2, e006.	0.7	6
128	Differences in gene expression profiling and biomarkers between histological colorectal carcinoma subsets from the serrated pathway. Histopathology, 2019, 75, 496-507.	2.9	6
129	Mip6 binds directly to the Mex67 UBA domain to maintain low levels of Msn2/4 stressâ€dependent mRNAs. EMBO Reports, 2019, 20, e47964.	4.5	6
130	A multi-omics dataset of heat-shock response in the yeast RNA binding protein Mip6. Scientific Data, 2020, 7, 69.	5.3	6
131	MultiBaC: an R package to remove batch effects in multi-omic experiments. Bioinformatics, 2022, 38, 2657-2658.	4.1	6
132	Transdifferentiation of MALME-3M and MCF-7 Cells toward Adipocyte-like Cells is Dependent on Clathrin-mediated Endocytosis. SpringerPlus, 2012, 1, 44.	1.2	5
133	A Multiomics Study To Unravel the Effects of Developmental Exposure to Endosulfan in Rats: Molecular Explanation for Sex-Dependent Effects. ACS Chemical Neuroscience, 2019, 10, 4264-4279.	3.5	5
134	Identification of miRNA from Bouteloua gracilis, a drought tolerant grass, by deep sequencing and their in silico analysis. Computational Biology and Chemistry, 2017, 66, 26-35.	2.3	4
135	MirCure: a tool for quality control, filter and curation of microRNAs of animals and plants. Bioinformatics, 2020, 36, i618-i624.	4.1	4
136	A Nextflow pipeline for T-cell receptor repertoire reconstruction and analysis from RNA sequencing data. ImmunoInformatics, 2022, 6, 100012.	2.2	4
137	Omics Data Integration in Systems Biology. Comprehensive Analytical Chemistry, 2014, 64, 441-459.	1.3	2
138	A multi-omic study for uncovering molecular mechanisms associated with hyperammonemia-induced cerebellar function impairment in rats. Cell Biology and Toxicology, 2021, 37, 129-149.	5.3	2
139	GAIT-GM integrative cross-omics analyses reveal cholinergic defects in a C. elegans model of Parkinsonâ€™s disease. Scientific Reports, 2022, 12, 3268.	3.3	2
140	SEQUENCING OF 150 CITRUS VARIETIES: LINKING GENOTYPES TO PHENOTYPES. Acta Horticulturae, 2015, , 585-589.	0.2	1
141	Gene expression profile and molecular pathway datasets resulting from benzo(a)pyrene exposure in the liver and testis of adult tilapia. Data in Brief, 2018, 20, 1500-1509.	1.0	1
142	The STATegra project: new statistical tools for analysis and integration of diverse omics data. EMBnet Journal, 2014, 20, 768.	0.6	1
143	Padhoc: a computational pipeline for pathway reconstruction on the fly. Bioinformatics, 2020, 36, i795-i803.	4.1	1
144	Variation in leaf transcriptome responses to elevated ozone corresponds with physiological sensitivity to ozone across maize inbred lines. Genetics, 2022, 221, .	2.9	1

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145	Expression Profiling as Biomarkers in Colorectal Serrated Carcinoma. , 2014, , 1-23.		0
146	Global Methylome Scores Correlate with Histological Subtypes of Colorectal Carcinoma and Show Different Associations with Common Clinical and Molecular Features. Cancers, 2021, 13, 5165.	3.7	0
147	Calcium signaling in water stress-induced leaf abscission in citrus plants. , 2007, , 303-304.		0
148	Expression Profiling as Biomarkers in Colorectal Serrated Carcinoma. Biomarkers in Disease, 2015, , 631-657.	0.1	0