Liliana D Florea

List of Publications by Year
in descending order

72 papers	20,097 citations	147566 31 h-index	118652 62 g-index
84 all docs	84 docs citations	84 times ranked	23176 citing authors

#	Article	IF	Citations
1	Impact of lifestyle and demographics on the gut microbiota of acne patients and the response to minocycline. Journal of Dermatological Treatment, 2021, 32, 934-935.	1.1	4
2	Comparison of the skin microbiota in acne and rosacea. Experimental Dermatology, 2021, 30, 1375-1380.	1.4	19
3	Study of Tofacitinib in Refractory Dermatomyositis: An Open‐Label Pilot Study of Ten Patients. Arthritis and Rheumatology, 2021, 73, 858-865.	2.9	93
4	Excessive O-GlcNAcylation Causes Heart Failure and Sudden Death. Circulation, 2021, 143, 1687-1703.	1.6	65
5	Jutils: a visualization toolkit for differential alternative splicing events. Bioinformatics, 2021, 37, 4272-4274.	1.8	3
6	CaMKII oxidation is a critical performance/disease trade-off acquired at the dawn of vertebrate evolution. Nature Communications, 2021, 12, 3175.	5.8	19
7	Detection of Alu Exonization Events in Human Frontal Cortex From RNA-Seq Data. Frontiers in Molecular Biosciences, 2021, 8, 727537.	1.6	7
8	Somatic reversion impacts myelodysplastic syndromes and acute myeloid leukemia evolution in the short telomere disorders. Journal of Clinical Investigation, 2021, 131, .	3.9	33
9	Development of Methods to Extract RNA From Archived Pediatric Needle Liver Biopsies to Produce Sequencing Data. Journal of Pediatric Gastroenterology and Nutrition, 2021, 72, 436-441.	0.9	2
10	Characterization and Analysis of the Skin Microbiota in Rosacea: A Case–Control Study. American Journal of Clinical Dermatology, 2020, 21, 139-147.	3.3	37
11	CaMKII oxidation is a performance-disease tradeoff in vertebrate evolution. Journal of Molecular and Cellular Cardiology, 2020, 140, 24.	0.9	0
12	Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. Epigenetics, 2020, 15, 959-971.	1.3	17
13	Minocycline and Its Impact on Microbial Dysbiosis in the Skin and Gastrointestinal Tract of Acne Patients. Annals of Dermatology, 2020, 32, 21.	0.3	35
14	Variability in skin microbiota between smokers, former smokers, and nonsmokers. Journal of the American Academy of Dermatology, 2020, 83, 942-944.	0.6	4
15	A non-mosaic transchromosomic mouse model of Down syndrome carrying the long arm of human chromosome 21. ELife, 2020, 9, .	2.8	65
16	Abstract A25: Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. , 2020, , .		0
17	Changes in Gut Microbiome after Bariatric Surgery Versus Medical Weight Loss in a Pilot Randomized Trial. Obesity Surgery, 2019, 29, 3239-3245.	1.1	46
18	$ZCCHC8$, the nuclear exosome targeting component, is mutated in familial pulmonary fibrosis and is required for telomerase RNA maturation. Genes and Development, 2019, 33, 1381-1396.	2.7	85

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19	A Prospective Study of the Urinary and Gastrointestinal Microbiome in Prepubertal Males. Urology, 2019, 131, 204-210.	0.5	26
20	A multi-sample approach increases the accuracy of transcript assembly. Nature Communications, 2019, 10, 5000.	5.8	30
21	Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer. Bioinformatics, 2018, 34, 1859-1867.	1.8	11
22	Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. Translational Research, 2018, 202, 109-119.	2.2	15
23	Germline Mutations in DNA Repair Genes in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2017, 12, 1673-1678.	0.5	73
24	Abstract 4474: Functional characterization of alternatively splicedGSNin head and neck cancer. , 2017, , .		0
25	Abstract 3577: Splice expression variation analysis (SEVA) for differential gene isoform usage in cancer. , 2017, , .		0
26	JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples. , 2016, , .		0
27	JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples. , 2016, , .		0
28	Molecular Triage of Premalignant Lesions in Liquid-Based Cervical Cytology and Circulating Cell-Free DNA from Urine, Using a Panel of Methylated Human Papilloma Virus and Host Genes. Cancer Prevention Research, 2016, 9, 915-924.	0.7	29
29	Rascaf: Improving Genome Assembly with RNA Sequencing Data. Plant Genome, 2016, 9, plantgenome2016.03.0027.	1.6	50
30	CLASS2: accurate and efficient splice variant annotation from RNA-seq reads. Nucleic Acids Research, 2016, 44, e98-e98.	6.5	70
31	Abstract B11: Viral and host gene methylation in liquid prep: novel molecular screening and triage tools to reduce cervical cancer disparities. , 2016, , .		0
32	Abstract LB-133: Triage of high risk HPV positive women before colposcopy with reflex tests in pap smears and screening of high risk HPV in Transrenal DNA isolated from urine, using novel workflows to identify panels of methylated viral and human DNA. , 2016, , .		0
33	Viral non-coding RNA inhibits HNF4α expression in HCV associated hepatocellular carcinoma. Infectious Agents and Cancer, 2015, 10, 19.	1.2	4
34	Rcorrector: efficient and accurate error correction for Illumina RNA-seq reads. GigaScience, 2015, 4, 48.	3.3	381
35	Abstract A1-50: Genomic and epigenomic alterations in human and high-risk HPV DNA can discriminate normal from cervical dysplasia patients in urine. , 2015, , .		0
36	Lighter: fast and memory-efficient sequencing error correction without counting. Genome Biology, 2014, 15, 509.	3.8	201

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37	Loss of nuclear PTEN in HCV-infected human hepatocytes. Infectious Agents and Cancer, 2014, 9, 23.	1.2	10
38	CLASS: constrained transcript assembly of RNA-seq reads. BMC Bioinformatics, 2013, 14, S14.	1.2	30
39	RNA sequencing of cancer reveals novel splicing alterations. Scientific Reports, 2013, 3, 1689.	1.6	162
40	Genome-Guided Transcriptome Assembly in the Age of Next-Generation Sequencing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1234-1240.	1.9	16
41	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188.	0.8	372
42	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. F1000Research, 2013, 2, 188.	0.8	293
43	Transcriptomic landscape of breast cancers through mRNA sequencing. Scientific Reports, 2012, 2, 264.	1.6	83
44	Abstract A12: Web-based tools for visualization of the Human Papilloma Virus genome dynamics: A computational approach to cancer prevention and control. Cancer Prevention Research, 2012, 5, A12-A12.	0.7	0
45	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two Bos Taurus Assemblies. PLoS ONE, 2011, 6, e21400.	1.1	65
46	MicroRNA silencing of tumor suppressor DLC-1 promotes efficient hepatitis C virus replication in primary human hepatocytes. Hepatology, 2011, 53, 53-61.	3.6	75
47	<tt>Sim4db</tt> and <tt>Leaff</tt>: utilities for fast batch spliced alignment and sequence indexing. Bioinformatics, 2011, 27, 1869-1870.	1.8	18
48	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
49	Genes and genomes, an imperfect world: comparison of gene annotations of two Bos taurus draft assemblies. Genome Biology, 2010, 11, P13.	13.9	1
50	Spaced Seeds for Cross-species CDNA-to-genome Sequence Alignment. Communications in Information and Systems, 2010, 10, 115-136.	0.3	1
51	Sim4cc: a cross-species spliced alignment program. Nucleic Acids Research, 2009, 37, e80-e80.	6.5	16
52	Novel Splice Variants of sFlt1 are Upregulated in Preeclampsia. Placenta, 2009, 30, 250-255.	0.7	79
53	A method for identifying alternative or cryptic donor splice sites within gene and mRNA sequences. Comparisons among sequences from vertebrates, echinoderms and other groups. BMC Genomics, 2009, 10, 318.	1.2	5
54	A whole-genome assembly of the domestic cow, Bos taurus. Genome Biology, 2009, 10, R42.	13.9	1,005

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55	Universal seeds for cDNA-to-genome comparison. BMC Bioinformatics, 2008, 9, 36.	1.2	11
56	Effective cluster-based seed design for cross-species sequence comparisons. Bioinformatics, 2008, 24, 2926-2927.	1.8	3
57	Improving gene annotation using peptide mass spectrometry. Genome Research, 2007, 17, 231-239.	2.4	157
58	Designing Sensitive and Specific Spaced Seeds for Cross-Species mRNA-to-Genome Alignment. Journal of Computational Biology, 2007, 14, 113-130.	0.8	8
59	Bioinformatics of alternative splicing and its regulation. Briefings in Bioinformatics, 2006, 7, 55-69.	3.2	29
60	Finding Anchors for Genomic Sequence Comparison. Journal of Computational Biology, 2005, 12, 762-776.	0.8	8
61	Gene and alternative splicing annotation with AIR. Genome Research, 2005, 15, 54-66.	2.4	70
62	List of lists-annotated (LOLA): A database for annotation and comparison of published microarray gene lists. Gene, 2005, 360, 78-82.	1.0	54
63	Whole-genome shotgun assembly and comparison of human genome assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1916-1921.	3.3	164
64	Comparative immunopeptidomics of humans and their pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13268-13272.	3.3	38
65	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. Nature Genetics, 2004, 36, 1268-1274.	9.4	367
66	EnteriX 2003: visualization tools for genome alignments of Enterobacteriaceae. Nucleic Acids Research, 2003, 31, 3527-3532.	6.5	23
67	A non-redundant microarray of genes for two related bacteria. Nucleic Acids Research, 2003, 31, 1869-1876.	6.5	74
68	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. Genomics, 2002, 80, 681-690.	1.3	32
69	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
70	Complete genome sequence of Salmonella enterica serovar Typhimurium LT2. Nature, 2001, 413, 852-856.	13.7	1,712
71	Web-based visualization tools for bacterial genome alignments. Nucleic Acids Research, 2000, 28, 3486-3496.	6.5	29
72	A Computer Program for Aligning a cDNA Sequence with a Genomic DNA Sequence. Genome Research, 1998, 8, 967-974.	2.4	683