

Liliana D Florea

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

20,097
citations

147726

31
h-index

118793

62
g-index

84
all docs

84
docs citations

84
times ranked

23176
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
2	Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2. <i>Nature</i> , 2001, 413, 852-856.	13.7	1,712
3	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	13.9	1,005
4	A Computer Program for Aligning a cDNA Sequence with a Genomic DNA Sequence. <i>Genome Research</i> , 1998, 8, 967-974.	2.4	683
5	Rcorrector: efficient and accurate error correction for Illumina RNA-seq reads. <i>GigaScience</i> , 2015, 4, 48.	3.3	381
6	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	372
7	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of <i>Salmonella enterica</i> that cause typhoid. <i>Nature Genetics</i> , 2004, 36, 1268-1274.	9.4	367
8	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	2.6	348
9	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	293
10	Lighter: fast and memory-efficient sequencing error correction without counting. <i>Genome Biology</i> , 2014, 15, 509.	3.8	201
11	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1916-1921.	3.3	164
12	RNA sequencing of cancer reveals novel splicing alterations. <i>Scientific Reports</i> , 2013, 3, 1689.	1.6	162
13	Improving gene annotation using peptide mass spectrometry. <i>Genome Research</i> , 2007, 17, 231-239.	2.4	157
14	Study of Tofacitinib in Refractory Dermatomyositis: An Open-Label Pilot Study of Ten Patients. <i>Arthritis and Rheumatology</i> , 2021, 73, 858-865.	2.9	93
15	ZCCHC8, the nuclear exosome targeting component, is mutated in familial pulmonary fibrosis and is required for telomerase RNA maturation. <i>Genes and Development</i> , 2019, 33, 1381-1396.	2.7	85
16	Transcriptomic landscape of breast cancers through mRNA sequencing. <i>Scientific Reports</i> , 2012, 2, 264.	1.6	83
17	Novel Splice Variants of sFlt1 are Upregulated in Preeclampsia. <i>Placenta</i> , 2009, 30, 250-255.	0.7	79
18	MicroRNA silencing of tumor suppressor DLC-1 promotes efficient hepatitis C virus replication in primary human hepatocytes. <i>Hepatology</i> , 2011, 53, 53-61.	3.6	75

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19	A non-redundant microarray of genes for two related bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 1869-1876.	6.5	74
20	Germline Mutations in DNA Repair Genes in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2017, 12, 1673-1678.	0.5	73
21	Gene and alternative splicing annotation with AIR. <i>Genome Research</i> , 2005, 15, 54-66.	2.4	70
22	CLASS2: accurate and efficient splice variant annotation from RNA-seq reads. <i>Nucleic Acids Research</i> , 2016, 44, e98-e98.	6.5	70
23	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two <i>Bos Taurus</i> Assemblies. <i>PLoS ONE</i> , 2011, 6, e21400.	1.1	65
24	Excessive <i>O</i> -GlcNAcylation Causes Heart Failure and Sudden Death. <i>Circulation</i> , 2021, 143, 1687-1703.	1.6	65
25	A non-mosaic transchromosomal mouse model of Down syndrome carrying the long arm of human chromosome 21. <i>ELife</i> , 2020, 9, .	2.8	65
26	List of lists-annotated (LOLA): A database for annotation and comparison of published microarray gene lists. <i>Gene</i> , 2005, 360, 78-82.	1.0	54
27	Rascaf: Improving Genome Assembly with RNA Sequencing Data. <i>Plant Genome</i> , 2016, 9, plantgenome2016.03.0027.	1.6	50
28	Changes in Gut Microbiome after Bariatric Surgery Versus Medical Weight Loss in a Pilot Randomized Trial. <i>Obesity Surgery</i> , 2019, 29, 3239-3245.	1.1	46
29	Comparative immunopeptidomics of humans and their pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13268-13272.	3.3	38
30	Characterization and Analysis of the Skin Microbiota in Rosacea: A Case-Control Study. <i>American Journal of Clinical Dermatology</i> , 2020, 21, 139-147.	3.3	37
31	Minocycline and Its Impact on Microbial Dysbiosis in the Skin and Gastrointestinal Tract of Acne Patients. <i>Annals of Dermatology</i> , 2020, 32, 21.	0.3	35
32	Somatic reversion impacts myelodysplastic syndromes and acute myeloid leukemia evolution in the short telomere disorders. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	33
33	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. <i>Genomics</i> , 2002, 80, 681-690.	1.3	32
34	CLASS: constrained transcript assembly of RNA-seq reads. <i>BMC Bioinformatics</i> , 2013, 14, S14.	1.2	30
35	A multi-sample approach increases the accuracy of transcript assembly. <i>Nature Communications</i> , 2019, 10, 5000.	5.8	30
36	Web-based visualization tools for bacterial genome alignments. <i>Nucleic Acids Research</i> , 2000, 28, 3486-3496.	6.5	29

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37	Bioinformatics of alternative splicing and its regulation. <i>Briefings in Bioinformatics</i> , 2006, 7, 55-69.	3.2	29
38	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. <i>Cancer Prevention Research</i> , 2016, 9, 915-924.	0.7	29
39	A Prospective Study of the Urinary and Gastrointestinal Microbiome in Prepubertal Males. <i>Urology</i> , 2019, 131, 204-210.	0.5	26
40	EnteriX 2003: visualization tools for genome alignments of Enterobacteriaceae. <i>Nucleic Acids Research</i> , 2003, 31, 3527-3532.	6.5	23
41	Comparison of the skin microbiota in acne and rosacea. <i>Experimental Dermatology</i> , 2021, 30, 1375-1380.	1.4	19
42	CaMKII oxidation is a critical performance/disease trade-off acquired at the dawn of vertebrate evolution. <i>Nature Communications</i> , 2021, 12, 3175.	5.8	19
43	<tt>Sim4db</tt> and <tt>Leaff</tt>: utilities for fast batch spliced alignment and sequence indexing. <i>Bioinformatics</i> , 2011, 27, 1869-1870.	1.8	18
44	Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. <i>Epigenetics</i> , 2020, 15, 959-971.	1.3	17
45	Sim4cc: a cross-species spliced alignment program. <i>Nucleic Acids Research</i> , 2009, 37, e80-e80.	6.5	16
46	Genome-Guided Transcriptome Assembly in the Age of Next-Generation Sequencing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1234-1240.	1.9	16
47	Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. <i>Translational Research</i> , 2018, 202, 109-119.	2.2	15
48	Universal seeds for cDNA-to-genome comparison. <i>BMC Bioinformatics</i> , 2008, 9, 36.	1.2	11
49	Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer. <i>Bioinformatics</i> , 2018, 34, 1859-1867.	1.8	11
50	Loss of nuclear PTEN in HCV-infected human hepatocytes. <i>Infectious Agents and Cancer</i> , 2014, 9, 23.	1.2	10
51	Finding Anchors for Genomic Sequence Comparison. <i>Journal of Computational Biology</i> , 2005, 12, 762-776.	0.8	8
52	Designing Sensitive and Specific Spaced Seeds for Cross-Species mRNA-to-Genome Alignment. <i>Journal of Computational Biology</i> , 2007, 14, 113-130.	0.8	8
53	Detection of Alu Exonization Events in Human Frontal Cortex From RNA-Seq Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 727537.	1.6	7
54	A method for identifying alternative or cryptic donor splice sites within gene and mRNA sequences. Comparisons among sequences from vertebrates, echinoderms and other groups. <i>BMC Genomics</i> , 2009, 10, 318.	1.2	5

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55	Viral non-coding RNA inhibits HNF4 β expression in HCV associated hepatocellular carcinoma. <i>Infectious Agents and Cancer</i> , 2015, 10, 19.	1.2	4
56	Impact of lifestyle and demographics on the gut microbiota of acne patients and the response to minocycline. <i>Journal of Dermatological Treatment</i> , 2021, 32, 934-935.	1.1	4
57	Variability in skin microbiota between smokers, former smokers, and nonsmokers. <i>Journal of the American Academy of Dermatology</i> , 2020, 83, 942-944.	0.6	4
58	Effective cluster-based seed design for cross-species sequence comparisons. <i>Bioinformatics</i> , 2008, 24, 2926-2927.	1.8	3
59	Jutils: a visualization toolkit for differential alternative splicing events. <i>Bioinformatics</i> , 2021, 37, 4272-4274.	1.8	3
60	Development of Methods to Extract RNA From Archived Pediatric Needle Liver Biopsies to Produce Sequencing Data. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2021, 72, 436-441.	0.9	2
61	Genes and genomes, an imperfect world: comparison of gene annotations of two <i>Bos taurus</i> draft assemblies. <i>Genome Biology</i> , 2010, 11, P13.	13.9	1
62	Spaced Seeds for Cross-species CDNA-to-genome Sequence Alignment. <i>Communications in Information and Systems</i> , 2010, 10, 115-136.	0.3	1
63	JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples. , 2016, , .		0
64	JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples. , 2016, , .		0
65	CaMKII oxidation is a performance-disease tradeoff in vertebrate evolution. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 140, 24.	0.9	0
66	Abstract A12: Web-based tools for visualization of the Human Papilloma Virus genome dynamics: A computational approach to cancer prevention and control. <i>Cancer Prevention Research</i> , 2012, 5, A12-A12.	0.7	0
67	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
68	Abstract B11: Viral and host gene methylation in liquid prep: novel molecular screening and triage tools to reduce cervical cancer disparities. , 2016, , .		0
69	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
70	Abstract 4474: Functional characterization of alternatively spliced GSNin head and neck cancer. , 2017, , .		0
71	Abstract 3577: Splice expression variation analysis (SEVA) for differential gene isoform usage in cancer. , 2017, , .		0
72	Abstract A25: Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. , 2020, , .		0