

Sarah Djebali

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36 papers	24,281 citations	22 h-index	40 g-index
40 ext. papers	29,676 ext. citations	18.1 avg, IF	8.15 L-index

#	Paper	IF	Citations
36	Correlation Networks Provide New Insights into the Architecture of Testicular Steroid Pathways in Pigs. <i>Genes</i> , 2021 , 12,	4.2	1
35	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and -Regulation Analysis by Allele-Specific Expression in Livestock Species. <i>Frontiers in Genetics</i> , 2021 , 12, 655707	4.5	4
34	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
33	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
32	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020 , 30, 1047-1059	9.7	15
31	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. <i>Scientific Reports</i> , 2020 , 10, 20457	4.9	8
30	Analysis of pig transcriptomes suggests a global regulation mechanism enabling temporary bursts of circular RNAs. <i>RNA Biology</i> , 2019 , 16, 1190-1204	4.8	11
29	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019 , 17, 108	7.3	38
28	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
27	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , 2017 , 49, 6	4.9	45
26	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. <i>BMC Genomics</i> , 2017 , 18, 7	4.5	19
25	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. <i>Methods in Molecular Biology</i> , 2017 , 1468, 201-19	1.4	12
24	Gene-specific patterns of expression variation across organs and species. <i>Genome Biology</i> , 2016 , 17, 151	18.3	44
23	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016 , 17, 74	18.3	117
22	Human genomics. The human transcriptome across tissues and individuals. <i>Science</i> , 2015 , 348, 660-5	33.3	833
21	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015 , 6, 5903	17.4	56
20	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014 , 24, 212-26	9.7	143

19	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
18	Transcriptional Signatures of Viral Control in HIV-1 Infected South African Women. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, A64-A64	1.6	1
17	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
16	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
15	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. <i>Nucleic Acids Research</i> , 2013 , 41, 7220-30	20.1	11
14	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
13	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. <i>Genome Research</i> , 2012 , 22, 1616-25	9.7	317
12	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
11	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012 , 13, R53	18.3	182
10	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
9	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
8	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , 2012 , 7, e28213	3.7	51
7	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340
6	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
5	Efficient targeted transcript discovery via array-based normalization of RACE libraries. <i>Nature Methods</i> , 2008 , 5, 629-35	21.6	35
4	Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S7.1-10	18.3	13
3	Comparative analysis of neutrophil and monocyte epigenomes		2
2	Transcriptome and chromatin structure annotation of liver, CD4+ and CD8+ T cells from four livestock species		12

1 A limited set of transcriptional programs define major cell types

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