Sarah Djebali

List of Publications by Year
in descending order

33 papers	**32,456** citations	257450 **24** h-index	361022 **35** g-index
40 all docs	**40** docs citations	**40** times ranked	**52527** citing authors

#	Article	IF	Citations
1	Correlation Networks Provide New Insights into the Architecture of Testicular Steroid Pathways in Pigs. Genes, 2021, 12, 551.	2.4	3
2	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and Cis-Regulation Analysis by Allele-Specific Expression in Livestock Species. Frontiers in Genetics, 2021, 12, 655707.	2.3	30
3	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
4	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
5	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
6	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. Scientific Reports, 2020, 10, 20457.	3.3	20
7	Analysis of pig transcriptomes suggests a global regulation mechanism enabling temporary bursts of circular RNAs. RNA Biology, 2019, 16, 1190-1204.	3.1	15
8	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	3.8	109
9	An atlas of human long non-coding RNAs with accurate 5′ ends. Nature, 2017, 543, 199-204.	27.8	898
10	Long noncoding RNA repertoire in chicken liver and adipose tissue. Genetics Selection Evolution, 2017, 49, 6.	3.0	59
11	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7.	2.8	30
12	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. Methods in Molecular Biology, 2017, 1468, 201-219.	0.9	19
13	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	8.8	89
14	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	8.8	160
15	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
16	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	12.6	1,127
17	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	5.5	175
18	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444

#	Article	IF	Citations
19	Transcriptional Signatures of Viral Control in HIV-1 Infected South African Women. AIDS Research and Human Retroviruses, 2014, 30, A64-A64.	1.1	1
20	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
21	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	19.0	679
22	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. Nucleic Acids Research, 2013, 41, 7220-7230.	14.5	13
23	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
24	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
25	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. Genome Research, 2012, 22, 1616-1625.	5.5	401
26	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	5.5	4,428
27	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	9.6	231
28	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
29	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
30	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	2.5	61
31	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
32	Efficient targeted transcript discovery via array-based normalization of RACE libraries. Nature Methods, 2008, 5, 629-635.	19.0	41
33	Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA. Genome Biology, 2006, 7, S7.	9.6	14