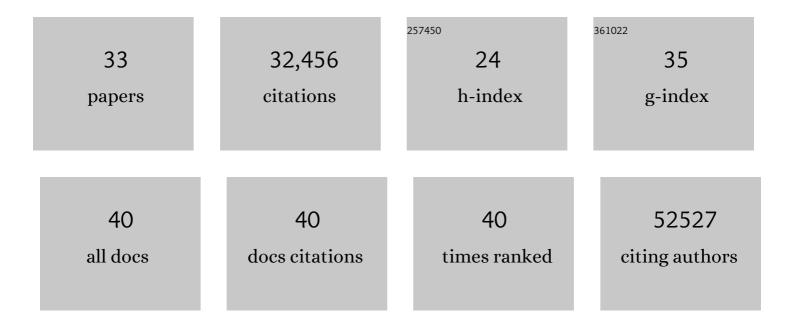
## Sarah Djebali

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2681485/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
3	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
4	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
5	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
6	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	12.6	1,127
7	An atlas of human long non-coding RNAs with accurate $5\hat{a}\in^2$ ends. Nature, 2017, 543, 199-204.	27.8	898
8	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	19.0	679
9	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
10	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for IncRNAs. Genome Research, 2012, 22, 1616-1625.	5.5	401
11	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
12	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	9.6	231
13	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
14	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
15	A benchmark for RNA-seq quantification pipelines. Genome Biology, 2016, 17, 74.	8.8	160
16	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
17	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	3.8	109
18	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	8.8	89

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19	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
20	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	2.5	61
21	Long noncoding RNA repertoire in chicken liver and adipose tissue. Genetics Selection Evolution, 2017, 49, 6.	3.0	59
22	Efficient targeted transcript discovery via array-based normalization of RACE libraries. Nature Methods, 2008, 5, 629-635.	19.0	41
23	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
24	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7.	2.8	30
25	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
26	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. Scientific Reports, 2020, 10, 20457.	3.3	20
27	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. Methods in Molecular Biology, 2017, 1468, 201-219.	0.9	19
28	Analysis of pig transcriptomes suggests a global regulation mechanism enabling temporary bursts of circular RNAs. RNA Biology, 2019, 16, 1190-1204.	3.1	15
29	Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA. Genome Biology, 2006, 7, S7.	9.6	14
30	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. Nucleic Acids Research, 2013, 41, 7220-7230.	14.5	13
31	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
32	Correlation Networks Provide New Insights into the Architecture of Testicular Steroid Pathways in Pigs. Genes, 2021, 12, 551.	2.4	3
33	Transcriptional Signatures of Viral Control in HIV-1 Infected South African Women. AIDS Research and Human Retroviruses, 2014, 30, A64-A64.	1.1	1