

Sarah Djebali

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2681485/publications.pdf>

Version: 2024-02-01

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	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	Landscape of transcription in human cells. <i>Nature</i> , 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. <i>Genome Research</i> , 2012, 22, 1775-1789.	5.5	4,428
4	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
5	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
6	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	12.6	1,127
7	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898
8	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
9	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 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 lncRNAs. <i>Genome Research</i> , 2012, 22, 1616-1625.	5.5	401
11	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	27.8	289
12	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	9.6	231
13	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	5.5	175
14	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	166
15	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	8.8	160
16	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
17	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019, 17, 108.	3.8	109
18	Gene-specific patterns of expression variation across organs and species. <i>Genome Biology</i> , 2016, 17, 151.	8.8	89

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19	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015, 6, 5903.	12.8	73
20	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.5	61
21	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , 2017, 49, 6.	3.0	59
22	Efficient targeted transcript discovery via array-based normalization of RACE libraries. <i>Nature Methods</i> , 2008, 5, 629-635.	19.0	41
23	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059.	5.5	32
24	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. <i>BMC Genomics</i> , 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. <i>Frontiers in Genetics</i> , 2021, 12, 655707.	2.3	30
26	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. <i>Scientific Reports</i> , 2020, 10, 20457.	3.3	20
27	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. <i>Methods in Molecular Biology</i> , 2017, 1468, 201-219.	0.9	19
28	Analysis of pig transcriptomes suggests a global regulation mechanism enabling temporary bursts of circular RNAs. <i>RNA Biology</i> , 2019, 16, 1190-1204.	3.1	15
29	Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA. <i>Genome Biology</i> , 2006, 7, S7.	9.6	14
30	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. <i>Nucleic Acids Research</i> , 2013, 41, 7220-7230.	14.5	13
31	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
32	Correlation Networks Provide New Insights into the Architecture of Testicular Steroid Pathways in Pigs. <i>Genes</i> , 2021, 12, 551.	2.4	3
33	Transcriptional Signatures of Viral Control in HIV-1 Infected South African Women. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A64-A64.	1.1	1