

Daniel R Zerbino

List of Publications by Citations

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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.

53 papers	37,217 citations	33 h-index	57 g-index
57 ext. papers	48,548 ext. citations	17.4 avg, IF	8.11 L-index

#	Paper	IF	Citations
53	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
52	Velvet: algorithms for de novo short read assembly using de Bruijn graphs. <i>Genome Research</i> , 2008 , 18, 821-9	9.7	7156
51	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012 , 487, 330-7	50.4	5640
50	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012 , 489, 519-25	50.4	2820
49	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761	20.1	1822
48	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D766-D773	20.1	1140
47	Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , 2012 , 28, 1086-92	7.2	1129
46	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1	1094
45	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
44	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D662-9	20.1	1013
43	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688	20.1	645
42	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016 , 167, 1369-1384.e19	56.2	556
41	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751	20.1	554
40	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
39	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1	404
38	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
37	Using the Velvet de novo assembler for short-read sequencing technologies. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 11, Unit 11.5	24.2	358

36	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891	20.1	324
35	The ensembl regulatory build. <i>Genome Biology</i> , 2015 , 16, 56	18.3	255
34	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
33	CHiCAGO: robust detection of DNA looping interactions in Capture Hi-C data. <i>Genome Biology</i> , 2016 , 17, 127	18.3	220
32	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016 , 48, 593-9	36.3	204
31	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011 , 21, 1512-28	9.7	170
30	Pebble and rock band: heuristic resolution of repeats and scaffolding in the velvet short-read de novo assembler. <i>PLoS ONE</i> , 2009 , 4, e8407	3.7	151
29	An analysis of core deformations in protein superfamilies. <i>Biophysical Journal</i> , 2005 , 88, 1291-9	2.9	91
28	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D916-D923	20.1	82
27	HAL: a hierarchical format for storing and analyzing multiple genome alignments. <i>Bioinformatics</i> , 2013 , 29, 1341-2	7.2	78
26	Ensembl 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	72
25	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
24	Improvements to services at the European Nucleotide Archive. <i>Nucleic Acids Research</i> , 2010 , 38, D39-45	20.1	47
23	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. <i>Bioinformatics</i> , 2014 , 30, 1008-9	7.2	44
22	Building a pan-genome reference for a population. <i>Journal of Computational Biology</i> , 2015 , 22, 387-401	1.7	41
21	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	35
20	eQTL Catalogue: a compendium of uniformly processed human gene expression and splicing QTLs		33
19	Ensembl regulation resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	33

18	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. <i>Nature Genetics</i> , 2021 , 53, 1290-1299	36.3	28
17	A new strategy for genome assembly using short sequence reads and reduced representation libraries. <i>Genome Research</i> , 2010 , 20, 249-56	9.7	24
16	An efficient conformational sampling method for homology modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 175-88	4.2	20
15	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021 , 184, 2633-2648.e19	56.2	20
14	Transcription and DNA Methylation Patterns of Blood-Derived CD8 T Cells Are Associated With Age and Inflammatory Bowel Disease But Do Not Predict Prognosis. <i>Gastroenterology</i> , 2021 , 160, 232-244.e7	13.3	17
13	Sequence tube maps: making graph genomes intuitive to commuters. <i>Bioinformatics</i> , 2019 , 35, 5318-5329	20.2	16
12	The open targets post-GWAS analysis pipeline. <i>Bioinformatics</i> , 2020 , 36, 2936-2937	7.2	13
11	Core deformations in protein families: a physical perspective. <i>Biophysical Chemistry</i> , 2005 , 115, 125-8	3.5	9
10	A unifying model of genome evolution under parsimony. <i>BMC Bioinformatics</i> , 2014 , 15, 206	3.6	8
9	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. <i>Briefings in Bioinformatics</i> , 2013 , 14, 548-55	13.4	7
8	Progress, Challenges, and Surprises in Annotating the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2020 , 21, 55-79	9.7	6
7	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. <i>BMC Bioinformatics</i> , 2016 , 17, 400	3.6	6
6	Building a Pangenome Reference for a Population. <i>Lecture Notes in Computer Science</i> , 2014 , 207-221	0.9	4
5	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
4	Sequence Ontology terminology for gene regulation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021 , 1864, 194745	6	3
3	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021 , 1865, 194768	6	1
2	Recommendations for the FAIRification of genomic track metadata. <i>F1000Research</i> , 2021 , 10,	3.6	1
1	The FAANG Data Portal: Global, Open-Access, "FAIR", and Richly Validated Genotype to Phenotype Data for High-Quality Functional Annotation of Animal Genomes. <i>Frontiers in Genetics</i> , 2021 , 12, 639238	4.5	0

