Daniel R Zerbino

List of Publications by Year in Descending Order

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	Ensembl 2022. *Nucleic Acids Research*, **2021**,	20.1	72
52	The gene regulation knowledge commons: the action area of GREEKC. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1865, 194768	6	1
51	Recommendations for the FAIRification of genomic track metadata. *F1000Research*, **2021**, 10,	3.6	1
50	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*, **2021**, 184, 2633-2648.e19	56.2	20
49	The FAANG Data Portal: Global, Open-Access, "FAIR", and Richly Validated Genotype to Phenotype Data for High-Quality Functional Annotation of Animal Genomes. *Frontiers in Genetics*, **2021**, 12, 639238	4.5	0
48	Ensembl 2021. *Nucleic Acids Research*, **2021**, 49, D884-D891	20.1	324
47	GENCODE 2021. *Nucleic Acids Research*, **2021**, 49, D916-D923	20.1	82
46	Transcription and DNA Methylation Patterns of Blood-Derived CD8 T Cells Are Associated With Age and Inflammatory Bowel Disease But Do Not Predict Prognosis. *Gastroenterology*, **2021**, 160, 232-244.e7	13.3	17
45	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. *Nucleic Acids Research*, **2021**,	20.1	3
44	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. *Nature Genetics*, **2021**, 53, 1290-1299	36.3	28
43	Sequence Ontology terminology for gene regulation. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194745	6	3
42	Progress, Challenges, and Surprises in Annotating the Human Genome. *Annual Review of Genomics and Human Genetics*, **2020**, 21, 55-79	9.7	6
41	The open targets post-GWAS analysis pipeline. *Bioinformatics*, **2020**, 36, 2936-2937	7.2	13
40	Ensembl 2020. *Nucleic Acids Research*, **2020**, 48, D682-D688	20.1	645
39	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
38	Sequence tube maps: making graph genomes intuitive to commuters. *Bioinformatics*, **2019**, 35, 5318-5320	7.2	16
37	GENCODE reference annotation for the human and mouse genomes. *Nucleic Acids Research*, **2019**, 47, D766-D773	20.1	1140

36	Ensembl 2019. *Nucleic Acids Research*, **2019**, 47, D745-D751	20.1	554
35	Ensembl 2018. *Nucleic Acids Research*, **2018**, 46, D754-D761	20.1	1822
34	Ensembl 2017. *Nucleic Acids Research*, **2017**, 45, D635-D642	20.1	404
33	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. *Database: the Journal of Biological Databases and Curation*, **2017**, 2017,	5	35
32	CHiCAGO: robust detection of DNA looping interactions in Capture Hi-C data. *Genome Biology*, **2016** , 17, 127	18.3	220
31	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19	56.2	556
30	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
29	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. *BMC Bioinformatics*, **2016**, 17, 400	3.6	6
28	Ensembl 2016. *Nucleic Acids Research*, **2016**, 44, D710-6	20.1	1094
27	Ensembl regulation resources. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	33
26	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, **2016**, 48, 593-9	36.3	204
25	The ensembl regulatory build. *Genome Biology*, **2015**, 16, 56	18.3	255
24	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
23	Ensembl 2015. *Nucleic Acids Research*, **2015**, 43, D662-9	20.1	1013
22	Building a pan-genome reference for a population. *Journal of Computational Biology*, **2015**, 22, 387-401	1.7	41
21	A unifying model of genome evolution under parsimony. *BMC Bioinformatics*, **2014**, 15, 206	3.6	8
20	Ensembl 2014. *Nucleic Acids Research*, **2014**, 42, D749-55	20.1	1087
19	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. *Bioinformatics*, **2014**, 30, 1008-9	7.2	44

18	Building a Pangenome Reference for a Population. *Lecture Notes in Computer Science*, **2014**, 207-221	0.9	4
17	Assessment of transcript reconstruction methods for RNA-seq. *Nature Methods*, **2013**, 10, 1177-84	21.6	477
16	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. *Briefings in Bioinformatics*, **2013**, 14, 548-55	13.4	7
15	HAL: a hierarchical format for storing and analyzing multiple genome alignments. *Bioinformatics*, **2013**, 29, 1341-2	7.2	78
14	Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. *Bioinformatics*, **2012**, 28, 1086-92	7.2	1129
13	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
12	Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **2012**, 489, 519-25	50.4	2820
11	Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome Research*, **2011**, 21, 2224-41	9.7	364
10	Cactus: Algorithms for genome multiple sequence alignment. *Genome Research*, **2011**, 21, 1512-28	9.7	170
9	Improvements to services at the European Nucleotide Archive. *Nucleic Acids Research*, **2010**, 38, D39-45	20.1	47
8	A new strategy for genome assembly using short sequence reads and reduced representation libraries. *Genome Research*, **2010**, 20, 249-56	9.7	24
7	Using the Velvet de novo assembler for short-read sequencing technologies. *Current Protocols in Bioinformatics*, **2010**, Chapter 11, Unit 11.5	24.2	358
6	Pebble and rock band: heuristic resolution of repeats and scaffolding in the velvet short-read de novo assembler. *PLoS ONE*, **2009**, 4, e8407	3.7	151
5	Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Research*, **2008**, 18, 821-9	9.7	7156
4	An efficient conformational sampling method for homology modeling. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 175-88	4.2	20
3	An analysis of core deformations in protein superfamilies. *Biophysical Journal*, **2005**, 88, 1291-9	2.9	91
2	Core deformations in protein families: a physical perspective. *Biophysical Chemistry*, **2005**, 115, 125-8	3.5	9
1	eQTL Catalogue: a compendium of uniformly processed human gene expression and splicing QTLs		33