Julien Gagneur

List of Publications by Year
in descending order

68 papers	8,632 citations	81900 39 h-index	91884 69 g-index
97 all docs	97 docs citations	97 times ranked	14050 citing authors

#	Article	IF	Citations
1	A physical and functional map of the human TNF-Î±/NF-Î²B signal transduction pathway. Nature Cell Biology, 2004, 6, 97-105.	10.3	970
2	Bidirectional promoters generate pervasive transcription in yeast. Nature, 2009, 457, 1033-1037.	27.8	872
3	Deep learning: new computational modelling techniques for genomics. Nature Reviews Genetics, 2019, 20, 389-403.	16.3	717
4	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. Molecular Systems Biology, 2019, 15, e8503.	7.2	576
5	Genetic diagnosis of Mendelian disorders via RNA sequencing. Nature Communications, 2017, 8, 15824.	12.8	432
6	TT-seq maps the human transient transcriptome. Science, 2016, 352, 1225-1228.	12.6	384
7	Combinatorial binding predicts spatio-temporal cis-regulatory activity. Nature, 2009, 462, 65-70.	27.8	361
8	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. G3: Genes, Genomes, Genetics, 2013, 3, 1213-1224.	1.8	355
9	Base-resolution models of transcription-factor binding reveal soft motif syntax. Nature Genetics, 2021, 53, 354-366.	21.4	325
10	Computation of elementary modes: a unifying framework and the new binary approach. BMC Bioinformatics, 2004, 5, 175.	2.6	207
11	Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. Cell, 2013, 155, 1075-1087.	28.9	201
12	GOing Bayesian: model-based gene set analysis of genome-scale data. Nucleic Acids Research, 2010, 38, 3523-3532.	14.5	190
13	Dynamic Regulation by Polycomb Group Protein Complexes Controls Pattern Formation and the Cell Cycle in Drosophila. Developmental Cell, 2008, 15, 877-889.	7.0	178
14	Antisense expression increases gene expression variability and locus interdependency. Molecular Systems Biology, 2011, 7, 468.	7.2	173
15	MMSplice: modular modeling improves the predictions of genetic variant effects on splicing. Genome Biology, 2019, 20, 48.	8.8	140
16	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. Nature Biotechnology, 2019, 37, 592-600.	17.5	118
17	OUTRIDER: A Statistical Method for Detecting Aberrantly Expressed Genes in RNA Sequencing Data. American Journal of Human Genetics, 2018, 103, 907-917.	6.2	112
18	Biallelic Mutations in NBAS Cause Recurrent Acute Liver Failure with Onset in Infancy. American Journal of Human Genetics, 2015, 97, 163-169.	6.2	110

#	Article	IF	Citations
19	Dissecting the Genetic Basis of Resistance to Malaria Parasites in Anopheles gambiae. Science, 2009, 326, 147-150.	12.6	106
20	Modular decomposition of protein-protein interaction networks. Genome Biology, 2004, 5, R57.	9.6	100
21	Chromatin-remodeling factor SMARCD2 regulates transcriptional networks controlling differentiation of neutrophil granulocytes. Nature Genetics, 2017, 49, 742-752.	21.4	87
22	Transcriptome-directed analysis for Mendelian disease diagnosis overcomes limitations of conventional genomic testing. Journal of Clinical Investigation, 2021, 131, .	8.2	87
23	An Evaluation of High-Throughput Approaches to QTL Mapping in Saccharomyces cerevisiae. Genetics, 2014, 196, 853-865.	2.9	86
24	Clinical implementation of RNA sequencing for Mendelian disease diagnostics. Genome Medicine, 2022, 14, 38.	8.2	85
25	Determinants of <scp>RNA</scp> metabolism in the Schizosaccharomyces pombe genome. Molecular Systems Biology, 2016, 12, 857.	7.2	81
26	Detection of aberrant splicing events in RNA-seq data using FRASER. Nature Communications, 2021, 12, 529.	12.8	78
27	A yeast-based assay identifies drugs active against human mitochondrial disorders. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11989-11994.	7.1	73
28	Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. PLoS ONE, 2017, 12, e0169249.	2.5	73
29	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. PLoS Genetics, 2013, 9, e1003803.	3.5	72
30	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. PLoS Genetics, 2006, 2, e170.	3.5	67
31	Mutations in MDH2, Encoding a Krebs Cycle Enzyme, Cause Early-Onset Severe Encephalopathy. American Journal of Human Genetics, 2017, 100, 151-159.	6.2	63
32	Cis-regulatory elements explain most of the mRNA stability variation across genes in yeast. Rna, 2017, 23, 1648-1659.	3.5	63
33	Quantification and discovery of sequence determinants of proteinâ€perâ€mRNA amount inÂ29Âhuman tissues. Molecular Systems Biology, 2019, 15, e8513.	7.2	63
34	Detection of aberrant gene expression events in RNA sequencing data. Nature Protocols, 2021, 16, 1276-1296.	12.0	58
35	Hierarchical analysis of dependency in metabolic networks. Bioinformatics, 2003, 19, 1027-1034.	4.1	56
36	Model-based gene set analysis for Bioconductor. Bioinformatics, 2011, 27, 1882-1883.	4.1	56

#	Article	IF	Citations
37	OCR-Stats: Robust estimation and statistical testing of mitochondrial respiration activities using Seahorse XF Analyzer. PLoS ONE, 2018, 13, e0199938.	2.5	55
38	Global donor and acceptor splicing site kinetics in human cells. ELife, 2019, 8, .	6.0	51
39	Quantification of Proteins and Histone Marks in Drosophila Embryos Reveals Stoichiometric Relationships Impacting Chromatin Regulation. Developmental Cell, 2019, 51, 632-644.e6.	7.0	50
40	Experimental Relocation of the Mitochondrial ATP9 Gene to the Nucleus Reveals Forces Underlying Mitochondrial Genome Evolution. PLoS Genetics, 2012, 8, e1002876.	3.5	48
41	Genotyping 1000 yeast strains by next-generation sequencing. BMC Genomics, 2013, 14, 90.	2.8	47
42	TTâ€seq captures enhancer landscapes immediately after Tâ€cell stimulation. Molecular Systems Biology, 2017, 13, 920.	7.2	44
43	Yeast Growth Plasticity Is Regulated by Environment-Specific Multi-QTL Interactions. G3: Genes, Genomes, Genetics, 2014, 4, 769-777.	1.8	34
44	4DXpress: a database for cross-species expression pattern comparisons. Nucleic Acids Research, 2007, 36, D847-D853.	14.5	33
45	Negative feedback buffers effects of regulatory variants. Molecular Systems Biology, 2015, 11, 785.	7.2	33
46	From molecular networks to qualitative cell behavior. FEBS Letters, 2005, 579, 1867-1871.	2.8	31
47	Genomeâ€wide alleleâ€and strandâ€specific expression profiling. Molecular Systems Biology, 2009, 5, 274.	7.2	31
48	Mitochondrial protein sorting as a therapeutic target for ATP synthase disorders. Nature Communications, 2014, 5, 5585.	12.8	29
49	Modeling positional effects of regulatory sequences with spline transformations increases prediction accuracy of deep neural networks. Bioinformatics, 2018, 34, 1261-1269.	4.1	29
50	MTSplice predicts effects of genetic variants on tissue-specific splicing. Genome Biology, 2021, 22, 94.	8.8	23
51	Annotation of genomics data using bidirectional hidden Markov models unveils variations in Pol II transcription cycle. Molecular Systems Biology, 2014, 10, 768.	7.2	21
52	Inhibition of oxidative stress in cholinergic projection neurons fully rescues aging-associated olfactory circuit degeneration in Drosophila. ELife, 2018, 7, .	6.0	21
53	Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224.	2.5	18
54	Temporal Expression Profiling Identifies Pathways Mediating Effect of Causal Variant on Phenotype. PLoS Genetics, 2015, 11, e1005195.	3.5	17

#	Article	IF	Citations
55	Predicting mean ribosome load for 5â€™UTR of any length using deep learning. PLoS Computational Biology, 2021, 17, e1008982.	3.2	17
56	Selective Phenotyping, Entropy Reduction, and the Mastermind game. BMC Bioinformatics, 2011, 12, 406.	2.6	15
57	Caenorhabditis elegans CES-1 Snail Represses pig-1 MELK Expression To Control Asymmetric Cell Division. Genetics, 2017, 206, 2069-2084.	2.9	13
58	Capturing cellular machines by systematic screens of protein complexes. Trends in Microbiology, 2006, 14, 336-339.	7.7	10
59	Identification of mitochondrial disease genes through integrative analysis of multiple datasets. Methods, 2008, 46, 248-255.	3.8	10
60	CAGI 5 splicing challenge: Improved exon skipping and intron retention predictions with MMSplice. Human Mutation, 2019, 40, 1243-1251.	2.5	10
61	GenoGAM: genome-wide generalized additive models for ChIP-Seq analysis. Bioinformatics, 2017, 33, 2258-2265.	4.1	9
62	Measures of RNA metabolism rates: Toward a definition at the level of single bonds. Transcription, 2017, 8, 75-80.	3.1	8
63	Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data. Nature Biotechnology, 2022, 40, 741-750.	17.5	7
64	Meiotic Interactors of a Mitotic Gene TAO3 Revealed by Functional Analysis of its Rare Variant. G3: Genes, Genomes, Genetics, 2016, 6, 2255-2263.	1.8	5
65	Somatic alterations compromised molecular diagnosis of DOCK8 hyper-IgE syndrome caused by a novel intronic splice site mutation. Scientific Reports, 2018, 8, 16719.	3.3	5
66	Simultaneous characterization of sense and antisense genomic processes by the double-stranded hidden Markov model. Nucleic Acids Research, 2016, 44, e44-e44.	14.5	4
67	Bioinformatics advances biology and medicine by turning big data troves into knowledge. Informatik-Spektrum, 2017, 40, 153-160.	1.3	2
68	GenoGAM 2.0: scalable and efficient implementation of genome-wide generalized additive models for gigabase-scale genomes. BMC Bioinformatics, 2018, 19, 247.	2.6	1