Matthew Loose

List of Publications by Year
in descending order

43 papers	6,030 citations	304743 22 h-index	254184 43 g-index
79 all docs	79 docs citations	79 times ranked	9841 citing authors

#	Article	IF	Citations
1	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	17.5	1,443
2	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols, 2017, 12, 1261-1276.	12.0	898
3	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
4	Nanopore native RNA sequencing of a human poly(A) transcriptome. Nature Methods, 2019, 16, 1297-1305.	19.0	411
5	Same-Day Diagnostic and Surveillance Data for Tuberculosis via Whole-Genome Sequencing of Direct Respiratory Samples. Journal of Clinical Microbiology, 2017, 55, 1285-1298.	3.9	315
6	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	1.6	270
7	Real-time selective sequencing using nanopore technology. Nature Methods, 2016, 13, 751-754.	19.0	266
8	BulkVis: a graphical viewer for Oxford nanopore bulk FAST5 files. Bioinformatics, 2019, 35, 2193-2198.	4.1	204
9	Readfish enables targeted nanopore sequencing of gigabase-sized genomes. Nature Biotechnology, 2021, 39, 442-450.	17.5	197
10	Genetic regulatory networks programming hematopoietic stem cells and erythroid lineage specification. Developmental Biology, 2006, 294, 525-540.	2.0	147
11	A genetic regulatory network for Xenopus mesendoderm formation. Developmental Biology, 2004, 271, 467-478.	2.0	125
12	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. F1000Research, 2017, 6, 760.	1.6	107
13	Pluripotency and X chromosome dynamics revealed in pig pre-gastrulating embryos by single cell analysis. Nature Communications, 2019, 10, 500.	12.8	91
14	Transient Accumulation of 5-Carboxylcytosine Indicates Involvement of Active Demethylation in Lineage Specification of Neural Stem Cells. Cell Reports, 2014, 7, 1353-1361.	6.4	85
15	Exact and approximate distributions of protein and mRNA levels in the low-copy regime of gene expression. Journal of Mathematical Biology, 2012, 64, 829-854.	1.9	71
16	Acquisition of Germ Plasm Accelerates Vertebrate Evolution. Science, 2014, 344, 200-203.	12.6	48
17	Transcriptional networks regulating hematopoietic cell fate decisions. Current Opinion in Hematology, 2007, 14, 307-314.	2.5	44
18	Specification and epigenomic resetting of the pig germline exhibit conservation with the human lineage. Cell Reports, 2021, 34, 108735.	6.4	43

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19	Transcriptional Bursting Diversifies the Behaviour of a Toggle Switch: Hybrid Simulation of Stochastic Gene Expression. Bulletin of Mathematical Biology, 2013, 75, 351-371.	1.9	40
20	A conserved mechanism for vertebrate mesoderm specification in urodele amphibians and mammals. Developmental Biology, 2010, 343, 138-152.	2.0	39
21	Examining diabetic heel ulcers through an ecological lens: microbial community dynamics associated with healing and infection. Journal of Medical Microbiology, 2019, 68, 230-240.	1.8	34
22	Reply to â€˜Errors in long-read assemblies can critically affect protein predictionâ€™. Nature Biotechnology, 2019, 37, 127-128.	17.5	29
23	Global genetic regulatory networks controlling hematopoietic cell fates. Current Opinion in Hematology, 2006, 13, 229-236.	2.5	28
24	The Impact of Real-Time Whole-Genome Sequencing in Controlling Healthcare-Associated SARS-CoV-2 Outbreaks. Journal of Infectious Diseases, 2022, 225, 10-18.	4.0	25
25	The potential impact of nanopore sequencing on human genetics. Human Molecular Genetics, 2017, 26, R202-R207.	2.9	24
26	A bistable genetic switch which does not require high co-operativity at the promoter: a two-timescale model for the PU.1-GATA-1 interaction. Mathematical Medicine and Biology, 2009, 26, 117-132.	1.2	19
27	Rapid-CNS2: rapid comprehensive adaptive nanopore-sequencing of CNS tumors, a proof-of-concept study. Acta Neuropathologica, 2022, 143, 609-612.	7.7	19
28	AlignWise: a tool for identifying protein-coding sequence and correcting frame-shifts. BMC Bioinformatics, 2015, 16, 376.	2.6	18
29	Genome Profiling of SARS-CoV-2 in Indonesia, ASEAN and the Neighbouring East Asian Countries: Features, Challenges and Achievements. Viruses, 2022, 14, 778.	3.3	14
30	Inference, Validation, and Dynamic Modeling of Transcription Networks in Multipotent Hematopoietic Cells. Annals of the New York Academy of Sciences, 2007, 1106, 30-40.	3.8	13
31	Genetic variation at mouse and human ribosomal DNA influences associated epigenetic states. Genome Biology, 2022, 23, 54.	8.8	11
32	Retrospective screening of routine respiratory samples revealed undetected community transmission and missed intervention opportunities for SARS-CoV-2 in the United Kingdom. Journal of General Virology, 2021, 102, .	2.9	10
33	Virtual Genome Walking across the 32â€‰Gb Ambystoma mexicanum genome; assembling gene models and intronic sequence. Scientific Reports, 2018, 8, 618.	3.3	9
34	Dissection of a Ciona regulatory element reveals complexity of cross-species enhancer activity. Developmental Biology, 2014, 390, 261-272.	2.0	8
35	minoTour, real-time monitoring and analysis for nanopore sequencers. Bioinformatics, 2022, 38, 1133-1135.	4.1	8
36	Germ Layer Induction in ESCâ€"Following the Vertebrate Roadmap. Current Protocols in Stem Cell Biology, 2007, 1, Unit 1D.1.	3.0	5

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37	Finding the Needle: Targeted Nanopore Sequencing and CRISPR-Cas9. CRISPR Journal, 2018, 1, 265-267.	2.9	4
38	myGRN: A database and visualisation system for the storage and analysis of developmental genetic regulatory networks. BMC Developmental Biology, 2009, 9, 33.	2.1	3
39	The genome sequence of the European golden eagle, Aquila chrysaetos chrysaetos Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	1.8	3
40	The UK Leicester COVID-19 â€˜exceedanceâ€™ Mayâ€"July 2020: An analysis of hospitalised cases. Journal of Infection, 2021, 83, e5-e7.	3.3	1
41	Mathematical modelling of a microRNA-regulated gene network in <i>Caenorhabditis elegans</i>. Mathematical Biosciences and Engineering, 2020, 17, 2881-2904.	1.9	1
42	Gene Regulatory Networks in the Genomics Era. Genomics, Proteomics and Bioinformatics, 2013, 11, 133-134.	6.9	0
43	A disruptive sequencer meets disruptive publishing. F1000Research, 2015, 4, 1074.	1.6	0