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	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
2	minoTour, real-time monitoring and analysis for nanopore sequencers. Bioinformatics, 2022, 38, 1133-1135.	4.1	8
3	Genetic variation at mouse and human ribosomal DNA influences associated epigenetic states. Genome Biology, 2022, 23, 54.	8.8	11
4	Rapid-CNS2: rapid comprehensive adaptive nanopore-sequencing of CNS tumors, a proof-of-concept study. Acta Neuropathologica, 2022, 143, 609-612.	7.7	19
5	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
6	Readfish enables targeted nanopore sequencing of gigabase-sized genomes. Nature Biotechnology, 2021, 39, 442-450.	17.5	197
7	Specification and epigenomic resetting of the pig germline exhibit conservation with the human lineage. Cell Reports, 2021, 34, 108735.	6.4	43
8	The genome sequence of the European golden eagle, Aquila chrysaetos chrysaetos Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	1.8	3
9	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
10	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
11	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
12	Mathematical modelling of a microRNA-regulated gene network in <i>Caenorhabditis elegans</i>. Mathematical Biosciences and Engineering, 2020, 17, 2881-2904.	1.9	1
13	Reply to â€˜Errors in long-read assemblies can critically affect protein predictionâ€™. Nature Biotechnology, 2019, 37, 127-128.	17.5	29
14	Pluripotency and X chromosome dynamics revealed in pig pre-gastrulating embryos by single cell analysis. Nature Communications, 2019, 10, 500.	12.8	91
15	Nanopore native RNA sequencing of a human poly(A) transcriptome. Nature Methods, 2019, 16, 1297-1305.	19.0	411
16	BulkVis: a graphical viewer for Oxford nanopore bulk FAST5 files. Bioinformatics, 2019, 35, 2193-2198.	4.1	204
17	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
18	Nanopore sequencing and assembly of a human genome with ultra-long reads. Nature Biotechnology, 2018, 36, 338-345.	17.5	1,443

#	Article	IF	Citations
19	Virtual Genome Walking across the 32‰Gb Ambystoma mexicanum genome; assembling gene models and intronic sequence. Scientific Reports, 2018, 8, 618.	3.3	9
20	Finding the Needle: Targeted Nanopore Sequencing and CRISPR-Cas9. CRISPR Journal, 2018, 1, 265-267.	2.9	4
21	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
22	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
23	The potential impact of nanopore sequencing on human genetics. Human Molecular Genetics, 2017, 26, R202-R207.	2.9	24
24	MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry. F1000Research, 2017, 6, 760.	1.6	107
25	Real-time selective sequencing using nanopore technology. Nature Methods, 2016, 13, 751-754.	19.0	266
26	AlignWise: a tool for identifying protein-coding sequence and correcting frame-shifts. BMC Bioinformatics, 2015, 16, 376.	2.6	18
27	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	1.6	270
28	A disruptive sequencer meets disruptive publishing. F1000Research, 2015, 4, 1074.	1.6	0
29	Dissection of a Ciona regulatory element reveals complexity of cross-species enhancer activity. Developmental Biology, 2014, 390, 261-272.	2.0	8
30	Acquisition of Germ Plasm Accelerates Vertebrate Evolution. Science, 2014, 344, 200-203.	12.6	48
31	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
32	Gene Regulatory Networks in the Genomics Era. Genomics, Proteomics and Bioinformatics, 2013, 11, 133-134.	6.9	0
33	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
34	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
35	A conserved mechanism for vertebrate mesoderm specification in urodele amphibians and mammals. Developmental Biology, 2010, 343, 138-152.	2.0	39
36	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

#	Article	IF	Citations
37	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
38	Transcriptional networks regulating hematopoietic cell fate decisions. Current Opinion in Hematology, 2007, 14, 307-314.	2.5	44
39	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
40	Germ Layer Induction in ESCâ€"Following the Vertebrate Roadmap. Current Protocols in Stem Cell Biology, 2007, 1, Unit 1D.1.	3.0	5
41	Genetic regulatory networks programming hematopoietic stem cells and erythroid lineage specification. Developmental Biology, 2006, 294, 525-540.	2.0	147
42	Global genetic regulatory networks controlling hematopoietic cell fates. Current Opinion in Hematology, 2006, 13, 229-236.	2.5	28
43	A genetic regulatory network for Xenopus mesendoderm formation. Developmental Biology, 2004, 271, 467-478.	2.0	125