

Ira W Deveson

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

2,109
citations

361413

20
h-index

289244

40
g-index

56
all docs

56
docs citations

56
times ranked

3741
citing authors

#	ARTICLE	IF	CITATIONS
1	InterARTIC: an interactive web application for whole-genome nanopore sequencing analysis of SARS-CoV-2 and other viruses. <i>Bioinformatics</i> , 2022, 38, 1443-1446.	4.1	8
2	Assessment of Inter-Laboratory Differences in SARS-CoV-2 Consensus Genome Assemblies between Public Health Laboratories in Australia. <i>Viruses</i> , 2022, 14, 185.	3.3	4
3	Using synthetic chromosome controls to evaluate the sequencing of difficult regions within the human genome. <i>Genome Biology</i> , 2022, 23, 19.	8.8	4
4	Fast nanopore sequencing data analysis with SLOW5. <i>Nature Biotechnology</i> , 2022, 40, 1026-1029.	17.5	40
5	Sex-specific splicing of Z- and W-borne <i>nr5a1</i> alleles suggests sex determination is controlled by chromosome conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
6	Long read sequencing overcomes challenges in the diagnosis of <i>SORD</i> neuropathy. <i>Journal of the Peripheral Nervous System</i> , 2022, 27, 120-126.	3.1	6
7	Comprehensive genetic diagnosis of tandem repeat expansion disorders with programmable targeted nanopore sequencing. <i>Science Advances</i> , 2022, 8, eabm5386.	10.3	68
8	Truncated <i>jarid2</i> and <i>kdm6b</i> transcripts are associated with temperature-induced sex reversal during development in a dragon lizard. <i>Science Advances</i> , 2022, 8, eabk0275.	10.3	6
9	Ultra-deep sequencing data from a liquid biopsy proficiency study demonstrating analytic validity. <i>Scientific Data</i> , 2022, 9, 170.	5.3	4
10	Persistent high-level shedding of cultivable SARS-CoV-2 Delta virus 33 days after onset of COVID-19 in a hospitalized patient with pneumonia. <i>Journal of Medical Virology</i> , 2022, 94, 4043-4046.	5.0	4
11	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. <i>Scientific Reports</i> , 2021, 11, 3934.	3.3	55
12	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
13	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
14	Two transcriptionally distinct pathways drive female development in a reptile with both genetic and temperature dependent sex determination. <i>PLoS Genetics</i> , 2021, 17, e1009465.	3.5	25
15	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	115
16	An update on the neurological short tandem repeat expansion disorders and the emergence of long-read sequencing diagnostics. <i>Acta Neuropathologica Communications</i> , 2021, 9, 98.	5.2	83
17	Oncogenic cooperation between TCF7-SPI1 and NRAS(G12D) requires β -catenin activity to drive T-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2021, 12, 4164.	12.8	9
18	No evidence of human genome integration of SARS-CoV-2 found by long-read DNA sequencing. <i>Cell Reports</i> , 2021, 36, 109530.	6.4	39

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19	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. <i>Cell Reports</i> , 2021, 36, 109722.	6.4	39
20	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	129
21	Chimeric synthetic reference standards enable cross-validation of positive and negative controls in SARS-CoV-2 molecular tests. <i>Scientific Reports</i> , 2021, 11, 2636.	3.3	2
22	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. <i>Cell Reports Methods</i> , 2021, 1, 100106.	2.9	9
23	Genopo: a nanopore sequencing analysis toolkit for portable Android devices. <i>Communications Biology</i> , 2020, 3, 538.	4.4	19
24	A universal and independent synthetic DNA ladder for the quantitative measurement of genomic features. <i>Nature Communications</i> , 2020, 11, 3609.	12.8	7
25	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. <i>Nature Communications</i> , 2020, 11, 6272.	12.8	183
26	Use of synthetic DNA spike-in controls (sequins) for human genome sequencing. <i>Nature Protocols</i> , 2019, 14, 2119-2151.	12.0	22
27	Diagnosis of fusion genes using targeted RNA sequencing. <i>Nature Communications</i> , 2019, 10, 1388.	12.8	122
28	Chiral DNA sequences as commutable controls for clinical genomics. <i>Nature Communications</i> , 2019, 10, 1342.	12.8	11
29	Universal Alternative Splicing of Noncoding Exons. <i>Cell Systems</i> , 2018, 6, 245-255.e5.	6.2	110
30	Synthetic microbe communities provide internal reference standards for metagenome sequencing and analysis. <i>Nature Communications</i> , 2018, 9, 3096.	12.8	81
31	Differential intron retention in <i>Jumonji</i> chromatin modifier genes is implicated in reptile temperature-dependent sex determination. <i>Science Advances</i> , 2017, 3, e1700731.	10.3	111
32	Reference standards for next-generation sequencing. <i>Nature Reviews Genetics</i> , 2017, 18, 473-484.	16.3	194
33	Target RNA Secondary Structure Is a Major Determinant of miR159 Efficacy. <i>Plant Physiology</i> , 2017, 174, 1764-1778.	4.8	34
34	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. <i>Trends in Genetics</i> , 2017, 33, 464-478.	6.7	181
35	ANAQUIN: a software toolkit for the analysis of spike-in controls for next generation sequencing. <i>Bioinformatics</i> , 2017, 33, 1723-1724.	4.1	17
36	Representing genetic variation with synthetic DNA standards. <i>Nature Methods</i> , 2016, 13, 784-791.	19.0	37

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37	Spliced synthetic genes as internal controls in RNA sequencing experiments. <i>Nature Methods</i> , 2016, 13, 792-798.	19.0	123
38	MicroRNAs with analogous target complementarities perform with highly variable efficacies in <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2013, 587, 3703-3708.	2.8	15
39	Expression of human ARGONAUTE 2 inhibits endogenous microRNA activity in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 96.	3.6	2