Robert P Davey

List of Publications by Year
in descending order

29 papers	2,473 citations	687363 13 h-index	610901 24 g-index
38 all docs	38 docs citations	38 times ranked	4232 citing authors

#	Article	IF	Citations
1	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
2	ISA API: An open platform for interoperable life science experimental metadata. GigaScience, 2021, 10, .	6.4	19
3	Colombia's cyberinfrastructure for biodiversity: Building data infrastructure in emerging countries to foster socioeconomic growth. Plants People Planet, 2020, 2, 229-236.	3.3	3
4	CropSight: a scalable and open-source information management system for distributed plant phenotyping and IoT-based crop management. GigaScience, 2019, 8, .	6.4	48
5	A Galaxy-based training resource for single-cell RNA-sequencing quality control and analyses. GigaScience, 2019, 8, .	6.4	4
6	GeneSeqToFamily: a Galaxy workflow to find gene families based on the Ensembl Compara GeneTrees pipeline. GigaScience, 2018, 7, 1-10.	6.4	9
7	Aequatus: an open-source homology browser. GigaScience, 2018, 7, .	6.4	1
8	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. Genome Research, 2017, 27, 885-896.	5.5	464
9	Data management and best practice for plant science. Nature Plants, 2017, 3, 17086.	9.3	38
10	Developing data interoperability using standards: A wheat community use case. F1000Research, 2017, 6, 1843.	1.6	14
11	Developing data interoperability using standards: A wheat community use case. F1000Research, 2017, 6, 1843.	1.6	20
12	Prevalence and Dynamics of Ribosomal DNA Micro-heterogeneity Are Linked to Population History in Two Contrasting Yeast Species. Scientific Reports, 2016, 6, 28555.	3.3	4
13	Ribosomal DNA Sequence Heterogeneity Reflects Intraspecies Phylogenies and Predicts Genome Structure in Two Contrasting Yeast Species. Systematic Biology, 2014, 63, 543-554.	5.6	38
14	The Open Science Peer Review Oath. F1000Research, 2014, 3, 271.	1.6	15
15	An Open Science Peer Review Oath. F1000Research, 2014, 3, 271.	1.6	25
16	wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53.	1.6	4
17	wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53.	1.6	3
18	Sequencing quality assessment tools to enable data-driven informatics for high throughput genomics. Frontiers in Genetics, 2013, 4, 288.	2.3	163

#	Article	IF	Citations
19	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. F1000Research, 2013, 2, 248.	1.6	14
20	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. F1000Research, 2013, 2, 248.	1.6	12
21	TURNIP: tracking unresolved nucleotide polymorphisms in large hard-to-assemble regions of repetitive DNA sequence. Bioinformatics, 2010, 26, 2908-2909.	4.1	3
22	Repetitive sequence variation and dynamics in the ribosomal DNA array of Saccharomyces cerevisiae as revealed by whole-genome resequencing. Genome Research, 2009, 19, 626-635.	5.5	82
23	Population genomics of domestic and wild yeasts. Nature, 2009, 458, 337-341.	27.8	1,391
24	MPP: a microarray-to-phylogeny pipeline for analysis of gene and marker content datasets. Bioinformatics, 2007, 23, 1023-1025.	4.1	4
25	Data management challenges for artificial intelligence in plant and agricultural research. F1000Research, 0, 10, 324.	1.6	7
26	COPO: a metadata platform for brokering FAIR data in the life sciences. F1000Research, 0, 9, 495.	1.6	27
27	DNAContentViewer a BioJS component to visualise GC/AT Content. F1000Research, 0, 3, 54.	1.6	1
28	Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR. F1000Research, 0, 10, 1238.	1.6	3
29	Specimen and sample metadata standards for biodiversity genomics: a proposal from the Darwin Tree of Life project. Wellcome Open Research, 0, 7, 187.	1.8	11