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List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

16,461
citations

39113

52
h-index

56606

87
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101
all docs

101
docs citations

101
times ranked

28198
citing authors

#	ARTICLE	IF	CITATIONS
1	Uses and benefits of digital sequence information from plant genetic resources: Lessons learnt from botanical collections. <i>Plants People Planet</i> , 2022, 4, 33-43.	1.6	10
2	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
3	Standards recommendations for the Earth BioGenome Project. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	33
4	Green plant genomes: What we know in an era of rapidly expanding opportunities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	65
5	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021, 49, D1452-D1463.	6.5	83
6	ELIXIRâ€œEXCELERATE: establishing Europe's data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.	3.5	18
7	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021, 113, 3666-3680.	1.3	17
8	Ensembl Genomes 2020â€œenabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	6.5	416
9	Conservation Policy: Helping or hindering science to unlock properties of plants and fungi. <i>Plants People Planet</i> , 2020, 2, 535-545.	1.6	18
10	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	50
11	Selecting for useful properties of plants and fungi â€œ Novel approaches, opportunities, and challenges. <i>Plants People Planet</i> , 2020, 2, 409-420.	1.6	17
12	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	3.5	84
13	Factors Affecting Targeted Sequencing of 353 Nuclear Genes From Herbarium Specimens Spanning the Diversity of Angiosperms. <i>Frontiers in Plant Science</i> , 2019, 10, 1102.	1.7	124
14	Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. <i>Frontiers in Microbiology</i> , 2019, 10, 2477.	1.5	9
15	Plant genome sequences: past, present, future. <i>Current Opinion in Plant Biology</i> , 2019, 48, 1-8.	3.5	107
16	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	6.5	489
17	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018, 46, D1181-D1189.	6.5	147
18	Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. <i>New Phytologist</i> , 2018, 217, 1407-1419.	3.5	85

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19	Integrative analysis of large scale transcriptome data draws a comprehensive landscape of <i>Phaeodactylum tricornutum</i> genome and evolutionary origin of diatoms. <i>Scientific Reports</i> , 2018, 8, 4834.	1.6	131
20	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , 2018, 46, D869-D874.	6.5	172
21	The genome of the biting midge <i>Culicoides sonorensis</i> and gene expression analyses of vector competence for bluetongue virus. <i>BMC Genomics</i> , 2018, 19, 624.	1.2	19
22	Using WormBase ParaSite: An Integrated Platform for Exploring Helminth Genomic Data. <i>Methods in Molecular Biology</i> , 2018, 1757, 471-491.	0.4	48
23	Databases and Tools for the Analysis of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 377-394.	0.3	1
24	WormBase ParaSite â™™ a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017, 215, 2-10.	0.5	527
25	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. <i>Genome Research</i> , 2017, 27, 885-896.	2.4	464
26	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
27	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
28	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 1-31.	0.4	189
29	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
30	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	1.6	8
31	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016, 12, 44.	1.9	109
32	Gramene database: Navigating plant comparative genomics resources. <i>Current Plant Biology</i> , 2016, 7-8, 10-15.	2.3	51
33	Advancing vector biology research: a community survey for future directions, research applications and infrastructure requirements. <i>Pathogens and Global Health</i> , 2016, 110, 164-172.	1.0	3
34	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016, 44, D1133-D1140.	6.5	138
35	PhytoPath: an integrative resource for plant pathogen genomics. <i>Nucleic Acids Research</i> , 2016, 44, D688-D693.	6.5	42
36	Ensembl Genomes 2016: more genomes, more complexity. <i>Nucleic Acids Research</i> , 2016, 44, D574-D580.	6.5	530

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37	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , 2016, 44, D774-D780.	6.5	329
38	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2016, 1374, 115-140.	0.4	216
39	Towards recommendations for metadata and data handling in plant phenotyping. <i>Journal of Experimental Botany</i> , 2015, 66, 5417-5427.	2.4	116
40	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	6.5	95
41	Triticeae Resources in Ensembl Plants. <i>Plant and Cell Physiology</i> , 2015, 56, e3-e3.	1.5	59
42	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	6.5	103
43	De Novo Transcriptome Assembly and Analyses of Gene Expression during Photomorphogenesis in Diploid Wheat <i>Triticum monococcum</i> . <i>PLoS ONE</i> , 2014, 9, e96855.	1.1	55
44	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , 2014, 42, D789-D793.	6.5	149
45	Gramene 2013: comparative plant genomics resources. <i>Nucleic Acids Research</i> , 2014, 42, D1193-D1199.	6.5	163
46	Ensembl Genomes 2013: scaling up access to genome-wide data. <i>Nucleic Acids Research</i> , 2014, 42, D546-D552.	6.5	205
47	Ribosomal DNA intergenic spacer 1 region is useful when identifying <i>Candida parapsilosis</i> spp. complex based on high-resolution melting analysis. <i>Medical Mycology</i> , 2014, 52, 472-481.	0.3	12
48	Studying Culicoides vectors of BTV in the post-genomic era: Resources, bottlenecks to progress and future directions. <i>Virus Research</i> , 2014, 182, 43-49.	1.1	49
49	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
50	WormBase. <i>Worm</i> , 2012, 1, 15-21.	1.0	14
51	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , 2012, 40, D559-D564.	6.5	191
52	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , 2012, 40, D91-D97.	6.5	179
53	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012, 40, D695-D699.	6.5	288
54	WormBase 2012: more genomes, more data, new website. <i>Nucleic Acids Research</i> , 2012, 40, D735-D741.	6.5	175

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55	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	13.7	983
56	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	13.7	1,086
57	Ensembl BioMarts: a hub for data retrieval across taxonomic space. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar030-bar030.	1.4	1,186
58	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
59	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
60	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2011, 477, 419-423.	13.7	593
61	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011, 39, D1085-D1094.	6.5	182
62	Ensembl Genomes: Extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , 2010, 38, D563-D569.	6.5	138
63	An International Bioinformatics Infrastructure to Underpin the <i>Arabidopsis</i> Community. <i>Plant Cell</i> , 2010, 22, 2530-2536.	3.1	23
64	Genomic information infrastructure after the deluge. <i>Genome Biology</i> , 2010, 11, 402.	13.9	19
65	In Silico Characterization of Proteins: UniProt, InterPro and Integr8. <i>Molecular Biotechnology</i> , 2008, 38, 165-177.	1.3	53
66	Building a Biological Space Based on Protein Sequence Similarities and Biological Ontologies. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2008, 11, 653-660.	0.6	1
67	The EMBL Nucleotide Sequence and Genome Reviews Databases. , 2007, 406, 1-21.		14
68	Genome Reviews: Standardizing Content and Representation of Information about Complete Genomes. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 114-118.	1.0	25
69	Linking publication, gene and protein data. <i>Nature Cell Biology</i> , 2006, 8, 1183-1189.	4.6	33
70	Biological Databases: Infrastructure, Content and Integration. , 2005, , 11-28.		3
71	Databases and Resources for in silico Proteome Analysis. <i>Methods of Biochemical Analysis</i> , 2005, , 395-414.	0.2	1
72	The Integr8 project--a resource for genomic and proteomic data. <i>In Silico Biology</i> , 2005, 5, 179-85.	0.4	21

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73	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , 2004, 33, D297-D302.	6.5	125
74	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
75	The HUPO PSI's Molecular Interaction formatâ€”a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	9.4	581
76	The International Protein Index: An integrated database for proteomics experiments. <i>Proteomics</i> , 2004, 4, 1985-1988.	1.3	685
77	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2004, 33, D141-D146.	6.5	140
78	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. <i>Comparative and Functional Genomics</i> , 2003, 4, 16-19.	2.0	26
79	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. <i>Comparative and Functional Genomics</i> , 2003, 4, 203-206.	2.0	16
80	Automated annotation of microbial proteomes in SWISS-PROT. <i>Computational Biology and Chemistry</i> , 2003, 27, 49-58.	1.1	125
81	The Gene Ontology Annotation (GOA) Project: Implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003, 13, 662-672.	2.4	297
82	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 414-417.	6.5	64
83	Integr8: enhanced inter-operability of European molecular biology databases. <i>Methods of Information in Medicine</i> , 2003, 42, 154-60.	0.7	4
84	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002, 3, 285-295.	3.2	54
85	Proteome Analysis Database: online application of InterPro and CluSTr for the functional classification of proteins in whole genomes. <i>Nucleic Acids Research</i> , 2001, 29, 44-48.	6.5	84
86	VARSP LIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 2000, 16, 1048-1049.	1.8	47
87	Cell cycle, DNA damage and heat shock regulate. <i>Molecular Genetics and Genomics</i> , 1996, 252, 284.	2.4	2
88	Positive and negative roles for cdc10 in cell cycle gene expression. <i>Nucleic Acids Research</i> , 1995, 23, 4761-4768.	6.5	37
89	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
90	Data management challenges for artificial intelligence in plant and agricultural research. <i>F1000Research</i> , 0, 10, 324.	0.8	7

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91	Ten Simples Rules on How to Organise a Bioinformatics Hackathon. EMBnet Journal, 0, 26, e983.	0.2	0
92	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. F1000Research, 0, 11, 231.	0.8	2
93	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. F1000Research, 0, 11, 231.	0.8	4