

Kersey Pj

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

11,968
citations

48
h-index

101
g-index

101
ext. papers

14,911
ext. citations

12.5
avg, IF

6.3
L-index

#	Paper	IF	Citations
95	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012 , 487, 94-8	50.4	859
94	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017 , 544, 427-433	33.4	822
93	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012 , 491, 705-710	50.4	821
92	Ensembl BioMart: a hub for data retrieval across taxonomic space. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar030	5	751
91	The International Protein Index: an integrated database for proteomics experiments. <i>Proteomics</i> , 2004 , 4, 1985-8	4.8	650
90	The HUPO PSI Σ molecular interaction format--a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004 , 22, 177-83	44.5	504
89	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2011 , 477, 419-23	50.4	495
88	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
87	Ensembl Genomes 2016: more genomes, more complexity. <i>Nucleic Acids Research</i> , 2016 , 44, D574-80	20.1	408
86	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
85	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018 , 46, D802-D808	20.1	330
84	WormBase ParaSite - a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017 , 215, 2-10	1.9	264
83	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	9.7	262
82	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
81	The Gene Ontology Annotation (GOA) project: implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003 , 13, 662-72	9.7	251
80	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012 , 40, D695-9	20.1	221
79	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , 2016 , 44, D774-80	20.1	217

78	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020 , 48, D689-D695	20.1	214
77	Ensembl Genomes 2013: scaling up access to genome-wide data. <i>Nucleic Acids Research</i> , 2014 , 42, D546-552	20.1	179
76	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , 2012 , 40, D559-64	20.1	166
75	WormBase 2012: more genomes, more data, new website. <i>Nucleic Acids Research</i> , 2012 , 40, D735-41	20.1	159
74	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011 , 39, D1085-94	20.1	145
73	Gramene 2013: comparative plant genomics resources. <i>Nucleic Acids Research</i> , 2014 , 42, D1193-9	20.1	143
72	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , 2012 , 40, D91-7	20.1	141
71	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , 2018 , 46, D869-D874	20.1	138
70	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2016 , 1374, 115-40	1.4	129
69	Ensembl Genomes: extending Ensembl across the taxonomic space. <i>Nucleic Acids Research</i> , 2010 , 38, D563-9	20.1	127
68	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , 2014 , 42, D789-93	20.1	126
67	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2005 , 33, D141-6	20.1	122
66	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017 , 45, D128-D134	20.1	119
65	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , 2005 , 33, D297-302	20.1	116
64	Automated annotation of microbial proteomes in SWISS-PROT. <i>Computational Biology and Chemistry</i> , 2003 , 27, 49-58	3.6	112
63	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018 , 46, D1181-D1189	20.1	107
62	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016 , 44, D1133-40	20.1	102
61	Towards recommendations for metadata and data handling in plant phenotyping. <i>Journal of Experimental Botany</i> , 2015 , 66, 5417-27	7	94

60	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L. <i>Scientific Data</i> , 2017 , 4, 170044	8.2	93
59	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D123-9	20.1	89
58	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016 , 12, 44	5.8	83
57	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015 , 43, D656-61	20.1	74
56	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, 48347	4.9	64
55	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, 44-8	20.1	63
54	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. <i>Methods in Molecular Biology</i> , 2017 , 1533, 1-31	1.4	61
53	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	9.8	59
52	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	6.2	55
51	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003 , 31, 414-7	20.1	55
50	Plant genome sequences: past, present, future. <i>Current Opinion in Plant Biology</i> , 2019 , 48, 1-8	9.9	55
49	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011 , 17, 1941-6	5.8	54
48	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002 , 3, 285-95	13.4	48
47	In silico characterization of proteins: UniProt, InterPro and Integr8. <i>Molecular Biotechnology</i> , 2008 , 38, 165-77	3	47
46	Triticeae resources in Ensembl Plants. <i>Plant and Cell Physiology</i> , 2015 , 56, e3	4.9	44
45	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	3.7	44
44	VARSP LIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 2000 , 16, 1048-9	7.2	44
43	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020 , 227, 260-273	9.8	42

42	Studying Culicoides vectors of BTV in the post-genomic era: resources, bottlenecks to progress and future directions. <i>Virus Research</i> , 2014 , 182, 43-9	6.4	41
41	Positive and negative roles for cdc10 in cell cycle gene expression. <i>Nucleic Acids Research</i> , 1995 , 23, 4761-8.	28.1	36
40	Gramene Database: Navigating Plant Comparative Genomics Resources. <i>Current Plant Biology</i> , 2016 , 7-8, 10-15	3.3	35
39	PhytoPath: an integrative resource for plant pathogen genomics. <i>Nucleic Acids Research</i> , 2016 , 44, D688-93.	23.1	31
38	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021 , 49, D1452-D1463	20.1	29
37	Linking publication, gene and protein data. <i>Nature Cell Biology</i> , 2006 , 8, 1183-9	23.4	28
36	Genome Reviews: standardizing content and representation of information about complete genomes. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 114-8	3.8	25
35	An international bioinformatics infrastructure to underpin the Arabidopsis community. <i>Plant Cell</i> , 2010 , 22, 2530-6	11.6	22
34	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. <i>Comparative and Functional Genomics</i> , 2003 , 4, 16-9		22
33	Using WormBase ParaSite: An Integrated Platform for Exploring Helminth Genomic Data. <i>Methods in Molecular Biology</i> , 2018 , 1757, 471-491	1.4	22
32	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020 , 13, 1341-1344	14.4	21
31	The Integr8 project--a resource for genomic and proteomic data. <i>In Silico Biology</i> , 2005 , 5, 179-85	2	21
30	Genomic information infrastructure after the deluge. <i>Genome Biology</i> , 2010 , 11, 402	18.3	16
29	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,	11.5	15
28	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, 203-6		14
27	Conservation Policy: Helping or hindering science to unlock properties of plants and fungi. <i>Plants People Planet</i> , 2020 , 2, 535-545	4.1	13
26	The EMBL Nucleotide Sequence and Genome Reviews Databases. <i>Methods in Molecular Biology</i> , 2007 , 406, 1-21	1.4	12
25	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	4.5	12

24	WormBase: Annotating many nematode genomes. <i>Worm</i> , 2012 , 1, 15-21		11
23	ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021 , 40, e107409	13	11
22	Selecting for useful properties of plants and fungi [Novel approaches, opportunities, and challenges. <i>Plants People Planet</i> , 2020 , 2, 409-420	4.1	9
21	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,	11.5	9
20	Ribosomic 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, 472-81	3.9	8
19	Computational Pan-Genomics: Status, Promises and Challenges		6
18	Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. <i>Frontiers in Microbiology</i> , 2019 , 10, 2477	5.7	6
17	A Comprehensive Phylogenomic Platform for Exploring the Angiosperm Tree of Life		6
16	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.06.0038	4.4	5
15	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021 , 113, 3666-3680	4.3	5
14	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
13	Integr8: enhanced inter-operability of European molecular biology databases. <i>Methods of Information in Medicine</i> , 2003 , 42, 154-60	1.5	4
12	Biological Databases: Infrastructure, Content and Integration 2005 , 11-28		3
11	Uses and benefits of digital sequence information from plant genetic resources: Lessons learnt from botanical collections. <i>Plants People Planet</i> ,	4.1	3
10	Cell cycle, DNA damage and heat shock regulate. <i>Molecular Genetics and Genomics</i> , 1996 , 252, 284		2
9	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. <i>F1000Research</i> , 11 , 231	3.6	2
8	Databases and Tools for the Analysis of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018 , 377-394	4.8	1
7	Building a biological space based on protein sequence similarities and biological ontologies. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2008 , 11, 653-60	1.3	1

6	Databases and Resources for in silico Proteome Analysis. <i>Methods of Biochemical Analysis</i> , 2005 , 395-414		1
5	COPO: a metadata platform for brokering FAIR data in the life sciences		1
4	Data management challenges for artificial intelligence in plant and agricultural research. <i>F1000Research</i> , 10 , 324	3.6	1
3	Advancing vector biology research: a community survey for future directions, research applications and infrastructure requirements. <i>Pathogens and Global Health</i> , 2016 , 110, 164-72	3.1	0
2	Computational Methods and Bioinformatic Tools	769-904	
1	Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR. <i>F1000Research</i> , 11 , 231	3.6	