Kersey Pj

List of Publications by Year in Descending Order

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	The Earth BioGenome Project 2020: Starting the clock.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	15
94	Standards recommendations for the Earth BioGenome Project.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	4
93	Green plant genomes: What we know in an era of rapidly expanding opportunities.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	9
92	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. *Nucleic Acids Research*, **2021**, 49, D1452-D1463	20.1	29
91	ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. *EMBO Journal*, **2021**, 40, e107409	13	11
90	The salmon louse genome: Copepod features and parasitic adaptations. *Genomics*, **2021**, 113, 3666-3680	4.3	5
89	Selecting for useful properties of plants and fungi Novel approaches, opportunities, and challenges. *Plants People Planet*, **2020**, 2, 409-420	4.1	9
88	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. *New Phytologist*, **2020**, 227, 260-273	9.8	42
87	Ensembl Genomes 2020-enabling non-vertebrate genomic research. *Nucleic Acids Research*, **2020**, 48, D689-D695	20.1	214
86	Conservation Policy: Helping or hindering science to unlock properties of plants and fungi. *Plants People Planet*, **2020**, 2, 535-545	4.1	13
85	Mobilizing Crop Biodiversity. *Molecular Plant*, **2020**, 13, 1341-1344	14.4	21
84	Factors Affecting Targeted Sequencing of 353 Nuclear Genes From Herbarium Specimens Spanning the Diversity of Angiosperms. *Frontiers in Plant Science*, **2019**, 10, 1102	6.2	55
83	Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. *Frontiers in Microbiology*, **2019**, 10, 2477	5.7	6
82	Plant genome sequences: past, present, future. *Current Opinion in Plant Biology*, **2019**, 48, 1-8	9.9	55
81	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. *Nucleic Acids Research*, **2018**, 46, D802-D808	20.1	330
80	Gramene 2018: unifying comparative genomics and pathway resources for plant research. *Nucleic Acids Research*, **2018**, 46, D1181-D1189	20.1	107
79	Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. *New Phytologist*, **2018**, 217, 1407-1419	9.8	59

78	Integrative analysis of large scale transcriptome data draws a comprehensive landscape of Phaeodactylum tricornutum genome and evolutionary origin of diatoms. *Scientific Reports*, **2018**, 8, 4834	4.9	64
77	WormBase 2017: molting into a new stage. *Nucleic Acids Research*, **2018**, 46, D869-D874	20.1	138
76	Databases and Tools for the Analysis of the Barley Genome. *Compendium of Plant Genomes*, **2018**, 377-394	0.8	1
75	The genome of the biting midge Culicoides sonorensis and gene expression analyses of vector competence for bluetongue virus. *BMC Genomics*, **2018**, 19, 624	4.5	12
74	Using WormBase ParaSite: An Integrated Platform for Exploring Helminth Genomic Data. *Methods in Molecular Biology*, **2018**, 1757, 471-491	1.4	22
73	WormBase ParaSite - a comprehensive resource for helminth genomics. *Molecular and Biochemical Parasitology*, **2017**, 215, 2-10	1.9	264
72	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	9.7	262
71	A chromosome conformation capture ordered sequence of the barley genome. *Nature*, **2017**, 544, 427-433	50.4	822
70	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L. *Scientific Data*, **2017**, 4, 170044	8.2	93
69	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. *Methods in Molecular Biology*, **2017**, 1533, 1-31	1.4	61
68	RNAcentral: a comprehensive database of non-coding RNA sequences. *Nucleic Acids Research*, **2017**, 45, D128-D134	20.1	119
67	Advancing vector biology research: a community survey for future directions, research applications and infrastructure requirements. *Pathogens and Global Health*, **2016**, 110, 164-72	3.1	0
66	Gramene 2016: comparative plant genomics and pathway resources. *Nucleic Acids Research*, **2016**, 44, D1133-40	20.1	102
65	PhytoPath: an integrative resource for plant pathogen genomics. *Nucleic Acids Research*, **2016**, 44, D688-93	20.1	31
64	Ensembl Genomes 2016: more genomes, more complexity. *Nucleic Acids Research*, **2016**, 44, D574-80	20.1	408
63	WormBase 2016: expanding to enable helminth genomic research. *Nucleic Acids Research*, **2016**, 44, D774-80	20.1	217
62	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. *Methods in Molecular Biology*, **2016**, 1374, 115-40	1.4	129
61	transPLANT Resources for Triticeae Genomic Data. *Plant Genome*, **2016**, 9, plantgenome2015.06.0038	4.4	5

60	Measures for interoperability of phenotypic data: minimum information requirements and formatting. *Plant Methods*, **2016**, 12, 44	5.8	83
59	Gramene Database: Navigating Plant Comparative Genomics Resources. *Current Plant Biology*, **2016**, 7-8, 10-15	3.3	35
58	PomBase 2015: updates to the fission yeast database. *Nucleic Acids Research*, **2015**, 43, D656-61	20.1	74
57	Triticeae resources in Ensembl Plants. *Plant and Cell Physiology*, **2015**, 56, e3	4.9	44
56	RNAcentral: an international database of ncRNA sequences. *Nucleic Acids Research*, **2015**, 43, D123-9	20.1	89
55	Towards recommendations for metadata and data handling in plant phenotyping. *Journal of Experimental Botany*, **2015**, 66, 5417-27	7	94
54	Ensembl Genomes 2013: scaling up access to genome-wide data. *Nucleic Acids Research*, **2014**, 42, D546-52	20.1	179
53	Ribosomic DNA intergenic spacer 1 region is useful when identifying Candida parapsilosis spp. complex based on high-resolution melting analysis. *Medical Mycology*, **2014**, 52, 472-81	3.9	8
52	Studying Culicoides vectors of BTV in the post-genomic era: resources, bottlenecks to progress and future directions. *Virus Research*, **2014**, 182, 43-9	6.4	41
51	De novo transcriptome assembly and analyses of gene expression during photomorphogenesis in diploid wheat Triticum monococcum. *PLoS ONE*, **2014**, 9, e96855	3.7	44
50	WormBase 2014: new views of curated biology. *Nucleic Acids Research*, **2014**, 42, D789-93	20.1	126
49	Gramene 2013: comparative plant genomics resources. *Nucleic Acids Research*, **2014**, 42, D1193-9	20.1	143
48	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. *GigaScience*, **2013**, 2, 10	7.6	461
47	Analysis of the bread wheat genome using whole-genome shotgun sequencing. *Nature*, **2012**, 491, 705-10	50.4	821
46	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature*, **2012**, 487, 94-8	50.4	859
45	WormBase: Annotating many nematode genomes. *Worm*, **2012**, 1, 15-21		11
44	The Gene Ontology: enhancements for 2011. *Nucleic Acids Research*, **2012**, 40, D559-64	20.1	166
43	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. *Nucleic Acids Research*, **2012**, 40, D91-7	20.1	141

42	PomBase: a comprehensive online resource for fission yeast. *Nucleic Acids Research*, **2012**, 40, D695-9	20.1	221
41	WormBase 2012: more genomes, more data, new website. *Nucleic Acids Research*, **2012**, 40, D735-41	20.1	159
40	Ensembl BioMarts: a hub for data retrieval across taxonomic space. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar030	5	751
39	Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome Research*, **2011**, 21, 2224-41	9.7	364
38	RNAcentral: A vision for an international database of RNA sequences. *Rna*, **2011**, 17, 1941-6	5.8	54
37	Multiple reference genomes and transcriptomes for Arabidopsis thaliana. *Nature*, **2011**, 477, 419-23	50.4	495
36	Gramene database in 2010: updates and extensions. *Nucleic Acids Research*, **2011**, 39, D1085-94	20.1	145
35	Ensembl Genomes: extending Ensembl across the taxonomic space. *Nucleic Acids Research*, **2010**, 38, D563-9	20.1	127
34	An international bioinformatics infrastructure to underpin the Arabidopsis community. *Plant Cell*, **2010**, 22, 2530-6	11.6	22
33	Genomic information infrastructure after the deluge. *Genome Biology*, **2010**, 11, 402	18.3	16
32	Building a biological space based on protein sequence similarities and biological ontologies. *Combinatorial Chemistry and High Throughput Screening*, **2008**, 11, 653-60	1.3	1
31	In silico characterization of proteins: UniProt, InterPro and Integr8. *Molecular Biotechnology*, **2008**, 38, 165-77	3	47
30	The EMBL Nucleotide Sequence and Genome Reviews Databases. *Methods in Molecular Biology*, **2007**, 406, 1-21	1.4	12
29	Genome Reviews: standardizing content and representation of information about complete genomes. *OMICS A Journal of Integrative Biology*, **2006**, 10, 114-8	3.8	25
28	Linking publication, gene and protein data. *Nature Cell Biology*, **2006**, 8, 1183-9	23.4	28
27	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. *Nucleic Acids Research*, **2005**, 33, D297-302	20.1	116
26	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. *Nucleic Acids Research*, **2005**, 33, D141-6	20.1	122
25	Biological Databases: Infrastructure, Content and Integration **2005**, 11-28		3

24   Databases and Resources for in silico Proteome Analysis. *Methods of Biochemical Analysis*, **2005**, 395-414   1

23   The Integr8 project--a resource for genomic and proteomic data. *In Silico Biology*, **2005**, 5, 179-85   2   21

22   Integrative annotation of 21,037 human genes validated by full-length cDNA clones. *PLoS Biology*, **2004**, 2, e162   9.7   255

21   The HUPO PSI's molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83   44.5   504

20   The International Protein Index: an integrated database for proteomics experiments. *Proteomics*, **2004**, 4, 1985-8   4.8   650

19   The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. *Comparative and Functional Genomics*, **2003**, 4, 16-9   22

18   Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. *Comparative and Functional Genomics*, **2003**, 4, 203-6   14

17   Automated annotation of microbial proteomes in SWISS-PROT. *Computational Biology and Chemistry*, **2003**, 27, 49-58   3.6   112

16   The Gene Ontology Annotation (GOA) project: implementation of GO in SWISS-PROT, TrEMBL, and InterPro. *Genome Research*, **2003**, 13, 662-72   9.7   251

15   The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. *Nucleic Acids Research*, **2003**, 31, 414-7   20.1   55

14   Integr8: enhanced inter-operability of European molecular biology databases. *Methods of Information in Medicine*, **2003**, 42, 154-60   1.5   4

13   Applications of InterPro in protein annotation and genome analysis. *Briefings in Bioinformatics*, **2002**, 3, 285-95   13.4   48

12   Proteome Analysis Database: online application of InterPro and CluSTr for the functional classification of proteins in whole genomes. *Nucleic Acids Research*, **2001**, 29, 44-8   20.1   63

11   VARSPLIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. *Bioinformatics*, **2000**, 16, 1048-9   7.2   44

10   Cell cycle, DNA damage and heat shock regulate. *Molecular Genetics and Genomics*, **1996**, 252, 284   2

9   Positive and negative roles for cdc10 in cell cycle gene expression. *Nucleic Acids Research*, **1995**, 23, 4761-8   28.1   36

8   Computational Methods and Bioinformatic Tools769-904

7   COPO: a metadata platform for brokering FAIR data in the life sciences   1

List of Publications