

Peter Cock

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

9,572
citations

172457

29
h-index

138484

58
g-index

67
all docs

67
docs citations

67
times ranked

15862
citing authors

#	ARTICLE	IF	CITATIONS
1	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009, 25, 1422-1423.	4.1	4,097
2	The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. <i>Nucleic Acids Research</i> , 2010, 38, 1767-1771.	14.5	1,340
3	Using Tablet for visual exploration of second-generation sequencing data. <i>Briefings in Bioinformatics</i> , 2013, 14, 193-202.	6.5	836
4	Resistance gene enrichment sequencing (<sc>R</sc>en<sc>S</sc>eq) enables reannotation of the <sc>NB</sc>â€<sc>LRR</sc> gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. <i>Plant Journal</i> , 2013, 76, 530-544.	5.7	367
5	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002219.	4.7	351
6	Identification and localisation of the NB-LRR gene family within the potato genome. <i>BMC Genomics</i> , 2012, 13, 75.	2.8	290
7	NCBI BLAST+ integrated into Galaxy. <i>GigaScience</i> , 2015, 4, 39.	6.4	213
8	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014, 15, R43.	9.6	212
9	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. <i>PeerJ</i> , 2013, 1, e167.	2.0	159
10	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	8.8	156
11	Bio.Phylo: A unified toolkit for processing, analyzing and visualizing phylogenetic trees in Biopython. <i>BMC Bioinformatics</i> , 2012, 13, 209.	2.6	117
12	Identification and functional characterization of effectors in expressed sequence tags from various life cycle stages of the potato cyst nematode <i>Globodera pallida</i>. <i>Molecular Plant Pathology</i> , 2009, 10, 815-828.	4.2	96
13	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. <i>BMC Genomics</i> , 2016, 17, 172.	2.8	92
14	Identification and characterization of parasitism genes from the pinewood nematode <i>Bursaphelenchus xylophilus</i> reveals a multilayered detoxification strategy. <i>Molecular Plant Pathology</i> , 2016, 17, 286-295.	4.2	91
15	Raspberry leaf blotch virus, a putative new member of the genus Emaravirus, encodes a novel genomic RNA. <i>Journal of General Virology</i> , 2012, 93, 430-437.	2.9	85
16	Genomic characterisation of the effector complement of the potato cyst nematode <i>Globodera pallida</i> . <i>BMC Genomics</i> , 2014, 15, 923.	2.8	81
17	Two-component systems of the myxobacteria: structure, diversity and evolutionary relationships. <i>Microbiology (United Kingdom)</i> , 2008, 154, 360-372.	1.8	64
18	Evolution of prokaryotic two-component systems: insights from comparative genomics. <i>Amino Acids</i> , 2009, 37, 459-466.	2.7	58

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19	Genetic characterization of the HrpL regulon of the fire blight pathogen <i>Erwinia amylovora</i> reveals novel virulence factors. <i>Molecular Plant Pathology</i> , 2012, 13, 160-173.	4.2	54
20	Distinct Circular Single-Stranded DNA Viruses Exist in Different Soil Types. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3934-3945.	3.1	54
21	Shared Transcriptional Control and Disparate Gain and Loss of Aphid Parasitism Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 2716-2733.	2.5	53
22	Genome-Wide Identification of Genes Regulated by the Rcs Phosphorelay System in <i>Erwinia amylovora</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 6-17.	2.6	52
23	Evolution of Prokaryotic Two-Component System Signaling Pathways: Gene Fusions and Fissions. <i>Molecular Biology and Evolution</i> , 2007, 24, 2355-2357.	8.9	47
24	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014, 5, 5.	1.6	47
25	Novel Bacteriophages Containing a Genome of Another Bacteriophage within Their Genomes. <i>PLoS ONE</i> , 2012, 7, e40683.	2.5	46
26	Community-driven development for computational biology at Sprints, Hackathons and Codefests. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	42
27	Newly identified RNAs of raspberry leaf blotch virus encoding a related group of proteins. <i>Journal of General Virology</i> , 2015, 96, 3432-3439.	2.9	42
28	The Transcriptome of <i>Nacobbus aberrans</i> Reveals Insights into the Evolution of Sedentary Endoparasitism in Plant-Parasitic Nematodes. <i>Genome Biology and Evolution</i> , 2014, 6, 2181-2194.	2.5	39
29	Computation of Balanced Equivalence Relations and Their Lattice for a Coupled Cell Network. <i>SIAM Journal on Applied Dynamical Systems</i> , 2013, 12, 352-382.	1.6	32
30	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , 2013, 4, 6.	1.6	26
31	Evolution of Gene Overlaps: Relative Reading Frame Bias in Prokaryotic Two-Component System Genes. <i>Journal of Molecular Evolution</i> , 2007, 64, 457-462.	1.8	25
32	A metagenetic approach to determine the diversity and distribution of cyst nematodes at the level of the country, the field and the individual. <i>Molecular Ecology</i> , 2015, 24, 5842-5851.	3.9	22
33	Evidence for an Opportunistic and Endophytic Lifestyle of the <i>Bursaphelenchus xylophilus</i> -Associated Bacteria <i>Serratia marcescens</i> PWN146 Isolated from Wilting <i>Pinus pinaster</i> . <i>Microbial Ecology</i> , 2016, 72, 669-681.	2.8	22
34	FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. <i>Journal of Biomedical Semantics</i> , 2016, 7, 39.	1.6	22
35	From plants to nematodes: <i>Serratia grimesii</i> BXF1 genome reveals an adaptation to the modulation of multi-species interactions. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
36	The genome and genetics of a high oxidative stress tolerant <i>Serratia</i> sp. LCN16 isolated from the plant parasitic nematode <i>Bursaphelenchus xylophilus</i> . <i>BMC Genomics</i> , 2016, 17, 301.	2.8	18

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37	PHYTO-THREATS: Addressing Threats to UK Forests and Woodlands from Phytophthora; Identifying Risks of Spread in Trade and Methods for Mitigation. <i>Forests</i> , 2021, 12, 1617.	2.1	18
38	DNA Metabarcoding and Isolation by Baiting Complement Each Other in Revealing Phytophthora Diversity in Anthropized and Natural Ecosystems. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 330.	3.5	17
39	Evolution of Relative Reading Frame Bias in Unidirectional Prokaryotic Gene Overlaps. <i>Molecular Biology and Evolution</i> , 2010, 27, 753-756.	8.9	14
40	Comparison of transcript profiles in different life stages of the nematode <i>Globodera pallida</i> under different host potato genotypes. <i>Molecular Plant Pathology</i> , 2012, 13, 1120-1134.	4.2	14
41	Characterisation of the transcriptome of <i>Aphelenchoides besseyi</i> and identification of a GHF 45 cellulase. <i>Nematology</i> , 2014, 16, 99-107.	0.6	14
42	Partial sequence and RT-PCR diagnostic test for the plant rhabdovirus Raspberry vein chlorosis virus. <i>Plant Pathology</i> , 2011, 60, 462-467.	2.4	12
43	Activation of hatching in diapaused and quiescent <i>Globodera pallida</i> . <i>Parasitology</i> , 2013, 140, 445-454.	1.5	12
44	Phytophthora austrocedri in Argentina and Co-Inhabiting Phytophthoras: Roles of Anthropogenic and Abiotic Factors in Species Distribution and Diversity. <i>Forests</i> , 2020, 11, 1223.	2.1	11
45	Parallel Microbial Ecology of Pasteuria and Nematode Species in Scottish Soils. <i>Frontiers in Plant Science</i> , 2019, 10, 1763.	3.6	9
46	Kodoja: A workflow for virus detection in plants using k-mer analysis of RNA-sequencing data. <i>Journal of General Virology</i> , 2019, 100, 533-542.	2.9	9
47	Two-Component Signal Transduction Systems of the Myxobacteria. , 0, , 169-189.		8
48	The Genomic Impact of Selection for Virulence against Resistance in the Potato Cyst Nematode, <i>Globodera pallida</i> . <i>Genes</i> , 2020, 11, 1429.	2.4	8
49	Gene expression changes in diapause or quiescent potato cyst nematode, <i>Globodera pallida</i> , eggs after hydration or exposure to tomato root diffusate. <i>PeerJ</i> , 2016, 4, e1654.	2.0	8
50	Galaxy as a Platform for Identifying Candidate Pathogen Effectors. <i>Methods in Molecular Biology</i> , 2014, 1127, 3-15.	0.9	5
51	Sprints, Hackathons and Codefests as community gluons in computational biology. <i>EMBnet Journal</i> , 2013, 19, 40.	0.6	5
52	The 2015 Bioinformatics Open Source Conference (BOSC 2015). <i>PLoS Computational Biology</i> , 2016, 12, e1004691.	3.2	4
53	The Bioinformatics Open Source Conference (BOSC) 2013. <i>Bioinformatics</i> , 2015, 31, 299-300.	4.1	3
54	BOSC 2019, the 20th annual Bioinformatics Open Source Conference. <i>F1000Research</i> , 2019, 8, 2132.	1.6	3

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55	The 2017 Bioinformatics Open Source Conference (BOSC). F1000Research, 2017, 6, 1858.	1.6	2
56	The 2016 Bioinformatics Open Source Conference (BOSC). F1000Research, 2016, 5, 2464.	1.6	2
57	The 21st annual Bioinformatics Open Source Conference (BOSC 2020, part of BCC2020). F1000Research, 2020, 9, 1160.	1.6	1
58	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0