Peter Cock

List of Publications by Year
in descending order

58￼papers	9,572￼citations	172386￼29￼h-index	138417￼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. Bioinformatics, 2009, 25, 1422-1423.	1.8	4,097
2	The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. Nucleic Acids Research, 2010, 38, 1767-1771.	6.5	1,340
3	Using Tablet for visual exploration of second-generation sequencing data. Briefings in Bioinformatics, 2013, 14, 193-202.	3.2	836
4	Resistance gene enrichment sequencing (<scp>R</scp>en<scp>S</scp>eq) enables reannotation of the <scp>NB</scp>â€‹<scp>LRR</scp> gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. Plant Journal, 2013, 76, 530-544.	2.8	367
5	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen Bursaphelenchus xylophilus. PLoS Pathogens, 2011, 7, e1002219.	2.1	351
6	Identification and localisation of the NB-LRR gene family within the potato genome. BMC Genomics, 2012, 13, 75.	1.2	290
7	NCBI BLAST+ integrated into Galaxy. GigaScience, 2015, 4, 39.	3.3	213
8	The genome and life-stage specific transcriptomes of Globodera pallida elucidate key aspects of plant parasitism by a cyst nematode. Genome Biology, 2014, 15, R43.	13.9	212
9	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. PeerJ, 2013, 1, e167.	0.9	159
10	The genome of the yellow potato cyst nematode, Globodera rostochiensis, reveals insights into the basis of parasitism and virulence. Genome Biology, 2016, 17, 124.	3.8	156
11	Bio.Phylo: A unified toolkit for processing, analyzing and visualizing phylogenetic trees in Biopython. BMC Bioinformatics, 2012, 13, 209.	1.2	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>. Molecular Plant Pathology, 2009, 10, 815-828.	2.0	96
13	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. BMC Genomics, 2016, 17, 172.	1.2	92
14	Identification and characterization of parasitism genes from the pinewood nematode <i>Bursaphelenchus xylophilus</i> reveals a multilayered detoxification strategy. Molecular Plant Pathology, 2016, 17, 286-295.	2.0	91
15	Raspberry leaf blotch virus, a putative new member of the genus Emaravirus, encodes a novel genomic RNA. Journal of General Virology, 2012, 93, 430-437.	1.3	85
16	Genomic characterisation of the effector complement of the potato cyst nematode Globodera pallida. BMC Genomics, 2014, 15, 923.	1.2	81
17	Two-component systems of the myxobacteria: structure, diversity and evolutionary relationships. Microbiology (United Kingdom), 2008, 154, 360-372.	0.7	64
18	Evolution of prokaryotic two-component systems: insights from comparative genomics. Amino Acids, 2009, 37, 459-466.	1.2	58

#	Article	IF	Citations
19	Genetic characterization of the HrpL regulon of the fire blight pathogen *Erwinia amylovora* reveals novel virulence factors. Molecular Plant Pathology, 2012, 13, 160-173.	2.0	54
20	Distinct Circular Single-Stranded DNA Viruses Exist in Different Soil Types. Applied and Environmental Microbiology, 2015, 81, 3934-3945.	1.4	54
21	Shared Transcriptional Control and Disparate Gain and Loss of Aphid Parasitism Genes. Genome Biology and Evolution, 2018, 10, 2716-2733.	1.1	53
22	Genome-Wide Identification of Genes Regulated by the Rcs Phosphorelay System in *Erwinia amylovora*. Molecular Plant-Microbe Interactions, 2012, 25, 6-17.	1.4	52
23	Evolution of Prokaryotic Two-Component System Signaling Pathways: Gene Fusions and Fissions. Molecular Biology and Evolution, 2007, 24, 2355-2357.	3.5	47
24	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	0.9	47
25	Novel Bacteriophages Containing a Genome of Another Bacteriophage within Their Genomes. PLoS ONE, 2012, 7, e40683.	1.1	46
26	Community-driven development for computational biology at Sprints, Hackathons and Codefests. BMC Bioinformatics, 2014, 15, S7.	1.2	42
27	Newly identified RNAs of raspberry leaf blotch virus encoding a related group of proteins. Journal of General Virology, 2015, 96, 3432-3439.	1.3	42
28	The Transcriptome of Nacobbus aberrans Reveals Insights into the Evolution of Sedentary Endoparasitism in Plant-Parasitic Nematodes. Genome Biology and Evolution, 2014, 6, 2181-2194.	1.1	39
29	Computation of Balanced Equivalence Relations and Their Lattice for a Coupled Cell Network. SIAM Journal on Applied Dynamical Systems, 2013, 12, 352-382.	0.7	32
30	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	0.9	26
31	Evolution of Gene Overlaps: Relative Reading Frame Bias in Prokaryotic Two-Component System Genes. Journal of Molecular Evolution, 2007, 64, 457-462.	0.8	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. Molecular Ecology, 2015, 24, 5842-5851.	2.0	22
33	Evidence for an Opportunistic and Endophytic Lifestyle of the Bursaphelenchus xylophilus-Associated Bacteria Serratia marcescens PWN146 Isolated from Wilting Pinus pinaster. Microbial Ecology, 2016, 72, 669-681.	1.4	22
34	FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. Journal of Biomedical Semantics, 2016, 7, 39.	0.9	22
35	From plants to nematodes: Serratia grimesii BXF1 genome reveals an adaptation to the modulation of multi-species interactions. Microbial Genomics, 2018, 4, .	1.0	19
36	The genome and genetics of a high oxidative stress tolerant Serratia sp. LCN16 isolated from the plant parasitic nematode Bursaphelenchus xylophilus. BMC Genomics, 2016, 17, 301.	1.2	18

#	Article	IF	Citations
37	PHYTO-THREATS: Addressing Threats to UK Forests and Woodlands from Phytophthora; Identifying Risks of Spread in Trade and Methods for Mitigation. Forests, 2021, 12, 1617.	0.9	18
38	DNA Metabarcoding and Isolation by Baiting Complement Each Other in Revealing Phytophthora Diversity in Anthropized and Natural Ecosystems. Journal of Fungi (Basel, Switzerland), 2022, 8, 330.	1.5	17
39	Evolution of Relative Reading Frame Bias in Unidirectional Prokaryotic Gene Overlaps. Molecular Biology and Evolution, 2010, 27, 753-756.	3.5	14
40	Comparison of transcript profiles in different life stages of the nematode *Globodera pallida* under different host potato genotypes. Molecular Plant Pathology, 2012, 13, 1120-1134.	2.0	14
41	Characterisation of the transcriptome of Aphelenchoides besseyi and identification of a GHF 45 cellulase. Nematology, 2014, 16, 99-107.	0.2	14
42	Partial sequence and RTâ€PCR diagnostic test for the plant rhabdovirus Raspberry vein chlorosis virus. Plant Pathology, 2011, 60, 462-467.	1.2	12
43	Activation of hatching in diapaused and quiescent *Globodera pallida*. Parasitology, 2013, 140, 445-454.	0.7	12
44	Phytophthora austrocedri in Argentina and Co-Inhabiting Phytophthoras: Roles of Anthropogenic and Abiotic Factors in Species Distribution and Diversity. Forests, 2020, 11, 1223.	0.9	11
45	Parallel Microbial Ecology of Pasteuria and Nematode Species in Scottish Soils. Frontiers in Plant Science, 2019, 10, 1763.	1.7	9
46	Kodoja: A workflow for virus detection in plants using k-mer analysis of RNA-sequencing data. Journal of General Virology, 2019, 100, 533-542.	1.3	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, Globodera pallida. Genes, 2020, 11, 1429.	1.0	8
49	Gene expression changes in diapause or quiescent potato cyst nematode, *Globodera pallida*, eggs after hydration or exposure to tomato root diffusate. PeerJ, 2016, 4, e1654.	0.9	8
50	Galaxy as a Platform for Identifying Candidate Pathogen Effectors. Methods in Molecular Biology, 2014, 1127, 3-15.	0.4	5
51	Sprints, Hackathons and Codefests as community gluons in computational biology. EMBnet Journal, 2013, 19, 40.	0.2	5
52	The 2015 Bioinformatics Open Source Conference (BOSC 2015). PLoS Computational Biology, 2016, 12, e1004691.	1.5	4
53	The Bioinformatics Open Source Conference (BOSC) 2013. Bioinformatics, 2015, 31, 299-300.	1.8	3
54	BOSC 2019, the 20th annual Bioinformatics Open Source Conference. F1000Research, 2019, 8, 2132.	0.8	3

#	Article	IF	Citations
55	The 2017 Bioinformatics Open Source Conference (BOSC). F1000Research, 2017, 6, 1858.	0.8	2
56	The 2016 Bioinformatics Open Source Conference (BOSC). F1000Research, 2016, 5, 2464.	0.8	2
57	The 21st annual Bioinformatics Open Source Conference (BOSC 2020, part of BCC2020). F1000Research, 2020, 9, 1160.	0.8	1
58	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	0.8	0