

# Peter Cock

## List of Publications by Year in descending order

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58  
papers

9,572  
citations

172386

29  
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138417

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67  
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67  
docs citations

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times ranked

15862  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Metabarcoding and Isolation by Baiting Complement Each Other in Revealing Phytophthora Diversity in Anthropized and Natural Ecosystems. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 330.	1.5	17
2	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.	0.9	18
3	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.	0.9	11
4	The Genomic Impact of Selection for Virulence against Resistance in the Potato Cyst Nematode, <i>Globodera pallida</i> . <i>Genes</i> , 2020, 11, 1429.	1.0	8
5	The 21st annual Bioinformatics Open Source Conference (BOSC 2020, part of BCC2020). <i>F1000Research</i> , 2020, 9, 1160.	0.8	1
6	Parallel Microbial Ecology of Pasteuria and Nematode Species in Scottish Soils. <i>Frontiers in Plant Science</i> , 2019, 10, 1763.	1.7	9
7	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.	1.3	9
8	BOSC 2019, the 20th annual Bioinformatics Open Source Conference. <i>F1000Research</i> , 2019, 8, 2132.	0.8	3
9	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, .	1.0	19
10	Shared Transcriptional Control and Disparate Gain and Loss of Aphid Parasitism Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 2716-2733.	1.1	53
11	The 2017 Bioinformatics Open Source Conference (BOSC). <i>F1000Research</i> , 2017, 6, 1858.	0.8	2
12	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.	2.0	91
13	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.	1.2	18
14	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.	1.4	22
15	FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. <i>Journal of Biomedical Semantics</i> , 2016, 7, 39.	0.9	22
16	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. <i>BMC Genomics</i> , 2016, 17, 172.	1.2	92
17	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.	3.8	156
18	The 2016 Bioinformatics Open Source Conference (BOSC). <i>F1000Research</i> , 2016, 5, 2464.	0.8	2

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19	The 2015 Bioinformatics Open Source Conference (BOSC 2015). PLoS Computational Biology, 2016, 12, e1004691.	1.5	4
20	Gene expression changes in diapause or quiescent potato cyst nematode, <i>Globodera pallida</i> , eggs after hydration or exposure to tomato root diffusate. PeerJ, 2016, 4, e1654.	0.9	8
21	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
22	Distinct Circular Single-Stranded DNA Viruses Exist in Different Soil Types. Applied and Environmental Microbiology, 2015, 81, 3934-3945.	1.4	54
23	NCBI BLAST+ integrated into Galaxy. GigaScience, 2015, 4, 39.	3.3	213
24	The Bioinformatics Open Source Conference (BOSC) 2013. Bioinformatics, 2015, 31, 299-300.	1.8	3
25	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
26	Characterisation of the transcriptome of <i>Aphelenchoides besseyi</i> and identification of a GHF 45 cellulase. Nematology, 2014, 16, 99-107.	0.2	14
27	The Transcriptome of <i>Nacobbus aberrans</i> Reveals Insights into the Evolution of Sedentary Endoparasitism in Plant-Parasitic Nematodes. Genome Biology and Evolution, 2014, 6, 2181-2194.	1.1	39
28	Genomic characterisation of the effector complement of the potato cyst nematode <i>Globodera pallida</i> . BMC Genomics, 2014, 15, 923.	1.2	81
29	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
30	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. Genome Biology, 2014, 15, R43.	13.9	212
31	Community-driven development for computational biology at Sprints, Hackathons and Codefests. BMC Bioinformatics, 2014, 15, S7.	1.2	42
32	Galaxy as a Platform for Identifying Candidate Pathogen Effectors. Methods in Molecular Biology, 2014, 1127, 3-15.	0.4	5
33	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	0.9	26
34	Resistance gene enrichment sequencing (R-Seq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. Plant Journal, 2013, 76, 530-544.	2.8	367
35	Using Tablet for visual exploration of second-generation sequencing data. Briefings in Bioinformatics, 2013, 14, 193-202.	3.2	836
36	Activation of hatching in diapaused and quiescent <i>Globodera pallida</i> . Parasitology, 2013, 140, 445-454.	0.7	12

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37	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
38	Sprints, Hackathons and Codefests as community gluons in computational biology. EMBnet Journal, 2013, 19, 40.	0.2	5
39	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. PeerJ, 2013, 1, e167.	0.9	159
40	Genome-Wide Identification of Genes Regulated by the Rcs Phosphorelay System in <i>Erwinia amylovora</i> . Molecular Plant-Microbe Interactions, 2012, 25, 6-17.	1.4	52
41	Identification and localisation of the NB-LRR gene family within the potato genome. BMC Genomics, 2012, 13, 75.	1.2	290
42	Bio.Phylo: A unified toolkit for processing, analyzing and visualizing phylogenetic trees in Biopython. BMC Bioinformatics, 2012, 13, 209.	1.2	117
43	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
44	Genetic characterization of the HrpL regulon of the fire blight pathogen <i>Erwinia amylovora</i> reveals novel virulence factors. Molecular Plant Pathology, 2012, 13, 160-173.	2.0	54
45	Comparison of transcript profiles in different life stages of the nematode <i>Globodera pallida</i> under different host potato genotypes. Molecular Plant Pathology, 2012, 13, 1120-1134.	2.0	14
46	Novel Bacteriophages Containing a Genome of Another Bacteriophage within Their Genomes. PLoS ONE, 2012, 7, e40683.	1.1	46
47	Partial sequence and RT-PCR diagnostic test for the plant rhabdovirus Raspberry vein chlorosis virus. Plant Pathology, 2011, 60, 462-467.	1.2	12
48	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . PLoS Pathogens, 2011, 7, e1002219.	2.1	351
49	Evolution of Relative Reading Frame Bias in Unidirectional Prokaryotic Gene Overlaps. Molecular Biology and Evolution, 2010, 27, 753-756.	3.5	14
50	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
51	Evolution of prokaryotic two-component systems: insights from comparative genomics. Amino Acids, 2009, 37, 459-466.	1.2	58
52	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
53	Biopython: freely available Python tools for computational molecular biology and bioinformatics. Bioinformatics, 2009, 25, 1422-1423.	1.8	4,097
54	Two-component systems of the myxobacteria: structure, diversity and evolutionary relationships. Microbiology (United Kingdom), 2008, 154, 360-372.	0.7	64

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55	Evolution of Prokaryotic Two-Component System Signaling Pathways: Gene Fusions and Fissions. Molecular Biology and Evolution, 2007, 24, 2355-2357.	3.5	47
56	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
57	Two-Component Signal Transduction Systems of the Myxobacteria. , 0, , 169-189.		8
58	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	0.8	0