

John Parkinson

List of Publications by Year in Descending Order

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Version: 2024-04-27

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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.

119
papers

9,650
citations

47
h-index

97
g-index

137
ext. papers

11,181
ext. citations

10
avg, IF

5.37
L-index

#	Paper	IF	Citations
119	Performance of distinct microbial based solutions in a <i>Campylobacter</i> infection challenge model in poultry.. <i>Animal Microbiome</i> , 2022 , 4, 2	4.1	1
118	Effects of therapeutic levels of dietary antibiotics on the cecal microbiome composition of broiler chickens.. <i>Poultry Science</i> , 2022 , 101, 101864	3.9	0
117	Micronutrient supplements can promote disruptive protozoan and fungal communities in the developing infant gut. <i>Nature Communications</i> , 2021 , 12, 6729	17.4	3
116	<i>E.coli</i> Nissle increases transcription of flagella assembly and formate hydrogenlyase genes in response to colitis. <i>Gut Microbes</i> , 2021 , 13, 1994832	8.8	0
115	A new platform for high-throughput therapy testing on iPSC-derived lung progenitor cells from cystic fibrosis patients. <i>Stem Cell Reports</i> , 2021 , 16, 2825-2837	8	5
114	Blindly Controlled Magnetically Actuated Capsule for Noninvasive Sampling of the Gastrointestinal Microbiome. <i>IEEE/ASME Transactions on Mechatronics</i> , 2021 , 1-1	5.5	6
113	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020 , 10, 333-350.e14	10.6	13
112	Accumulation of genetic variants associated with immunity in the selective breeding of broilers. <i>BMC Genetics</i> , 2020 , 21, 5	2.6	2
111	A systematic pipeline for classifying bacterial operons reveals the evolutionary landscape of biofilm machineries. <i>PLoS Computational Biology</i> , 2020 , 16, e1007721	5	14
110	Discovery and characterization of a Gram-positive Pel polysaccharide biosynthetic gene cluster. <i>PLoS Pathogens</i> , 2020 , 16, e1008281	7.6	16
109	Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. <i>ELife</i> , 2020 , 9,	8.9	6
108	Commensal gut microbiota can modulate adaptive immune responses in chickens vaccinated with whole inactivated avian influenza virus subtype H9N2. <i>Vaccine</i> , 2019 , 37, 6640-6647	4.1	18
107	PopNetD3-A Network-Based Web Resource for Exploring Population Structure. <i>Genome Biology and Evolution</i> , 2019 , 11, 1730-1735	3.9	1
106	Influenza A virus subtype H9N2 infection disrupts the composition of intestinal microbiota of chickens. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	27
105	Improved enzyme annotation with EC-specific cutoffs using DETECT v2. <i>Bioinformatics</i> , 2018 , 34, 3393-3395	3.95	11
104	Comparative transcriptomic analyses and single-cell RNA sequencing of the freshwater planarian <i>Schmidtea mediterranea</i> identify major cell types and pathway conservation. <i>Genome Biology</i> , 2018 , 19, 124	18.3	24
103	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018 , 36, 103-112	44.5	68

102	Lactobacillus elicits a Marmite effect on the chicken cecal microbiome. <i>Npj Biofilms and Microbiomes</i> , 2018 , 4, 27	8.2	12
101	Design and application of a novel two-amplicon approach for defining eukaryotic microbiota. <i>Microbiome</i> , 2018 , 6, 228	16.6	8
100	Analyzing Metabolic Pathways in Microbiomes. <i>Methods in Molecular Biology</i> , 2018 , 1849, 291-307	1.4	
99	Characterization of Eukaryotic Microbiome Using 18S Amplicon Sequencing. <i>Methods in Molecular Biology</i> , 2018 , 1849, 29-48	1.4	5
98	Gut microbiota-mediated protection against influenza virus subtype H9N2 in chickens is associated with modulation of the innate responses. <i>Scientific Reports</i> , 2018 , 8, 13189	4.9	40
97	Genomics of apicomplexan parasites. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017 , 52, 254-273	8.7	16
96	Chemogenetic Interrogation of a Brain-wide Fear Memory Network in Mice. <i>Neuron</i> , 2017 , 94, 363-374.e43.9	43.9	119
95	PopNet: A Markov Clustering Approach to Study Population Genetic Structure. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1799-1811	8.3	3
94	Malaria parasites possess a telomere repeat-binding protein that shares ancestry with transcription factor IIIA. <i>Nature Microbiology</i> , 2017 , 2, 17033	26.6	12
93	Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. <i>Microbiome</i> , 2017 , 5, 117	16.6	8
92	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- κ B Signaling. <i>Cell Systems</i> , 2017 , 5, 564-577.e12	10.6	37
91	Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. <i>Microbiome</i> , 2016 , 4, 2	16.6	67
90	PhyloPro2.0: a database for the dynamic exploration of phylogenetically conserved proteins and their domain architectures across the Eukarya. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	5
89	Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic <i>Toxoplasma gondii</i> genomes. <i>Nature Communications</i> , 2016 , 7, 10147	17.4	151
88	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2016 , 2, 16216	26.6	69
87	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. <i>Data in Brief</i> , 2016 , 6, 715-21	1.2	5
86	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in <i>Escherichia coli</i> . <i>Cell Reports</i> , 2016 , 14, 648-661	10.6	23
85	The role of palmitoylation for protein recruitment to the inner membrane complex of the malaria parasite. <i>Journal of Biological Chemistry</i> , 2015 , 290, 1712-28	5.4	46

84	Hyperscape: visualization for complex biological networks. <i>Bioinformatics</i> , 2015 , 31, 3390-1	7.2	5
83	Systems-based analysis of the <i>Sarcocystis neuropa</i> genome identifies pathways that contribute to a heteroxenous life cycle. <i>MBio</i> , 2015 , 6,	7.8	37
82	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015 , 525, 339-44	50.4	325
81	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. <i>PLoS ONE</i> , 2015 , 10, e0130902	3.7	17
80	Comparative Genomics and Evolutionary Modularity of Prokaryotes. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 883, 77-96	3.6	1
79	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014 , 24, 1676-85	9.7	121
78	New tricks for "old" domains: how novel architectures and promiscuous hubs contributed to the organization and evolution of the ECM. <i>Genome Biology and Evolution</i> , 2014 , 6, 2897-917	3.9	11
77	Quantitative genome-wide genetic interaction screens reveal global epistatic relationships of protein complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004120	6	71
76	Comparison of assembly algorithms for improving rate of metatranscriptomic functional annotation. <i>Microbiome</i> , 2014 , 2, 39	16.6	39
75	IDBA-MT: de novo assembler for metatranscriptomic data generated from next-generation sequencing technology. <i>Journal of Computational Biology</i> , 2013 , 20, 540-50	1.7	32
74	Sequencing and annotation of the <i>Ophiostoma ulmi</i> genome. <i>BMC Genomics</i> , 2013 , 14, 162	4.5	34
73	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013 , 496, 57-63	50.4	483
72	Metabolic reconstruction identifies strain-specific regulation of virulence in <i>Toxoplasma gondii</i> . <i>Molecular Systems Biology</i> , 2013 , 9, 708	12.2	35
71	Identification of a functional connectome for long-term fear memory in mice. <i>PLoS Computational Biology</i> , 2013 , 9, e1002853	5	148
70	The apicomplexan inner membrane complex. <i>Frontiers in Bioscience - Landmark</i> , 2013 , 18, 982-92	2.8	20
69	The VPS33B-binding protein VPS16B is required in megakaryocyte and platelet granule biogenesis. <i>Blood</i> , 2012 , 120, 5032-40	2.2	67
68	Polymorphisms in the human tropoelastin gene modify in vitro self-assembly and mechanical properties of elastin-like polypeptides. <i>PLoS ONE</i> , 2012 , 7, e46130	3.7	15
67	Toward a systems level view of the ECM and related proteins: a framework for the systematic definition and analysis of biological systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 1522-44	4.2	20

66	A transcriptomic analysis of <i>Echinococcus granulosus</i> larval stages: implications for parasite biology and host adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1897	4.8	51
65	Comparative genomics of the apicomplexan parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : Coccidia differing in host range and transmission strategy. <i>PLoS Pathogens</i> , 2012 , 8, e1002567	7.6	154
64	Modelling the self-assembly of elastomeric proteins provides insights into the evolution of their domain architectures. <i>PLoS Computational Biology</i> , 2012 , 8, e1002406	5	8
63	Evolution and architecture of the inner membrane complex in asexual and sexual stages of the malaria parasite. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2113-32	8.3	77
62	Integrated bioinformatic and targeted deletion analyses of the SRS gene superfamily identify SRS29C as a negative regulator of <i>Toxoplasma</i> virulence. <i>MBio</i> , 2012 , 3,	7.8	53
61	Generation and analysis of a mouse intestinal metatranscriptome through Illumina based RNA-sequencing. <i>PLoS ONE</i> , 2012 , 7, e36009	3.7	49
60	Genetic interaction maps in <i>Escherichia coli</i> reveal functional crosstalk among cell envelope biogenesis pathways. <i>PLoS Genetics</i> , 2011 , 7, e1002377	6	76
59	Mutations in NBEAL2, encoding a BEACH protein, cause gray platelet syndrome. <i>Nature Genetics</i> , 2011 , 43, 738-40	36.3	207
58	Post-genomics resources and tools for studying apicomplexan metabolism. <i>Trends in Parasitology</i> , 2011 , 27, 131-40	6.4	12
57	DAnCER: disease-annotated chromatin epigenetics resource. <i>Nucleic Acids Research</i> , 2011 , 39, D889-94	20.1	16
56	PhyloPro: a web-based tool for the generation and visualization of phylogenetic profiles across Eukarya. <i>Bioinformatics</i> , 2011 , 27, 877-8	7.2	8
55	Characterization of the <i>Arabidopsis thaliana</i> exocyst complex gene families by phylogenetic, expression profiling, and subcellular localization studies. <i>New Phytologist</i> , 2010 , 185, 401-19	9.8	63
54	DETECT--a density estimation tool for enzyme classification and its application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2010 , 26, 1690-8	7.2	28
53	A comprehensive analysis of structural and sequence conservation in the TetR family transcriptional regulators. <i>Journal of Molecular Biology</i> , 2010 , 400, 847-64	6.5	101
52	The evolutionary landscape of the chromatin modification machinery reveals lineage specific gains, expansions, and losses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 2075-89	4.2	15
51	Expanding the landscape of chromatin modification (CM)-related functional domains and genes in human. <i>PLoS ONE</i> , 2010 , 5, e14122	3.7	9
50	Identification of a VPS33B-Binding Protein That Facilitates Alpha Granule Formation In Human Megakaryocytes and Platelets.. <i>Blood</i> , 2010 , 116, 1444-1444	2.2	
49	A family of diverse Kunitz inhibitors from <i>Echinococcus granulosus</i> potentially involved in host-parasite cross-talk. <i>PLoS ONE</i> , 2009 , 4, e7009	3.7	30

48	Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4-2 using proteome arrays. <i>Molecular Systems Biology</i> , 2009 , 5, 333	12.2	100
47	The Modular Organization of Protein Interactions in Escherichia coli. <i>PLoS Computational Biology</i> , 2009 , 5, e1000523	5	60
46	The origins of apicomplexan sequence innovation. <i>Genome Research</i> , 2009 , 19, 1202-13	9.7	53
45	Expressed sequence tags: an overview. <i>Methods in Molecular Biology</i> , 2009 , 533, 1-12	1.4	74
44	Phylogenomic analysis of EST datasets. <i>Methods in Molecular Biology</i> , 2009 , 533, 257-76	1.4	2
43	The conservation and evolutionary modularity of metabolism. <i>Genome Biology</i> , 2009 , 10, R63	18.3	99
42	SubSequer: a graph-based approach for the detection and identification of repetitive elements in low-complexity sequences. <i>Bioinformatics</i> , 2008 , 24, 1016-7	7.2	1
41	A systematic analysis of intronic sequences downstream of 5Rsplice sites reveals a widespread role for U-rich motifs and TIA1/TIAL1 proteins in alternative splicing regulation. <i>Genome Research</i> , 2008 , 18, 1247-58	9.7	67
40	Bacteriome.org--an integrated protein interaction database for E. coli. <i>Nucleic Acids Research</i> , 2008 , 36, D632-6	20.1	43
39	Ubiquitination screen using protein microarrays for comprehensive identification of Rsp5 substrates in yeast. <i>Molecular Systems Biology</i> , 2007 , 3, 116	12.2	126
38	Comparative genomics of elastin: Sequence analysis of a highly repetitive protein. <i>Matrix Biology</i> , 2007 , 26, 524-40	11.4	54
37	The global landscape of sequence diversity. <i>Genome Biology</i> , 2007 , 8, R238	18.3	9
36	Draft genome of the filarial nematode parasite Brugia malayi. <i>Science</i> , 2007 , 317, 1756-60	33.3	513
35	Cell++--simulating biochemical pathways. <i>Bioinformatics</i> , 2006 , 22, 2918-25	7.2	29
34	Codon usage patterns in Nematoda: analysis based on over 25 million codons in thirty-two species. <i>Genome Biology</i> , 2006 , 7, R75	18.3	42
33	Sequences and domain structures of mammalian, avian, amphibian and teleost tropoelastins: Clues to the evolutionary history of elastins. <i>Matrix Biology</i> , 2006 , 25, 492-504	11.4	68
32	Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. <i>Nature</i> , 2006 , 440, 637-43	50.4	2327
31	PartiGeneDB--collating partial genomes. <i>Nucleic Acids Research</i> , 2005 , 33, D303-7	20.1	8

30	Potential roles for diatomists in nanotechnology. <i>Journal of Nanoscience and Nanotechnology</i> , 2005 , 5, 35-40	1.3	23
29	Interaction network containing conserved and essential protein complexes in Escherichia coli. <i>Nature</i> , 2005 , 433, 531-7	50.4	951
28	Large-scale modelling as a route to multiple surface comparisons of the CCP module family. <i>Protein Engineering, Design and Selection</i> , 2005 , 18, 379-88	1.9	43
27	NEMBASE: a resource for parasitic nematode ESTs. <i>Nucleic Acids Research</i> , 2004 , 32, D427-30	20.1	59
26	PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004 , 20, 1398-404	7.2	127
25	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004 , 36, 1259-67	36.3	209
24	Signal sequence analysis of expressed sequence tags from the nematode Nippostrongylus brasiliensis and the evolution of secreted proteins in parasites. <i>Genome Biology</i> , 2004 , 5, R39	18.3	54
23	Expressed sequence tags: analysis and annotation. <i>Methods in Molecular Biology</i> , 2004 , 270, 93-126	1.4	8
22	400000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003 , 19, 283-6	6.4	53
21	Caenorhabditis elegans-applications to nematode genomics. <i>Comparative and Functional Genomics</i> , 2003 , 4, 194-202		2
20	The earthworm Expressed Sequence Tag project. <i>Pedobiologia</i> , 2003 , 47, 447-451	1.7	15
19	SimiTri--visualizing similarity relationships for groups of sequences. <i>Bioinformatics</i> , 2003 , 19, 390-5	7.2	59
18	Making sense of EST sequences by CLOBBing them. <i>BMC Bioinformatics</i> , 2002 , 3, 31	3.6	74
17	IL-4 dependent alternatively-activated macrophages have a distinctive in vivo gene expression phenotype. <i>BMC Immunology</i> , 2002 , 3, 7	3.7	259
16	The Brugia malayi genome project: expressed sequence tags and gene discovery. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2002 , 96, 7-17	2	57
15	200000 nematode expressed sequence tags on the Net. <i>Trends in Parasitology</i> , 2001 , 17, 394-396	6.4	31
14	Conserved surface-exposed K/R-X-K/R motifs and net positive charge on poxvirus complement control proteins serve as putative heparin binding sites and contribute to inhibition of molecular interactions with human endothelial cells: a novel mechanism for evasion of host defense. <i>Journal of Virology</i> , 2000 , 74, 5659-66	6.6	88
13	Dissecting sites important for complement regulatory activity in membrane cofactor protein (MCP; CD46). <i>Journal of Biological Chemistry</i> , 2000 , 275, 37692-701	5.4	106

12	A family of secreted mucins from the parasitic nematode <i>Toxocara canis</i> bears diverse mucin domains but shares similar flanking six-cysteine repeat motifs. <i>Journal of Biological Chemistry</i> , 2000 , 275, 39600-7	5.4	66
11	Beyond micromachining: the potential of diatoms. <i>Trends in Biotechnology</i> , 1999 , 17, 190-6	15.1	181
10	Centric diatom morphogenesis: a model based on a DLA algorithm investigating the potential role of microtubules. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 1999 , 1452, 89-102	4.9	55
9	Central modules of the vaccinia virus complement control protein are not in extensive contact. <i>Biochemical Journal</i> , 1999 , 344, 167-175	3.8	35
8	Central modules of the vaccinia virus complement control protein are not in extensive contact. <i>Biochemical Journal</i> , 1999 , 344, 167	3.8	17
7	The mechanical properties of simulated collagen fibrils. <i>Journal of Biomechanics</i> , 1997 , 30, 549-54	2.9	39
6	Simple physical model of collagen fibrillogenesis based on diffusion limited aggregation. <i>Journal of Molecular Biology</i> , 1995 , 247, 823-831	6.5	47
5	Self-assembly of rodlike particles in two dimensions: A simple model for collagen fibrillogenesis. <i>Physical Review E</i> , 1994 , 50, 2963-2966	2.4	21
4	Discovery and characterization of a Gram-positive Pel polysaccharide biosynthetic gene cluster		2
3	A systematic pipeline for classifying bacterial operons reveals the evolutionary landscape of biofilm machineries		
2	Gist In ensemble approach to the taxonomic classification of metatranscriptomic sequence data		1
1	MetaPro: A scalable and reproducible data processing and analysis pipeline for metatranscriptomic investigation of microbial communities		1