

# John Parkinson

## List of Publications by Year in descending order

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Version: 2024-02-01

121  
papers

12,135  
citations

38720

50  
h-index

27389

106  
g-index

137  
all docs

137  
docs citations

137  
times ranked

16195  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.   | 13.7 | 2,681     |
| 2  | Interaction network containing conserved and essential protein complexes in <i>Escherichia coli</i> . <i>Nature</i> , 2005, 433, 531-537.  | 13.7 | 1,093     |
| 3  | The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.   | 13.7 | 603       |
| 4  | Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.   | 6.0  | 571       |
| 5  | Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.   | 13.7 | 478       |
| 6  | IL-4 dependent alternatively-activated macrophages have a distinctive in vivo gene expression phenotype. <i>BMC Immunology</i> , 2002, 3, 7.   | 0.9  | 290       |
| 7  | Identification of a Functional Connectome for Long-Term Fear Memory in Mice. <i>PLoS Computational Biology</i> , 2013, 9, e1002853.  | 1.5  | 246       |
| 8  | Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic <i>Toxoplasma gondii</i> genomes. <i>Nature Communications</i> , 2016, 7, 10147.                                   | 5.8  | 243       |
| 9  | A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004, 36, 1259-1267.  | 9.4  | 239       |
| 10 | Mutations in NBEAL2, encoding a BEACH protein, cause gray platelet syndrome. <i>Nature Genetics</i> , 2011, 43, 738-740.   | 9.4  | 239       |
| 11 | Chemogenetic Interrogation of a Brain-wide Fear Memory Network in Mice. <i>Neuron</i> , 2017, 94, 363-374.e4.  | 3.8  | 211       |
| 12 | 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. | 2.1  | 206       |
| 13 | Beyond micromachining: the potential of diatoms. <i>Trends in Biotechnology</i> , 1999, 17, 190-196.   | 4.9  | 204       |
| 14 | Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.  | 2.4  | 176       |
| 15 | Ubiquitination screen using protein microarrays for comprehensive identification of Rsp5 substrates in yeast. <i>Molecular Systems Biology</i> , 2007, 3, 116.   | 3.2  | 145       |
| 16 | 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, 2113-2132.                                     | 3.5  | 135       |
| 17 | The conservation and evolutionary modularity of metabolism. <i>Genome Biology</i> , 2009, 10, R63.   | 13.9 | 134       |
| 18 | A Comprehensive Analysis of Structural and Sequence Conservation in the TetR Family Transcriptional Regulators. <i>Journal of Molecular Biology</i> , 2010, 400, 847-864.  | 2.0  | 134       |

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|----|--|-----|-----------|
| 19 | PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004, 20, 1398-1404.  | 1.8 | 129       |
| 20 | Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4a using proteome arrays. <i>Molecular Systems Biology</i> , 2009, 5, 333.  | 3.2 | 128       |
| 21 | Dissecting Sites Important for Complement Regulatory Activity in Membrane Cofactor Protein (MCP). <i>J Biol Chem</i> , 2007, 282, 11743-11752.   | 1.6 | 126       |
| 22 | Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. <i>Microbiome</i> , 2016, 4, 2.  | 4.9 | 118       |
| 23 | Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.  | 9.4 | 110       |
| 24 | The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.  | 5.9 | 107       |
| 25 | 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.  | 1.5 | 96        |
| 26 | Genetic Interaction Maps in <i>Escherichia coli</i> Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002377.   | 1.5 | 95        |
| 27 | 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, 5659-5666. | 1.5 | 94        |
| 28 | A systematic analysis of intronic sequences downstream of 5' splice sites reveals a widespread role for U-rich motifs and TIA1/TIAL1 proteins in alternative splicing regulation. <i>Genome Research</i> , 2008, 18, 1247-1258.  | 2.4 | 90        |
| 29 | Making sense of EST sequences by CLOBBing them. <i>BMC Bioinformatics</i> , 2002, 3, 31.   | 1.2 | 86        |
| 30 | Expressed Sequence Tags: An Overview. <i>Methods in Molecular Biology</i> , 2009, 533, 1-12.   | 0.4 | 86        |
| 31 | 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, 39600-39607.   | 1.6 | 81        |
| 32 | 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, .   | 1.8 | 81        |
| 33 | 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, 401-419.  | 3.5 | 77        |
| 34 | 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.  | 1.5 | 76        |
| 35 | The VPS33B-binding protein VPS16B is required in megakaryocyte and platelet $\alpha$ -granule biogenesis. <i>Blood</i> , 2012, 120, 5032-5040.   | 0.6 | 76        |
| 36 | The Modular Organization of Protein Interactions in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2009, 5, e1000523.   | 1.5 | 72        |

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|----|---|------|-----------|
| 37 | 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.           | 1.3  | 72        |
| 38 | 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. | 1.9  | 68        |
| 39 | The <i>Brugia malayi</i> genome project: expressed sequence tags and gene discovery. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2002, 96, 7-17.                      | 0.7  | 67        |
| 40 | Comparative genomics of elastin: Sequence analysis of a highly repetitive protein. <i>Matrix Biology</i> , 2007, 26, 524-540.   | 1.5  | 67        |
| 41 | Comparison of assembly algorithms for improving rate of metatranscriptomic functional annotation. <i>Microbiome</i> , 2014, 2, 39.  | 4.9  | 67        |
| 42 | The Role of Palmitoylation for Protein Recruitment to the Inner Membrane Complex of the Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2015, 290, 1712-1728.                              | 1.6  | 66        |
| 43 | NEMBASE: a resource for parasitic nematode ESTs. <i>Nucleic Acids Research</i> , 2004, 32, 427D-430.  | 6.5  | 65        |
| 44 | 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.                | 1.6  | 64        |
| 45 | The origins of apicomplexan sequence innovation. <i>Genome Research</i> , 2009, 19, 1202-1213.  | 2.4  | 63        |
| 46 | Simple physical model of collagen fibrillogenesis based on diffusion limited aggregation. <i>Journal of Molecular Biology</i> , 1995, 247, 823-831.   | 2.0  | 62        |
| 47 | SimiTri-visualizing similarity relationships for groups of sequences. <i>Bioinformatics</i> , 2003, 19, 390-395.  | 1.8  | 62        |
| 48 | 400,000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003, 19, 283-286.  | 1.5  | 61        |
| 49 | Codon usage patterns in Nematoda: analysis based on over 25 million codons in thirty-two species. <i>Genome Biology</i> , 2006, 7, R75.   | 13.9 | 60        |
| 50 | Signal sequence analysis of expressed sequence tags from the nematode <i>Nippostrongylus brasiliensis</i> and the evolution of secreted proteins in parasites. <i>Genome Biology</i> , 2004, 5, R39.  | 13.9 | 59        |
| 51 | Generation and Analysis of a Mouse Intestinal Metatranscriptome through Illumina Based RNA-Sequencing. <i>PLoS ONE</i> , 2012, 7, e36009.   | 1.1  | 52        |
| 52 | Systems-Based Analysis of the <i>Sarcocystis neurona</i> Genome Identifies Pathways That Contribute to a Heteroxenous Life Cycle. <i>MBio</i> , 2015, 6, .  | 1.8  | 49        |
| 53 | Metabolic reconstruction identifies strain-specific regulation of virulence in <i>Toxoplasma gondii</i> . <i>Molecular Systems Biology</i> , 2013, 9, 708.  | 3.2  | 48        |
| 54 | BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.  | 2.9  | 48        |

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|----|---|-----|-----------|
| 55 | Bacteriome.org an integrated protein interaction database for E. coli. <i>Nucleic Acids Research</i> , 2007, 36, D632-D636.   | 6.5 | 47        |
| 56 | Large-scale modelling as a route to multiple surface comparisons of the CCP module family. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 379-388.  | 1.0 | 45        |
| 57 | IDBA-MT: <i>De Novo</i> Assembler for Metatranscriptomic Data Generated from Next-Generation Sequencing Technology. <i>Journal of Computational Biology</i> , 2013, 20, 540-550.  | 0.8 | 45        |
| 58 | A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- $\kappa$ B Signaling. <i>Cell Systems</i> , 2017, 5, 564-577.e12.                     | 2.9 | 44        |
| 59 | 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. | 3.8 | 44        |
| 60 | The mechanical properties of simulated collagen fibrils. <i>Journal of Biomechanics</i> , 1997, 30, 549-554.  | 0.9 | 41        |
| 61 | Sequencing and annotation of the <i>Ophiostoma ulmigenome</i> . <i>BMC Genomics</i> , 2013, 14, 162.  | 1.2 | 40        |
| 62 | Identification of Candidate Adherent-Invasive E. coli Signature Transcripts by Genomic/Transcriptomic Analysis. <i>PLoS ONE</i> , 2015, 10, e0130902.   | 1.1 | 40        |
| 63 | Influenza A virus subtype H9N2 infection disrupts the composition of intestinal microbiota of chickens. <i>FEMS Microbiology Ecology</i> , 2018, 94, .  | 1.3 | 39        |
| 64 | Central modules of the vaccinia virus complement control protein are not in extensive contact. <i>Biochemical Journal</i> , 1999, 344, 167-175.   | 1.7 | 38        |
| 65 | 200,000 nematode expressed sequence tags on the Net. <i>Trends in Parasitology</i> , 2001, 17, 394-396.   | 1.5 | 36        |
| 66 | A membranous system in the spotlight. <i>Frontiers in Bioscience - Landmark</i> , 2013, 18, 982.  | 3.0 | 36        |
| 67 | Cell++ simulating biochemical pathways. <i>Bioinformatics</i> , 2006, 22, 2918-2925.  | 1.8 | 35        |
| 68 | DETECT—a Density Estimation Tool for Enzyme Classification and its application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2010, 26, 1690-1698.   | 1.8 | 35        |
| 69 | 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.   | 2.9 | 34        |
| 70 | 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.   | 1.1 | 33        |
| 71 | 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.                                 | 1.7 | 31        |
| 72 | Discovery and characterization of a Gram-positive Pel polysaccharide biosynthetic gene cluster. <i>PLoS Pathogens</i> , 2020, 16, e1008281.   | 2.1 | 30        |

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|----|---|-----|-----------|
| 73 | Potential Roles for Diatomists in Nanotechnology. <i>Journal of Nanoscience and Nanotechnology</i> , 2005, 5, 35-40.  | 0.9 | 29        |
| 74 | A systematic pipeline for classifying bacterial operons reveals the evolutionary landscape of biofilm machineries. <i>PLoS Computational Biology</i> , 2020, 16, e1007721.  | 1.5 | 28        |
| 75 | Self-assembly of rodlike particles in two dimensions: A simple model for collagen fibrillogenesis. <i>Physical Review E</i> , 1994, 50, 2963-2966.  | 0.8 | 26        |
| 76 | 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, 1522-1544. | 1.5 | 26        |
| 77 | Genomics of apicomplexan parasites. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 254-273.  | 2.3 | 26        |
| 78 | Blindly Controlled Magnetically Actuated Capsule for Noninvasive Sampling of the Gastrointestinal Microbiome. <i>IEEE/ASME Transactions on Mechatronics</i> , 2021, 26, 2616-2628.  | 3.7 | 22        |
| 79 | The earthworm Expressed Sequence Tag project. <i>Pedobiologia</i> , 2003, 47, 447-451.  | 0.5 | 21        |
| 80 | Improved enzyme annotation with EC-specific cutoffs using DETECT v2. <i>Bioinformatics</i> , 2018, 34, 3393-3395.   | 1.8 | 21        |
| 81 | Central modules of the vaccinia virus complement control protein are not in extensive contact. <i>Biochemical Journal</i> , 1999, 344, 167.   | 1.7 | 19        |
| 82 | DAnCER: Disease-Annotated Chromatin Epigenetics Resource. <i>Nucleic Acids Research</i> , 2011, 39, D889-D894.  | 6.5 | 19        |
| 83 | 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.   | 2.3 | 19        |
| 84 | <i>Lactobacillus</i> elicits a 'Marmite effect' on the chicken cecal microbiome. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 27.   | 2.9 | 18        |
| 85 | Design and application of a novel two-amplicon approach for defining eukaryotic microbiota. <i>Microbiome</i> , 2018, 6, 228.   | 4.9 | 18        |
| 86 | The evolutionary landscape of the chromatin modification machinery reveals lineage specific gains, expansions, and losses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2075-2089.                 | 1.5 | 17        |
| 87 | Malaria parasites possess a telomere repeat-binding protein that shares ancestry with transcription factor IIIA. <i>Nature Microbiology</i> , 2017, 2, 17033.   | 5.9 | 17        |
| 88 | Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. <i>Microbiome</i> , 2017, 5, 117.   | 4.9 | 17        |
| 89 | Micronutrient supplements can promote disruptive protozoan and fungal communities in the developing infant gut. <i>Nature Communications</i> , 2021, 12, 6729.  | 5.8 | 17        |
| 90 | 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.   | 1.1 | 16        |

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|-----|---|------|-----------|
| 91  | Post-genomics resources and tools for studying apicomplexan metabolism. Trends in Parasitology, 2011, 27, 131-140.  | 1.5  | 14        |
| 92  | New Tricks for "Old" Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. Genome Biology and Evolution, 2014, 6, 2897-2917.  | 1.1  | 14        |
| 93  | Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. ELife, 2020, 9, .   | 2.8  | 14        |
| 94  | Accumulation of genetic variants associated with immunity in the selective breeding of broilers. BMC Genetics, 2020, 21, 5.   | 2.7  | 13        |
| 95  | PhyloPro2.0: a database for the dynamic exploration of phylogenetically conserved proteins and their domain architectures across the Eukarya. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw013. | 1.4  | 12        |
| 96  | Expressed Sequence Tags: Analysis and Annotation<l>. , 2004, 270, 093-126.  |      | 11        |
| 97  | The global landscape of sequence diversity. Genome Biology, 2007, 8, R238.  | 13.9 | 11        |
| 98  | PhyloPro: a web-based tool for the generation and visualization of phylogenetic profiles across Eukarya. Bioinformatics, 2011, 27, 877-878.   | 1.8  | 10        |
| 99  | Characterization of Eukaryotic Microbiome Using 18S Amplicon Sequencing. Methods in Molecular Biology, 2018, 1849, 29-48.   | 0.4  | 10        |
| 100 | Expanding the Landscape of Chromatin Modification (CM)-Related Functional Domains and Genes in Human. PLoS ONE, 2010, 5, e14122.  | 1.1  | 10        |
| 101 | Modelling the Self-Assembly of Elastomeric Proteins Provides Insights into the Evolution of Their Domain Architectures. PLoS Computational Biology, 2012, 8, e1002406.  | 1.5  | 9         |
| 102 | PartiGeneDB--collating partial genomes. Nucleic Acids Research, 2004, 33, D303-D307.  | 6.5  | 8         |
| 103 | Performance of distinct microbial based solutions in a Campylobacter infection challenge model in poultry. Animal Microbiome, 2022, 4, 2.   | 1.5  | 8         |
| 104 | Hyperscape: visualization for complex biological networks. Bioinformatics, 2015, 31, 3390-3391.   | 1.8  | 7         |
| 105 | Effects of therapeutic levels of dietary antibiotics on the cecal microbiome composition of broiler chickens. Poultry Science, 2022, 101, 101864.   | 1.5  | 7         |
| 106 | Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. Data in Brief, 2016, 6, 715-721.   | 0.5  | 5         |
| 107 | PopNet: A Markov Clustering Approach to Study Population Genetic Structure. Molecular Biology and Evolution, 2017, 34, 1799-1811.   | 3.5  | 5         |
| 108 | SubSeqer: a graph-based approach for the detection and identification of repetitive elements in low-complexity sequences. Bioinformatics, 2008, 24, 1016-1017.  | 1.8  | 3         |

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|-----|--|-----|-----------|
| 109 | Caenorhabditis elegans Applications to Nematode Genomics. Comparative and Functional Genomics, 2003, 4, 194-202.   | 2.0 | 2         |
| 110 | Phylogenomic Analysis of EST Datasets. Methods in Molecular Biology, 2009, 533, 257-276.   | 0.4 | 2         |
| 111 | Comparative Genomics and Evolutionary Modularity of Prokaryotes. Advances in Experimental Medicine and Biology, 2015, 883, 77-96.                        | 0.8 | 2         |
| 112 | E.coli Nissle increases transcription of flagella assembly and formate hydrogenlyase genes in response to colitis. Gut Microbes, 2021, 13, 1994832.      | 4.8 | 2         |
| 113 | PopNetD A Network-Based Web Resource for Exploring Population Structure. Genome Biology and Evolution, 2019, 11, 1730-1735.                              | 1.1 | 1         |
| 114 | A MODEL OF TYPE I COLLAGEN FIBRILLOGENESIS BASED ON DIFFUSION LIMITED AGGREGATION. Journal of Biological Systems, 1995, 03, 1033-1039.                   | 0.5 | 0         |
| 115 | Exploring Parasite Gene Space. BMC Bioinformatics, 2005, 6, P27.   | 1.2 | 0         |
| 116 | Analyzing Metabolic Pathways in Microbiomes. Methods in Molecular Biology, 2018, 1849, 291-307.  | 0.4 | 0         |
| 117 | Identification of a VPS33B-Binding Protein That Facilitates Alpha Granule Formation In Human Megakaryocytes and Platelets.. Blood, 2010, 116, 1444-1444. | 0.6 | 0         |
| 118 | Title is missing!. , 2020, 16, e1007721.   |     | 0         |
| 119 | Title is missing!. , 2020, 16, e1007721.   |     | 0         |
| 120 | Title is missing!. , 2020, 16, e1007721.   |     | 0         |
| 121 | Title is missing!. , 2020, 16, e1007721.   |     | 0         |