

James David Wasmuth

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

3,018
citations

218677

26
h-index

276875

41
g-index

49
all docs

49
docs citations

49
times ranked

5064
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Draft Hybrid Genome Assembly of a Canadian <i>Cyclospora cayetanensis</i> Isolate. <i>Microbiology Resource Announcements</i> , 2022, 11, e0107221. | 0.6 | 4 |
| 2 | Genotyping Canadian <i>Cyclospora cayetanensis</i> Isolates to Supplement Cyclosporiasis Outbreak Investigations. <i>Microorganisms</i> , 2022, 10, 447. | 3.6 | 4 |
| 3 | Small Intestinal Levels of the Branched Short-Chain Fatty Acid Isovalerate Are Elevated during Infection with <i>Heligmosomoides polygyrus</i> and Can Promote Helminth Fecundity. <i>Infection and Immunity</i> , 2021, 89, e0022521. | 2.2 | 4 |
| 4 | Characterization of the β -tubulin gene family in <i>Ascaris lumbricoides</i> and <i>Ascaris suum</i> and its implication for the molecular detection of benzimidazole resistance. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009777. | 3.0 | 13 |
| 5 | Benchmarking hybrid assemblies of <i>Giardia</i> and prediction of widespread intra-isolate structural variation. <i>Parasites and Vectors</i> , 2020, 13, 108. | 2.5 | 8 |
| 6 | Horizontal transfer of a retrotransposon between parasitic nematodes and the common shrew. <i>Mobile DNA</i> , 2019, 10, 24. | 3.6 | 18 |
| 7 | Bovine viral diarrhea virus genomic variation within persistently infected cattle. <i>Infection, Genetics and Evolution</i> , 2018, 58, 218-223. | 2.3 | 20 |
| 8 | Improved enzyme annotation with EC-specific cutoffs using DETECT v2. <i>Bioinformatics</i> , 2018, 34, 3393-3395. | 4.1 | 21 |
| 9 | MIPhy: identify and quantify rapidly evolving members of large gene families. <i>PeerJ</i> , 2018, 6, e4873. | 2.0 | 11 |
| 10 | Expanding the view on the evolution of the nematode dauer signalling pathways: refinement through gene gain and pathway co-option. <i>BMC Genomics</i> , 2016, 17, 476. | 2.8 | 35 |
| 11 | Does the Arthropod Microbiota Impact the Establishment of Vector-Borne Diseases in Mammalian Hosts?. <i>PLoS Pathogens</i> , 2015, 11, e1004646. | 4.7 | 51 |
| 12 | Morphological Variability and Molecular Identification of <i>Uncinaria</i> spp. (Nematoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td). <i>Parasitology</i> , 2015, 101, 182-192. | 0.7 | 15 |
| 13 | Kablammo: an interactive, web-based BLAST results visualizer. <i>Bioinformatics</i> , 2015, 31, 1305-1306. | 4.1 | 63 |
| 14 | Exploring the Gastrointestinal "Nemabiome": Deep Amplicon Sequencing to Quantify the Species Composition of Parasitic Nematode Communities. <i>PLoS ONE</i> , 2015, 10, e0143559. | 2.5 | 181 |
| 15 | Figmap: a profile HMM to identify genes and bypass troublesome gene models in draft genomes. <i>Bioinformatics</i> , 2014, 30, 3266-3267. | 4.1 | 6 |
| 16 | Realizing the promise of parasite genomics. <i>Trends in Parasitology</i> , 2014, 30, 321-323. | 3.3 | 10 |
| 17 | Unravelling parasitic nematode natural history using population genetics. <i>Trends in Parasitology</i> , 2013, 29, 438-448. | 3.3 | 30 |
| 18 | The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , 2013, 14, R88. | 9.6 | 293 |

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|----|--|------|-----------|
| 19 | Characterization and comparative analysis of the complete <i>Haemonchus contortus</i> β -tubulin gene family and implications for benzimidazole resistance in strongylid nematodes. <i>International Journal for Parasitology</i> , 2013, 43, 465-475. | 3.1 | 53 |
| 20 | The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63. | 27.8 | 603 |
| 21 | HIV Infection Deregulates Tim-3 Expression on Innate Cells. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2013, 63, 161-167. | 2.1 | 43 |
| 22 | Metabolic reconstruction identifies strain-specific regulation of virulence in <i>Toxoplasma gondii</i> . <i>Molecular Systems Biology</i> , 2013, 9, 708. | 7.2 | 48 |
| 23 | HIV infection deregulates innate immunity to malaria despite combination antiretroviral therapy. <i>Aids</i> , 2013, 27, 325-335. | 2.2 | 19 |
| 24 | 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. | 3.0 | 72 |
| 25 | Comparative Genomics of the Apicomplexan Parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : <i>Coccidia</i> Differing in Host Range and Transmission Strategy. <i>PLoS Pathogens</i> , 2012, 8, e1002567. | 4.7 | 206 |
| 26 | 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, . | 4.1 | 81 |
| 27 | Identification of Two Novel Coccidian Species Shed by California Sea Lions (<i>Zalophus californianus</i>). <i>Journal of Parasitology</i> , 2012, 98, 347-354. | 0.7 | 10 |
| 28 | The VPS33B-binding protein VPS16B is required in megakaryocyte and platelet α -granule biogenesis. <i>Blood</i> , 2012, 120, 5032-5040. | 1.4 | 76 |
| 29 | NEMBASE4: The nematode transcriptome resource. <i>International Journal for Parasitology</i> , 2011, 41, 881-894. | 3.1 | 60 |
| 30 | Intergenic Sequence Comparison of <i>Escherichia coli</i> Isolates Reveals Lifestyle Adaptations but Not Host Specificity. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7620-7632. | 3.1 | 56 |
| 31 | DETECT—a Density Estimation Tool for Enzyme Classification and its application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2010, 26, 1690-1698. | 4.1 | 35 |
| 32 | Structural and Functional Characterization of SporoSAG. <i>Journal of Biological Chemistry</i> , 2010, 285, 12063-12070. | 3.4 | 37 |
| 33 | Identification of a VPS33B-Binding Protein That Facilitates Alpha Granule Formation In Human Megakaryocytes and Platelets. <i>Blood</i> , 2010, 116, 1444-1444. | 1.4 | 0 |
| 34 | Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4 ϵ using proteome arrays. <i>Molecular Systems Biology</i> , 2009, 5, 333. | 7.2 | 128 |
| 35 | The origins of apicomplexan sequence innovation. <i>Genome Research</i> , 2009, 19, 1202-1213. | 5.5 | 63 |
| 36 | Obtaining Accurate Translations from Expressed Sequence Tags. <i>Methods in Molecular Biology</i> , 2009, 533, 221-239. | 0.9 | 5 |

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|----|--|-----|-----------|
| 37 | Patterns of Molecular Evolution in <i>Caenorhabditis</i> Preclude Ancient Origins of Selfing. <i>Genetics</i> , 2008, 178, 2093-2104. | 2.9 | 87 |
| 38 | On the Extent and Origins of Genic Novelty in the Phylum Nematoda. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e258. | 3.0 | 68 |
| 39 | Ubiquitination screen using protein microarrays for comprehensive identification of Rsp5 substrates in yeast. <i>Molecular Systems Biology</i> , 2007, 3, 116. | 7.2 | 145 |
| 40 | The Evolution of Biased Codon and Amino Acid Usage in Nematode Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 2303-2315. | 8.9 | 84 |
| 41 | PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004, 20, 1398-1404. | 4.1 | 129 |
| 42 | prot4EST: translating expressed sequence tags from neglected genomes. <i>BMC Bioinformatics</i> , 2004, 5, 187. | 2.6 | 118 |