

# 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	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	27.8	603
2	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
3	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.	4.7	206
4	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
5	Ubiquitination screen using protein microarrays for comprehensive identification of Rsp5 substrates in yeast. <i>Molecular Systems Biology</i> , 2007, 3, 116.	7.2	145
6	PartiGene--constructing partial genomes. <i>Bioinformatics</i> , 2004, 20, 1398-1404.	4.1	129
7	Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4 <sup>Δ2</sup> using proteome arrays. <i>Molecular Systems Biology</i> , 2009, 5, 333.	7.2	128
8	prot4EST: translating expressed sequence tags from neglected genomes. <i>BMC Bioinformatics</i> , 2004, 5, 187.	2.6	118
9	Patterns of Molecular Evolution in <i>Caenorhabditis</i> Preclude Ancient Origins of Selfing. <i>Genetics</i> , 2008, 178, 2093-2104.	2.9	87
10	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
11	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
12	The VPS33B-binding protein VPS16B is required in megakaryocyte and platelet $\alpha$ -granule biogenesis. <i>Blood</i> , 2012, 120, 5032-5040.	1.4	76
13	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
14	On the Extent and Origins of Genic Novelty in the Phylum Nematoda. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e258.	3.0	68
15	The origins of apicomplexan sequence innovation. <i>Genome Research</i> , 2009, 19, 1202-1213.	5.5	63
16	Kablammo: an interactive, web-based BLAST results visualizer. <i>Bioinformatics</i> , 2015, 31, 1305-1306.	4.1	63
17	NEMBASE4: The nematode transcriptome resource. <i>International Journal for Parasitology</i> , 2011, 41, 881-894.	3.1	60
18	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

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19	Characterization and comparative analysis of the complete <i>Haemonchus contortus</i> $\beta$ -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	Does the Arthropod Microbiota Impact the Establishment of Vector-Borne Diseases in Mammalian Hosts?. <i>PLoS Pathogens</i> , 2015, 11, e1004646.	4.7	51
21	Metabolic reconstruction identifies strain-specific regulation of virulence in <i>Toxoplasma gondii</i> . <i>Molecular Systems Biology</i> , 2013, 9, 708.	7.2	48
22	HIV Infection Deregulates Tim-3 Expression on Innate Cells. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2013, 63, 161-167.	2.1	43
23	Structural and Functional Characterization of SporoSAG. <i>Journal of Biological Chemistry</i> , 2010, 285, 12063-12070.	3.4	37
24	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
25	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
26	Unravelling parasitic nematode natural history using population genetics. <i>Trends in Parasitology</i> , 2013, 29, 438-448.	3.3	30
27	Improved enzyme annotation with EC-specific cutoffs using DETECT v2. <i>Bioinformatics</i> , 2018, 34, 3393-3395.	4.1	21
28	Bovine viral diarrhoea virus genomic variation within persistently infected cattle. <i>Infection, Genetics and Evolution</i> , 2018, 58, 218-223.	2.3	20
29	HIV infection deregulates innate immunity to malaria despite combination antiretroviral therapy. <i>Aids</i> , 2013, 27, 325-335.	2.2	19
30	Horizontal transfer of a retrotransposon between parasitic nematodes and the common shrew. <i>Mobile DNA</i> , 2019, 10, 24.	3.6	18
31	Morphological Variability and Molecular Identification of <i>Uncinaria</i> spp. (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 55). <i>Parasitology</i> , 2015, 101, 182-192.	0.7	15
32	Characterization of the $\beta$ -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
33	MIPhy: identify and quantify rapidly evolving members of large gene families. <i>PeerJ</i> , 2018, 6, e4873.	2.0	11
34	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
35	Realizing the promise of parasite genomics. <i>Trends in Parasitology</i> , 2014, 30, 321-323.	3.3	10
36	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

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37	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
38	Obtaining Accurate Translations from Expressed Sequence Tags. <i>Methods in Molecular Biology</i> , 2009, 533, 221-239.	0.9	5
39	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
40	Draft Hybrid Genome Assembly of a Canadian <i>Cyclospora cayetanensis</i> Isolate. <i>Microbiology Resource Announcements</i> , 2022, 11, e0107221.	0.6	4
41	Genotyping Canadian <i>Cyclospora cayetanensis</i> Isolates to Supplement Cyclosporiasis Outbreak Investigations. <i>Microorganisms</i> , 2022, 10, 447.	3.6	4
42	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