

Joel B Dacks

List of Publications by Year in descending order

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131
papers

9,374
citations

41344

49
h-index

43889

91
g-index

153
all docs

153
docs citations

153
times ranked

9885
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	12.6	731
2	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	27.8	448
3	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic "supergroups". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3859-3864.	7.1	444
4	The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642.	28.9	399
5	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377
6	A Eukaryote without a Mitochondrial Organelle. <i>Current Biology</i> , 2016, 26, 1274-1284.	3.9	302
7	Evolution of the eukaryotic membrane-trafficking system: origin, tempo and mode. <i>Journal of Cell Science</i> , 2007, 120, 2977-2985.	2.0	245
8	Evolution of the Multivesicular Body ESCRT Machinery; Retention Across the Eukaryotic Lineage. <i>Traffic</i> , 2008, 9, 1698-1716.	2.7	243
9	The Fifth Adaptor Protein Complex. <i>PLoS Biology</i> , 2011, 9, e1001170.	5.6	241
10	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>eLife</i> , 2015, 4, e06974.	6.0	198
11	Evolution of Filamentous Plant Pathogens: Gene Exchange across Eukaryotic Kingdoms. <i>Current Biology</i> , 2006, 16, 1857-1864.	3.9	197
12	Origin of H1 linker histones. <i>FASEB Journal</i> , 2001, 15, 34-42.	0.5	192
13	ARF GTPases and their GEFs and GAPs: concepts and challenges. <i>Molecular Biology of the Cell</i> , 2019, 30, 1249-1271.	2.1	188
14	Control systems for membrane fusion in the ancestral eukaryote; evolution of tethering complexes and SM proteins. <i>BMC Evolutionary Biology</i> , 2007, 7, 29.	3.2	186
15	Evolutionary Origins of the Eukaryotic Shikimate Pathway: Gene Fusions, Horizontal Gene Transfer, and Endosymbiotic Replacements. <i>Eukaryotic Cell</i> , 2006, 5, 1517-1531.	3.4	170
16	Molecular paleontology and complexity in the last eukaryotic common ancestor. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2013, 48, 373-396.	5.2	170
17	The First Sexual Lineage and the Relevance of Facultative Sex. <i>Journal of Molecular Evolution</i> , 1999, 48, 779-783.	1.8	143
18	Sculpting the endomembrane system in deep time: High resolution phylogenetics of Rab GTPases. <i>Journal of Cell Science</i> , 2012, 125, 2500-8.	2.0	139

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19	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. <i>Current Biology</i> , 2016, 26, 161-172.	3.9	137
20	A Role for the Ancient SNARE Syntaxin 17 in Regulating Mitochondrial Division. <i>Developmental Cell</i> , 2015, 32, 304-317.	7.0	126
21	Phylogeny of endocytic components yields insight into the process of nonendosymbiotic organelle evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 588-593.	7.1	120
22	Reconstructing/Deconstructing the Earliest Eukaryotes. <i>Cell</i> , 2001, 107, 419-425.	28.9	115
23	Characterization of TSET, an ancient and widespread membrane trafficking complex. <i>ELife</i> , 2014, 3, e02866.	6.0	114
24	First and last ancestors: reconstructing evolution of the endomembrane system with ESCRTs, vesicle coat proteins, and nuclear pore complexes. <i>Current Opinion in Cell Biology</i> , 2009, 21, 4-13.	5.4	112
25	Eukaryotic systematics: a user's guide for cell biologists and parasitologists. <i>Parasitology</i> , 2011, 138, 1638-1663.	1.5	106
26	Evolutionary reconstruction of the retromer complex and its function in <i>Trypanosoma brucei</i> . <i>Journal of Cell Science</i> , 2011, 124, 1496-1509.	2.0	102
27	Extreme genome diversity in the hyper-prevalent parasitic eukaryote <i>Blastocystis</i> . <i>PLoS Biology</i> , 2017, 15, e2003769.	5.6	99
28	Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.	3.8	98
29	Ancient Homology of the Mitochondrial Contact Site and Cristae Organizing System Points to an Endosymbiotic Origin of Mitochondrial Cristae. <i>Current Biology</i> , 2015, 25, 1489-1495.	3.9	95
30	Reconstructing the Evolution of the Endocytic System: Insights from Genomics and Molecular Cell Biology. <i>Advances in Experimental Medicine and Biology</i> , 2007, 607, 84-96.	1.6	94
31	The Ancient and Widespread Nature of the ER Mitochondria Encounter Structure. <i>Molecular Biology and Evolution</i> , 2013, 30, 2044-2049.	8.9	90
32	Rab protein evolution and the history of the eukaryotic endomembrane system. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3449-3465.	5.4	77
33	The changing view of eukaryogenesis – fossils, cells, lineages and how they all come together. <i>Journal of Cell Science</i> , 2016, 129, 3695-3703.	2.0	77
34	Tracing the Archaeal Origins of Eukaryotic Membrane-Trafficking System Building Blocks. <i>Molecular Biology and Evolution</i> , 2016, 33, 1528-1541.	8.9	77
35	Analyses of RNA Polymerase II Genes from Free-Living Protists: Phylogeny, Long Branch Attraction, and the Eukaryotic Big Bang. <i>Molecular Biology and Evolution</i> , 2002, 19, 830-840.	8.9	76
36	Evolution of specificity in the eukaryotic endomembrane system. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 330-340.	2.8	73

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37	Evolution and diversity of the Golgi body. <i>FEBS Letters</i> , 2009, 583, 3738-3745.	2.8	72
38	Oxymonads Are Closely Related to the Excavate Taxon <i>Trimastix</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 1034-1044.	8.9	67
39	Ultrastructural Description of <i>Breviata anathema</i> , N. Gen., N. Sp., the Organism Previously Studied as " <i>Mastigamoeba invertens</i> ". <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, 65-78.	1.7	64
40	Evolution of the Karyopherin- β Family of Nucleocytoplasmic Transport Factors; Ancient Origins and Continued Specialization. <i>PLoS ONE</i> , 2011, 6, e19308.	2.5	64
41	Novel syntaxin gene sequences from <i>Giardia</i> , <i>Trypanosoma</i> and algae: implications for the ancient evolution of the eukaryotic endomembrane system. <i>Journal of Cell Science</i> , 2002, 115, 1635-1642.	2.0	64
42	Comparative Genomic Analysis of Multi-Subunit Tethering Complexes Demonstrates an Ancient Pan-Eukaryotic Complement and Sculpting in Apicomplexa. <i>PLoS ONE</i> , 2013, 8, e76278.	2.5	61
43	Phylogenetic Artifacts Can be Caused by Leucine, Serine, and Arginine Codon Usage Heterogeneity: Dinoflagellate Plastid Origins as a Case Study. <i>Systematic Biology</i> , 2004, 53, 582-593.	5.6	60
44	Missing Pieces of an Ancient Puzzle: Evolution of the Eukaryotic Membrane-Trafficking System. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016048-a016048.	5.5	60
45	Evolutionary relationship between dinoflagellates bearing obligate diatom endosymbionts: insight into tertiary endosymbiosis.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 2075-2081.	1.7	58
46	Evolution of Tre-2/Bub2/Cdc16 (TBC) Rab GTPase-activating proteins. <i>Molecular Biology of the Cell</i> , 2013, 24, 1574-1583.	2.1	57
47	Novel syntaxin gene sequences from <i>Giardia</i> , <i>Trypanosoma</i> and algae: implications for the ancient evolution of the eukaryotic endomembrane system. <i>Journal of Cell Science</i> , 2002, 115, 1635-42.	2.0	57
48	Outerwear through the ages: evolutionary cell biology of vesicle coats. <i>Current Opinion in Cell Biology</i> , 2017, 47, 108-116.	5.4	56
49	Evidence for Golgi bodies in proposed 'Golgi-lacking' lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, S168-71.	2.6	55
50	ELMO Domains, Evolutionary and Functional Characterization of a Novel GTPase-activating Protein (GAP) Domain for Arf Protein Family GTPases. <i>Journal of Biological Chemistry</i> , 2012, 287, 39538-39553.	3.4	54
51	Evolution and Diversity of the Golgi. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a007849-a007849.	5.5	53
52	Implications of the new eukaryotic systematics for parasitologists. <i>Parasitology International</i> , 2008, 57, 97-104.	1.3	51
53	Arf3 Is Activated Uniquely at the trans-Golgi Network by Brefeldin A-inhibited Guanine Nucleotide Exchange Factors. <i>Molecular Biology of the Cell</i> , 2010, 21, 1836-1849.	2.1	49
54	The Oxymonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. <i>Molecular Biology and Evolution</i> , 2019, 36, 2292-2312.	8.9	49

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55	Evolutionary origins and specialisation of membrane transport. <i>Current Opinion in Cell Biology</i> , 2018, 53, 70-76.	5.4	47
56	Molecular Phylogeny of Three Oxymonad Genera: <i>Pyrsonympha</i> , <i>Dinenympha</i> and <i>Oxymonas</i> . <i>Journal of Eukaryotic Microbiology</i> , 2003, 50, 190-197.	1.7	46
57	Molecular and phylogenetic characterization of syntaxin genes from parasitic protozoa. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 123-136.	1.1	42
58	Pex3 peroxisome biogenesis proteins function in peroxisome inheritance as class V myosin receptors. <i>Journal of Cell Biology</i> , 2009, 187, 233-246.	5.2	42
59	Repeated secondary loss of adaptin complex genes in the Apicomplexa. <i>Parasitology International</i> , 2009, 58, 86-94.	1.3	42
60	Phylogenetic Placement of <i>Trichonympha</i> . <i>Journal of Eukaryotic Microbiology</i> , 1998, 45, 445-447.	1.7	41
61	Longin and <sc>GAF</sc> Domains: Structural Evolution and Adaptation to the Subcellular Trafficking Machinery. <i>Traffic</i> , 2014, 15, 104-121.	2.7	40
62	Reconstructing the Mosaic Glycolytic Pathway of the Anaerobic Eukaryote <i>Monocercomonoides</i> . <i>Eukaryotic Cell</i> , 2006, 5, 2138-2146.	3.4	38
63	The Single ENTHâ€Domain Protein of Trypanosomes; Endocytic Functions and Evolutionary Relationship with Epsin. <i>Traffic</i> , 2009, 10, 894-911.	2.7	38
64	Unexpected Ancient Paralogs and an Evolutionary Model for the COPII Coat Complex. <i>Genome Biology and Evolution</i> , 2015, 7, 1098-1109.	2.5	38
65	The Mitochondrial Genome and a 60â€b Nuclear DNA Segment from <i>Naegleria fowleri</i> , the Causative Agent of Primary Amoebic Meningoencephalitis. <i>Journal of Eukaryotic Microbiology</i> , 2013, 60, 179-191.	1.7	36
66	Ancient Complexity, Opisthokont Plasticity, and Discovery of the 11th Subfamily of Arf <sc>GAP</sc> Proteins. <i>Traffic</i> , 2013, 14, 636-649.	2.7	36
67	Evolution and Natural History of Membrane Trafficking in Eukaryotes. <i>Current Biology</i> , 2020, 30, R553-R564.	3.9	36
68	The cloning of one putative octopamine receptor and two putative serotonin receptors from the tobacco hawkmoth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 741-747.	2.7	35
69	Multivesicular bodies in the enigmatic amoeboflagellate <i>Breviata anathema</i> and the evolution of ESCRT 0. <i>Journal of Cell Science</i> , 2011, 124, 613-621.	2.0	35
70	A sophisticated, differentiated Golgi in the ancestor of eukaryotes. <i>BMC Biology</i> , 2018, 16, 27.	3.8	35
71	The Cell Biology of the Endocytic System from an Evolutionary Perspective. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016998-a016998.	5.5	34
72	How Oxymonads Lost Their Groove: An Ultrastructural Comparison of <i>Monocercomonoides</i> and Excavate Taxa. <i>Journal of Eukaryotic Microbiology</i> , 2002, 49, 239-248.	1.7	32

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73	The evolution of MICOS: Ancestral and derived functions and interactions. <i>Communicative and Integrative Biology</i> , 2015, 8, e1094593.	1.4	32
74	Interaction with the effector dynamin-related protein 1 (Drp1) is an ancient function of Rab32 subfamily proteins. <i>Cellular Logistics</i> , 2014, 4, e986399.	0.9	27
75	An evolutionary balance: conservation vs innovation in ciliate membrane trafficking. <i>Traffic</i> , 2017, 18, 18-28.	2.7	27
76	Evolutionary mechanisms for establishing eukaryotic cellular complexity. <i>Trends in Cell Biology</i> , 2014, 24, 435-442.	7.9	26
77	Next-Generation Sequencing Assessment of Eukaryotic Diversity in Oil Sands Tailings Ponds Sediments and Surface Water. <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 732-743.	1.7	26
78	Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate <i>Tetrahymena thermophila</i> . <i>Current Biology</i> , 2018, 28, 697-710.e13.	3.9	25
79	Resolving the homology-function relationship through comparative genomics of membrane-trafficking machinery and parasite cell biology. <i>Molecular and Biochemical Parasitology</i> , 2016, 209, 88-103.	1.1	24
80	Comparative analysis of plant genomes allows the definition of the "Phytolongins": a novel non-SNARE longin domain protein family. <i>BMC Genomics</i> , 2009, 10, 510.	2.8	23
81	A role for adaptor protein complex 1 in protein targeting to rhoptry organelles in <i>Plasmodium falciparum</i> . <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 699-710.	4.1	23
82	Evolution of the endomembrane systems of trypanosomatids: conservation and specialisation. <i>Journal of Cell Science</i> , 2017, 130, 1421-1434.	2.0	23
83	From all to (nearly) none. <i>Cellular Logistics</i> , 2014, 4, e28114.	0.9	22
84	Plastid Transcript Editing across Dinoflagellate Lineages Shows Lineage-Specific Application but Conserved Trends. <i>Genome Biology and Evolution</i> , 2018, 10, 1019-1038.	2.5	22
85	A pan-apicomplexan phosphoinositide-binding protein acts in malarial microneme exocytosis. <i>EMBO Reports</i> , 2019, 20, .	4.5	22
86	Ancient complement and lineage-specific evolution of the Sec7 ARF GEF proteins in eukaryotes. <i>Molecular Biology of the Cell</i> , 2019, 30, 1846-1863.	2.1	21
87	Mechanism and evolution of the Zn-fingernail required for interaction of VARP with VPS29. <i>Nature Communications</i> , 2020, 11, 5031.	12.8	21
88	Hydrogenosomal succinyl-CoA synthetase from the rumen-dwelling fungus <i>Neocallimastix patriciarum</i> ; an energy-producing enzyme of mitochondrial origin. <i>Gene</i> , 2006, 373, 75-82.	2.2	20
89	Cryptic organelle homology in apicomplexan parasites: insights from evolutionary cell biology. <i>Current Opinion in Microbiology</i> , 2013, 16, 424-431.	5.1	20
90	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	3.8	18

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91	A Eukaryote-Wide Perspective on the Diversity and Evolution of the ARF GTPase Protein Family. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	18
92	A comparative analysis of trypanosomatid SNARE proteins. <i>Parasitology International</i> , 2014, 63, 341-348.	1.3	17
93	Evolutionary cell biology: functional insight from "endless forms most beautiful". <i>Molecular Biology of the Cell</i> , 2015, 26, 4532-4538.	2.1	17
94	Seeing the endomembrane system for the trees: Evolutionary analysis highlights the importance of plants as models for eukaryotic membrane-trafficking. <i>Seminars in Cell and Developmental Biology</i> , 2018, 80, 142-152.	5.0	17
95	A Characterization of the <i>Manduca sexta</i> Serotonin Receptors in the Context of Olfactory Neuromodulation. <i>PLoS ONE</i> , 2013, 8, e69422.	2.5	16
96	An ancestral role in peroxisome assembly is retained by the divisional peroxin Pex11 in the yeast <i>Yarrowia lipolytica</i> . <i>Journal of Cell Science</i> , 2015, 128, 1327-1340.	2.0	16
97	Exclusive expression of the Rab11 effector SH3TC2 in Schwann cells links integrin- $\alpha 6$ and myelin maintenance to Charcot-Marie-Tooth disease type 4C. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1279-1290.	3.8	16
98	Nuclear condensation in protozoan gametes and the evolution of anisogamy. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 1999, 124, 287-295.	1.8	15
99	Phylogenetic Estimation of Community Composition and Novel Eukaryotic Lineages in Base Mine Lake: An Oil Sands Tailings Reclamation Site in Northern Alberta. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 86-99.	1.7	14
100	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2240-2259.	8.9	14
101	Progressive and Biased Divergent Evolution Underpins the Origin and Diversification of Peridinin Dinoflagellate Plastids. <i>Molecular Biology and Evolution</i> , 2016, 34, msw235.	8.9	13
102	Phylogenetic and Primary Sequence Characterization of Cathepsin B Cysteine Proteases from the Oxymonad Flagellate <i>Monocercomonoides</i> . <i>Journal of Eukaryotic Microbiology</i> , 2008, 55, 9-17.	1.7	12
103	Complex Patterns of Gene Fission in the Eukaryotic Folate Biosynthesis Pathway. <i>Genome Biology and Evolution</i> , 2014, 6, 2709-2720.	2.5	12
104	Membrane Trafficking Modulation during <i>Entamoeba</i> Encystation. <i>Scientific Reports</i> , 2017, 7, 12854.	3.3	12
105	Regulation of early endosomes across eukaryotes: Evolution and functional homology of Vps9 proteins. <i>Traffic</i> , 2018, 19, 546-563.	2.7	12
106	Emergent Complexity in Myosin V-Based Organelle Inheritance. <i>Molecular Biology and Evolution</i> , 2012, 29, 975-984.	8.9	11
107	An "ER-directed transcriptional response to unfolded protein stress in the absence of conserved sensor-transducer proteins in <i>Giardia lamblia</i> ". <i>Molecular Microbiology</i> , 2013, 88, 754-771.	2.5	11
108	Losses, Expansions, and Novel Subunit Discovery of Adaptor Protein Complexes in Haptophyte Algae. <i>Protist</i> , 2015, 166, 585-597.	1.5	11

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109	Recent gene duplications dominate evolutionary dynamics of adaptor protein complex subunits in embryophytes. <i>Traffic</i> , 2019, 20, 961-973.	2.7	10
110	A Phosphoinositide-Binding Protein Acts in the Trafficking Pathway of Hemoglobin in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>MBio</i> , 2022, 13, e0323921.	4.1	10
111	A Novel Rho-Like Protein TbrHP Is Involved in Spindle Formation and Mitosis in Trypanosomes. <i>PLoS ONE</i> , 2011, 6, e26890.	2.5	9
112	Unexpected organellar locations of ESCRT machinery in <i>Giardia intestinalis</i> and complex evolutionary dynamics spanning the transition to parasitism in the lineage Fornicata. <i>BMC Biology</i> , 2021, 19, 167.	3.8	8
113	Atypical Phenotypes From Flatworm Kv3 Channels. <i>Journal of Neurophysiology</i> , 2006, 95, 3035-3046.	1.8	7
114	Phylogenetic Analysis of Glycerol 3-Phosphate Acyltransferases in Opisthokonts Reveals Unexpected Ancestral Complexity and Novel Modern Biosynthetic Components. <i>PLoS ONE</i> , 2014, 9, e110684.	2.5	7
115	Evolutionary cell biology traces the rise of the exomer complex in Fungi from an ancient eukaryotic component. <i>Scientific Reports</i> , 2018, 8, 11154.	3.3	7
116	Identification and characterisation of the cryptic Golgi apparatus in <i>Naegleria gruberi</i> . <i>Journal of Cell Science</i> , 2018, 131, .	2.0	6
117	Evolution: Parallel Paths to Parasitism in the Apicomplexa. <i>Current Biology</i> , 2019, 29, R836-R839.	3.9	6
118	Proteomic Analysis of <i>Trichomonas vaginalis</i> Phagolysosome, Lysosomal Targeting, and Unconventional Secretion of Cysteine Peptidases. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100174.	3.8	6
119	Distribution of membrane trafficking system components across ciliate diversity highlights heterogeneous organelle-associated machinery. <i>Traffic</i> , 2022, .	2.7	6
120	The reduced ARF regulatory system in <i>Giardia intestinalis</i> pre-dates the transition to parasitism in the lineage Fornicata. <i>International Journal for Parasitology</i> , 2021, 51, 825-839.	3.1	5
121	Phylogeny and Evolution. , 2016, , 383-408.		4
122	Microbial Eukaryotes in Oil Sands Environments: Heterotrophs in the Spotlight. <i>Microorganisms</i> , 2019, 7, 178.	3.6	4
123	Phylogenetic and biochemical analysis of calsequestrin structure and association of its variants with cardiac disorders. <i>Scientific Reports</i> , 2020, 10, 18115.	3.3	4
124	Molecular evolutionary analysis of the <i>SM</i> and <i>SNARE</i> vesicle fusion machinery in ciliates shows concurrent expansions in late secretory machinery. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12919.	1.7	4
125	Genetic analysis of ID1-DBL2X predicts its validity as a vaccine candidate in Colombia and supports at least two independently introduced <i>Plasmodium falciparum</i> populations in the region. <i>Infection, Genetics and Evolution</i> , 2017, 55, 175-185.	2.3	3
126	Massive differential expansion of the <i>Trichomonas vaginalis</i> adaptin genomic complement. <i>Journal of Eukaryotic Microbiology</i> , 2005, 52, 7S-27S.	1.7	1

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127	The Ancient and Widespread Nature of the ER-Mitochondria Encounter Structure. <i>Molecular Biology and Evolution</i> , 2014, 31, 251-251.	8.9	1
128	Comparative genomic analysis illustrates evolutionary dynamics of multisubunit tethering complexes across green algal diversity. <i>Journal of Eukaryotic Microbiology</i> , 2023, 70, .	1.7	1
129	Cell biology of micro-organisms and the evolution of the eukaryotic cell. <i>Molecular Biology of the Cell</i> , 2012, 23, 974-974.	2.1	0
130	Evolving eukaryotes: an interview with Joel Dacks. <i>BMC Biology</i> , 2018, 16, 119.	3.8	0
131	Evolution of the eukaryotic endomembrane system –first and last ancestors. <i>FASEB Journal</i> , 2009, 23, 319.2.	0.5	0