Joel B Dacks

List of Publications by Year in Descending Order

132 papers	7,540 citations	47 h-index	85 g-index
153 ext. papers	8,715 ext. citations	7.2 avg, IF	5.87 L-index

#	Paper	IF	Citations
132	A Phosphoinositide-Binding Protein Acts in the Trafficking Pathway of Hemoglobin in the Malaria Parasite Plasmodium falciparum.. *MBio*, **2022**, e0323921	7.8	1
131	Distribution of Membrane Trafficking System Components Across Ciliate Diversity Highlights Heterogenous Organelle-Associated Machinery.. *Traffic*, **2022**,	5.7	1
130	Molecular Evolutionary Analysis of the SM and SNARE Vesicle Fusion Machinery in Ciliates shows Concurrent Expansions in Late Secretory Machinery.. *Journal of Eukaryotic Microbiology*, **2022**, e12919	3.6	0
129	Proteomic analysis of Trichomonas vaginalis phagolysosome, lysosomal targeting, and unconventional secretion of cysteine peptidases. *Molecular and Cellular Proteomics*, **2021**, 100174	7.6	0
128	Genomics and transcriptomics yields a system-level view of the biology of the pathogen Naegleria fowleri. *BMC Biology*, **2021**, 19, 142	7.3	7
127	The Mastigamoeba balamuthi Genome and the Nature of the Free-Living Ancestor of Entamoeba. *Molecular Biology and Evolution*, **2021**, 38, 2240-2259	8.3	7
126	A Eukaryote-Wide Perspective on the Diversity and Evolution of the ARF GTPase Protein Family. *Genome Biology and Evolution*, **2021**, 13,	3.9	2
125	Unexpected organellar locations of ESCRT machinery in Giardia intestinalis and complex evolutionary dynamics spanning the transition to parasitism in the lineage Fornicata. *BMC Biology*, **2021**, 19, 167	7.3	3
124	The reduced ARF regulatory system in Giardia intestinalis pre-dates the transition to parasitism in the lineage Fornicata. *International Journal for Parasitology*, **2021**, 51, 825-839	4.3	1
123	Evolution and Natural History of Membrane Trafficking in Eukaryotes. *Current Biology*, **2020**, 30, R553-R564	8.3	14
122	Mechanism and evolution of the Zn-fingernail required for interaction of VARP with VPS29. *Nature Communications*, **2020**, 11, 5031	17.4	6
121	Phylogenetic and biochemical analysis of calsequestrin structure and association of its variants with cardiac disorders. *Scientific Reports*, **2020**, 10, 18115	4.9	2
120	Phylogenetic Estimation of Community Composition and Novel Eukaryotic Lineages in Base Mine Lake: An Oil Sands Tailings Reclamation Site in Northern Alberta. *Journal of Eukaryotic Microbiology*, **2020**, 67, 86-99	3.6	5
119	Evolution: Parallel Paths to Parasitism in the Apicomplexa. *Current Biology*, **2019**, 29, R836-R839	6.3	2
118	Microbial Eukaryotes in Oil Sands Environments: Heterotrophs in the Spotlight. *Microorganisms*, **2019**, 7,	4.9	1
117	Ancient complement and lineage-specific evolution of the Sec7 ARF GEF proteins in eukaryotes. *Molecular Biology of the Cell*, **2019**, 30, 1846-1863	3.5	9
116	ARF GTPases and their GEFs and GAPs: concepts and challenges. *Molecular Biology of the Cell*, **2019**, 30, 1249-1271	3.5	86

115	A pan-apicomplexan phosphoinositide-binding protein acts in malarial microneme exocytosis. *EMBO Reports*, **2019**, 20,	6.5	10
114	Transcriptome, proteome and draft genome of Euglena gracilis. *BMC Biology*, **2019**, 17, 11	7.3	52
113	The Oxymonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. *Molecular Biology and Evolution*, **2019**, 36, 2292-2312	8.3	18
112	Recent gene duplications dominate evolutionary dynamics of adaptor protein complex subunits in embryophytes. *Traffic*, **2019**, 20, 961-973	5.7	5
111	Remodeling the Specificity of an Endosomal CORVET Tether Underlies Formation of Regulated Secretory Vesicles in the Ciliate Tetrahymena thermophila. *Current Biology*, **2018**, 28, 697-710.e13	6.3	14
110	Regulation of early endosomes across eukaryotes: Evolution and functional homology of Vps9 proteins. *Traffic*, **2018**, 19, 546-563	5.7	9
109	Plastid Transcript Editing across Dinoflagellate Lineages Shows Lineage-Specific Application but Conserved Trends. *Genome Biology and Evolution*, **2018**, 10, 1019-1038	3.9	17
108	Identification and characterisation of a cryptic Golgi complex in. *Journal of Cell Science*, **2018**, 131,	5.3	4
107	Seeing the endomembrane system for the trees: Evolutionary analysis highlights the importance of plants as models for eukaryotic membrane-trafficking. *Seminars in Cell and Developmental Biology*, **2018**, 80, 142-152	7.5	12
106	A sophisticated, differentiated Golgi in the ancestor of eukaryotes. *BMC Biology*, **2018**, 16, 27	7.3	21
105	Evolutionary cell biology traces the rise of the exomer complex in Fungi from an ancient eukaryotic component. *Scientific Reports*, **2018**, 8, 11154	4.9	3
104	Evolving eukaryotes: an interview with Joel Dacks. *BMC Biology*, **2018**, 16, 119	7.3	
103	Evolutionary origins and specialisation of membrane transport. *Current Opinion in Cell Biology*, **2018** , 53, 70-76	9	25
102	Outerwear through the ages: evolutionary cell biology of vesicle coats. *Current Opinion in Cell Biology*, **2017**, 47, 108-116	9	31
101	Evolution of the endomembrane systems of trypanosomatids - conservation and specialisation. *Journal of Cell Science*, **2017**, 130, 1421-1434	5.3	17
100	Membrane Trafficking Modulation during Entamoeba Encystation. *Scientific Reports*, **2017**, 7, 12854	4.9	9
99	Progressive and Biased Divergent Evolution Underpins the Origin and Diversification of Peridinin Dinoflagellate Plastids. *Molecular Biology and Evolution*, **2017**, 34, 361-379	8.3	12
98	Genetic analysis of ID1-DBL2X predicts its validity as a vaccine candidate in Colombia and supports at least two independently introduced Plasmodium falciparum populations in the region. *Infection, Genetics and Evolution*, **2017**, 55, 175-185	4.5	3

97	An evolutionary balance: conservation vs innovation in ciliate membrane trafficking. *Traffic*, **2017**, 18, 18-28	5.7	19
96	Extreme genome diversity in the hyper-prevalent parasitic eukaryote Blastocystis. *PLoS Biology*, **2017**, 15, e2003769	9.7	58
95	Phylogeny and Evolution **2016**, 383-408		3
94	Tracing the Archaeal Origins of Eukaryotic Membrane-Trafficking System Building Blocks. *Molecular Biology and Evolution*, **2016**, 33, 1528-41	8.3	55
93	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. *Current Biology*, **2016**, 26, 161-172	6.3	98
92	Next-Generation Sequencing Assessment of Eukaryotic Diversity in Oil Sands Tailings Ponds Sediments and Surface Water. *Journal of Eukaryotic Microbiology*, **2016**, 63, 732-743	3.6	19
91	Exclusive expression of the Rab11 effector SH3TC2 in Schwann cells links integrin-β and myelin maintenance to Charcot-Marie-Tooth disease type 4C. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2016**, 1862, 1279-90	6.9	10
90	A Eukaryote without a Mitochondrial Organelle. *Current Biology*, **2016**, 26, 1274-84	6.3	213
89	The changing view of eukaryogenesis - fossils, cells, lineages and how they all come together. *Journal of Cell Science*, **2016**, 129, 3695-3703	5.3	58
88	Resolving the homology-function relationship through comparative genomics of membrane-trafficking machinery and parasite cell biology. *Molecular and Biochemical Parasitology*, **2016**, 209, 88-103	1.9	17
87	An ancestral role in peroxisome assembly is retained by the divisional peroxin Pex11 in the yeast Yarrowia lipolytica. *Journal of Cell Science*, **2015**, 128, 1327-40	5.3	12
86	Losses, Expansions, and Novel Subunit Discovery of Adaptor Protein Complexes in Haptophyte Algae. *Protist*, **2015**, 166, 585-97	2.5	9
85	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. *ELife*, **2015**, 4, e06974	8.9	138
84	Ancient homology of the mitochondrial contact site and cristae organizing system points to an endosymbiotic origin of mitochondrial cristae. *Current Biology*, **2015**, 25, 1489-95	6.3	74
83	Unexpected ancient paralogs and an evolutionary model for the COPII coat complex. *Genome Biology and Evolution*, **2015**, 7, 1098-109	3.9	25
82	The evolution of MICOS: Ancestral and derived functions and interactions. *Communicative and Integrative Biology*, **2015**, 8, e1094593	1.7	22
81	Evolutionary cell biology: functional insight from "endless forms most beautiful". *Molecular Biology of the Cell*, **2015**, 26, 4532-8	3.5	13
80	A role for adaptor protein complex 1 in protein targeting to rhoptry organelles in Plasmodium falciparum. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2015**, 1853, 699-710	4.9	20

79	A role for the ancient SNARE syntaxin 17 in regulating mitochondrial division. *Developmental Cell*, **2015**, 32, 304-17	10.2	98
78	A comparative analysis of trypanosomatid SNARE proteins. *Parasitology International*, **2014**, 63, 341-8	2.1	16
77	Complex patterns of gene fission in the eukaryotic folate biosynthesis pathway. *Genome Biology and Evolution*, **2014**, 6, 2709-20	3.9	9
76	Missing pieces of an ancient puzzle: evolution of the eukaryotic membrane-trafficking system. *Cold Spring Harbor Perspectives in Biology*, **2014**, 6, a016048	10.2	49
75	The cell biology of the endocytic system from an evolutionary perspective. *Cold Spring Harbor Perspectives in Biology*, **2014**, 6, a016998	10.2	29
74	Phylogenetic analysis of glycerol 3-phosphate acyltransferases in opisthokonts reveals unexpected ancestral complexity and novel modern biosynthetic components. *PLoS ONE*, **2014**, 9, e110684	3.7	6
73	From all to (nearly) none: Tracing adaptin evolution in Fungi. *Cellular Logistics*, **2014**, 4, e28114		20
72	The Ancient and Widespread Nature of the ERMitochondria Encounter Structure. *Molecular Biology and Evolution*, **2014**, 31, 251-251	8.3	1
71	Interaction with the effector dynamin-related protein 1 (Drp1) is an ancient function of Rab32 subfamily proteins. *Cellular Logistics*, **2014**, 4, e986399		20
70	Longin and GAF domains: structural evolution and adaptation to the subcellular trafficking machinery. *Traffic*, **2014**, 15, 104-21	5.7	33
69	Evolutionary mechanisms for establishing eukaryotic cellular complexity. *Trends in Cell Biology*, **2014**, 24, 435-42	18.3	20
68	Characterization of TSET, an ancient and widespread membrane trafficking complex. *ELife*, **2014**, 3, e02866	8.9	88
67	Molecular paleontology and complexity in the last eukaryotic common ancestor. *Critical Reviews in Biochemistry and Molecular Biology*, **2013**, 48, 373-96	8.7	128
66	Pan genome of the phytoplankton Emiliania underpins its global distribution. *Nature*, **2013**, 499, 209-13	50.4	356
65	Cryptic organelle homology in apicomplexan parasites: insights from evolutionary cell biology. *Current Opinion in Microbiology*, **2013**, 16, 424-31	7.9	17
64	The mitochondrial genome and a 60-kb nuclear DNA segment from Naegleria fowleri, the causative agent of primary amoebic meningoencephalitis. *Journal of Eukaryotic Microbiology*, **2013**, 60, 179-91	3.6	31
63	The ancient and widespread nature of the ER-mitochondria encounter structure. *Molecular Biology and Evolution*, **2013**, 30, 2044-9	8.3	75
62	Evolution of Tre-2/Bub2/Cdc16 (TBC) Rab GTPase-activating proteins. *Molecular Biology of the Cell*, **2013**, 24, 1574-83	3.5	36

61	An ER-directed transcriptional response to unfolded protein stress in the absence of conserved sensor-transducer proteins in Giardia lamblia. *Molecular Microbiology*, **2013**, 88, 754-71	4.1	10
60	Ancient complexity, opisthokont plasticity, and discovery of the 11th subfamily of Arf GAP proteins. *Traffic*, **2013**, 14, 636-49	5.7	29
59	A characterization of the Manduca sexta serotonin receptors in the context of olfactory neuromodulation. *PLoS ONE*, **2013**, 8, e69422	3.7	13
58	Comparative genomic analysis of multi-subunit tethering complexes demonstrates an ancient pan-eukaryotic complement and sculpting in Apicomplexa. *PLoS ONE*, **2013**, 8, e76278	3.7	39
57	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature*, **2012**, 492, 59-65	50.4	304
56	ELMO domains, evolutionary and functional characterization of a novel GTPase-activating protein (GAP) domain for Arf protein family GTPases. *Journal of Biological Chemistry*, **2012**, 287, 39538-53	5.4	43
55	Cell biology of micro-organisms and the evolution of the eukaryotic cell. *Molecular Biology of the Cell*, **2012**, 23, 974-974	3.5	78
54	Sculpting the endomembrane system in deep time: high resolution phylogenetics of Rab GTPases. *Journal of Cell Science*, **2012**, 125, 2500-8	5.3	115
53	Emergent complexity in Myosin V-based organelle inheritance. *Molecular Biology and Evolution*, **2012**, 29, 975-84	8.3	10
52	Eukaryotic systematics: a user's guide for cell biologists and parasitologists. *Parasitology*, **2011**, 138, 1638-63	2.7	83
51	Evolution and diversity of the Golgi. *Cold Spring Harbor Perspectives in Biology*, **2011**, 3, a007849	10.2	44
50	Evolution of the karyopherin-β family of nucleocytoplasmic transport factors; ancient origins and continued specialization. *PLoS ONE*, **2011**, 6, e19308	3.7	43
49	A novel Rho-like protein TbRHP is involved in spindle formation and mitosis in trypanosomes. *PLoS ONE*, **2011**, 6, e26890	3.7	8
48	Multivesicular bodies in the enigmatic amoeboflagellate Breviata anathema and the evolution of ESCRT 0. *Journal of Cell Science*, **2011**, 124, 613-21	5.3	30
47	Evolutionary reconstruction of the retromer complex and its function in Trypanosoma brucei. *Journal of Cell Science*, **2011**, 124, 1496-509	5.3	85
46	The fifth adaptor protein complex. *PLoS Biology*, **2011**, 9, e1001170	9.7	205
45	Arf3 is activated uniquely at the trans-Golgi network by brefeldin A-inhibited guanine nucleotide exchange factors. *Molecular Biology of the Cell*, **2010**, 21, 1836-49	3.5	39
44	The genome of Naegleria gruberi illuminates early eukaryotic versatility. *Cell*, **2010**, 140, 631-42	56.2	346

43	Rab protein evolution and the history of the eukaryotic endomembrane system. *Cellular and Molecular Life Sciences*, **2010**, 67, 3449-65	10.3	69
42	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic "supergroups". *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 3859-64	11.5	401
41	Pex3 peroxisome biogenesis proteins function in peroxisome inheritance as class V myosin receptors. *Journal of Cell Biology*, **2009**, 187, 233-46	7.3	41
40	Comparative analysis of plant genomes allows the definition of the "Phytolongins": a novel non-SNARE longin domain protein family. *BMC Genomics*, **2009**, 10, 510	4.5	23
39	Evolution and diversity of the Golgi body. *FEBS Letters*, **2009**, 583, 3738-45	3.8	60
38	First and last ancestors: reconstructing evolution of the endomembrane system with ESCRTs, vesicle coat proteins, and nuclear pore complexes. *Current Opinion in Cell Biology*, **2009**, 21, 4-13	9	101
37	The single ENTH-domain protein of trypanosomes; endocytic functions and evolutionary relationship with epsin. *Traffic*, **2009**, 10, 894-911	5.7	36
36	Evolution of specificity in the eukaryotic endomembrane system. *International Journal of Biochemistry and Cell Biology*, **2009**, 41, 330-40	5.6	64
35	Repeated secondary loss of adaptin complex genes in the Apicomplexa. *Parasitology International*, **2009**, 58, 86-94	2.1	38
34	Evolution of the eukaryotic endomembrane system - first and last ancestors. *FASEB Journal*, **2009**, 23, 319.2	0.9	
33	Implications of the new eukaryotic systematics for parasitologists. *Parasitology International*, **2008**, 57, 97-104	2.1	47
32	Phylogeny of endocytic components yields insight into the process of nonendosymbiotic organelle evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 588-93	11.5	114
31	Evolution of the multivesicular body ESCRT machinery; retention across the eukaryotic lineage. *Traffic*, **2008**, 9, 1698-716	5.7	198
30	Phylogenetic and primary sequence characterization of cathepsin B cysteine proteases from the oxymonad flagellate Monocercomonoides. *Journal of Eukaryotic Microbiology*, **2008**, 55, 9-17	3.6	10
29	Control systems for membrane fusion in the ancestral eukaryote; evolution of tethering complexes and SM proteins. *BMC Evolutionary Biology*, **2007**, 7, 29	3	166
28	Reconstructing the evolution of the endocytic system: insights from genomics and molecular cell biology. *Advances in Experimental Medicine and Biology*, **2007**, 607, 84-96	3.6	84
27	Draft genome sequence of the sexually transmitted pathogen Trichomonas vaginalis. *Science*, **2007**, 315, 207-12	33.3	622
26	Evolution of the eukaryotic membrane-trafficking system: origin, tempo and mode. *Journal of Cell Science*, **2007**, 120, 2977-85	5.3	216

25	Evolution of filamentous plant pathogens: gene exchange across eukaryotic kingdoms. *Current Biology*, **2006**, 16, 1857-64	6.3	154
24	Evolutionary origins of the eukaryotic shikimate pathway: gene fusions, horizontal gene transfer, and endosymbiotic replacements. *Eukaryotic Cell*, **2006**, 5, 1517-31		155
23	Reconstructing the mosaic glycolytic pathway of the anaerobic eukaryote Monocercomonoides. *Eukaryotic Cell*, **2006**, 5, 2138-46		35
22	Hydrogenosomal succinyl-CoA synthetase from the rumen-dwelling fungus Neocallimastix patriciarum; an energy-producing enzyme of mitochondrial origin. *Gene*, **2006**, 373, 75-82	3.8	18
21	The cloning of one putative octopamine receptor and two putative serotonin receptors from the tobacco hawkmoth, Manduca sexta. *Insect Biochemistry and Molecular Biology*, **2006**, 36, 741-7	4.5	32
20	Atypical phenotypes from flatworm Kv3 channels. *Journal of Neurophysiology*, **2006**, 95, 3035-46	3.2	7
19	Ultrastructural description of Breviata anathema, n. gen., n. sp., the organism previously studied as "Mastigamoeba invertens". *Journal of Eukaryotic Microbiology*, **2006**, 53, 65-78	3.6	59
18	Massive differential expansion of the Trichomonas vaginalis adaptin genomic complement. *Journal of Eukaryotic Microbiology*, **2005**, 52, 7S-27S	3.6	1
17	Phylogenetic artifacts can be caused by leucine, serine, and arginine codon usage heterogeneity: dinoflagellate plastid origins as a case study. *Systematic Biology*, **2004**, 53, 582-93	8.4	54
16	Molecular and phylogenetic characterization of syntaxin genes from parasitic protozoa. *Molecular and Biochemical Parasitology*, **2004**, 136, 123-36	1.9	42
15	Molecular phylogeny of three oxymonad genera: Pyrsonympha, Dinenympha and Oxymonas. *Journal of Eukaryotic Microbiology*, **2003**, 50, 190-7	3.6	44
14	Evidence for Golgi bodies in proposed SGolgi-lackingSlineages. *Proceedings of the Royal Society B: Biological Sciences*, **2003**, 270 Suppl 2, S168-71	4.4	52
13	How oxymonads lost their groove: an ultrastructural comparison of Monocercomonoides and excavate taxa. *Journal of Eukaryotic Microbiology*, **2002**, 49, 239-48	3.6	28
12	Analyses of RNA Polymerase II genes from free-living protists: phylogeny, long branch attraction, and the eukaryotic big bang. *Molecular Biology and Evolution*, **2002**, 19, 830-40	8.3	74
11	Novel syntaxin gene sequences from Giardia, Trypanosoma and algae: implications for the ancient evolution of the eukaryotic endomembrane system. *Journal of Cell Science*, **2002**, 115, 1635-1642	5.3	49
10	Novel syntaxin gene sequences from Giardia, Trypanosoma and algae: implications for the ancient evolution of the eukaryotic endomembrane system. *Journal of Cell Science*, **2002**, 115, 1635-42	5.3	53
9	Oxymonads are closely related to the excavate taxon Trimastix. *Molecular Biology and Evolution*, **2001**, 18, 1034-44	8.3	62
8	Origin of H1 linker histones. *FASEB Journal*, **2001**, 15, 34-42	0.9	164

7	Reconstructing/deconstructing the earliest eukaryotes: how comparative genomics can help. *Cell*, **2001**, 107, 419-25	56.2	108
6	Evolutionary relationship between dinoflagellates bearing obligate diatom endosymbionts: insight into tertiary endosymbiosis. *International Journal of Systematic and Evolutionary Microbiology*, **2000**, 50 Pt 6, 2075-2081	2.2	54
5	The first sexual lineage and the relevance of facultative sex. *Journal of Molecular Evolution*, **1999**, 48, 779-83	3.1	108
4	Nuclear condensation in protozoan gametes and the evolution of anisogamy. *Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology*, **1999**, 124, 287-295	2.6	14
3	Phylogenetic placement of Trichonympha. *Journal of Eukaryotic Microbiology*, **1998**, 45, 445-7	3.6	38
2	A comparative ⊟mics approach to candidate pathogenicity factor discovery in the brain-eating amoebaNaegleria fowleri		8
1	Unlocking the biological potential of Euglena gracilis: evolution, cell biology and significance to parasitism		2