

# Damien Devos

## List of Publications by Year in descending order

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81  
papers

7,477  
citations

87843

38  
h-index

56687

83  
g-index

91  
all docs

91  
docs citations

91  
times ranked

10292  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural, Evolutionary, and Functional Analysis of the Protein O-Mannosyltransferase Family in Pathogenic Fungi. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 328.	1.5	3
2	Comparative Genomics of Peroxisome Biogenesis Proteins: Making Sense of the PEX Proteins. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 654163.	1.8	48
3	Homology and Modular Evolution of CATCHR at the Origin of the Eukaryotic Endomembrane System. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
4	Reconciling Asgardarchaeota Phylogenetic Proximity to Eukaryotes and Planctomycetes Cellular Features in the Evolution of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 3531-3542.	3.5	15
5	Functional diversity of isoprenoid lipids in <i>Methylobacterium extorquens</i> PA1. <i>Molecular Microbiology</i> , 2021, 116, 1064-1078.	1.2	12
6	<i>Hansenula polymorpha</i> Pex37 is a peroxisomal membrane protein required for organelle fission and segregation. <i>FEBS Journal</i> , 2020, 287, 1742-1757.	2.2	11
7	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
8	Complementary Tendencies in the Use of Regulatory Elements (Transcription Factors, Sigma Factors,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	1
9	Pex24 and Pex32 are required to tether peroxisomes to the ER for organelle biogenesis, positioning and segregation. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	21
10	Bringing the diversity of Planctomycetes into the light: Introduction to papers from the special issue on novel taxa of Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1715-1726.	0.7	4
11	<i>Thalassoglobus polymorphus</i> sp. nov., a novel Planctomycete isolated close to a public beach of Mallorca Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1915-1926.	0.7	15
12	<i>Maioricimonas rarisocia</i> gen. nov., sp. nov., a novel planctomycete isolated from marine sediments close to Mallorca Island. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1901-1913.	0.7	17
13	Origin and Evolution of Polycyclic Triterpene Synthesis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1925-1941.	3.5	38
14	Non-essentiality of canonical cell division genes in the planctomycete <i>Planctopirus limnophila</i> . <i>Scientific Reports</i> , 2020, 10, 66.	1.6	26
15	Peroxisome retention involves Inp1-dependent peroxisome-plasma membrane contact sites in yeast. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	12
16	Essentiality of sterol synthesis genes in the planctomycete bacterium <i>Gemmata obscuriglobus</i> . <i>Nature Communications</i> , 2019, 10, 2916.	5.8	19
17	Commentary: Manifold Routes to a Nucleus. <i>Frontiers in Microbiology</i> , 2019, 10, 1198.	1.5	4
18	Live-Cell Structural Biology to Solve Biological Mechanisms: The Case of the Exocyst. <i>Structure</i> , 2019, 27, 886-892.	1.6	3

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19	Planctomycetes. , 2019, , 614-614.		10
20	Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.	1.7	98
21	Introduction to papers from the third meeting on the Planctomycetes-Verrucomicrobia-Chlamydiae bacteria: new model organisms in the omics era. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 783-784.	0.7	2
22	The Paradigms They Are a-Changeinâ€™: past, present and future of PVC bacteria research. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 785-799.	0.7	49
23	Planctomycetes attached to algal surfaces: Insight into their genomes. <i>Genomics</i> , 2018, 110, 231-238.	1.3	39
24	PVCbase: an integrated web resource for the PVC bacterial proteomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	13
25	Nuclear Pore Complex Components in the Malaria Parasite <i>Plasmodium berghei</i> . <i>Scientific Reports</i> , 2018, 8, 11249.	1.6	19
26	ICBdocker: a Docker image for proteome annotation and visualization. <i>Bioinformatics</i> , 2018, 34, 3937-3938.	1.8	1
27	4Cin: A computational pipeline for 3D genome modeling and virtual Hi-C analyses from 4C data. <i>PLoS Computational Biology</i> , 2018, 14, e1006030.	1.5	9
28	The InÂVivo Architecture of the Exocyst Provides Structural Basis for Exocytosis. <i>Cell</i> , 2017, 168, 400-412.e18.	13.5	89
29	Determining the bacterial cell biology of Planctomycetes. <i>Nature Communications</i> , 2017, 8, 14853.	5.8	175
30	Regulatory landscape fusion in rhabdomyosarcoma through interactions between the PAX3 promoter and FOXO1 regulatory elements. <i>Genome Biology</i> , 2017, 18, 106.	3.8	24
31	Editorial: Planctomycetes-Verrucomicrobia-Chlamydiae Bacterial Superphylum: New Model Organisms for Evolutionary Cell Biology. <i>Frontiers in Microbiology</i> , 2017, 8, 1458.	1.5	28
32	Development of Genetic Tools for the Manipulation of the Planctomycetes. <i>Frontiers in Microbiology</i> , 2016, 7, 914.	1.5	38
33	Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum. <i>Frontiers in Microbiology</i> , 2016, 7, 1964.	1.5	45
34	The changing view of eukaryogenesis â€“ fossils, cells, lineages and how they all come together. <i>Journal of Cell Science</i> , 2016, 129, 3695-3703.	1.2	77
35	Efficient and automated large-scale detection of structural relationships in proteins with a flexible aligner. <i>BMC Bioinformatics</i> , 2016, 17, 20.	1.2	3
36	A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation. <i>Nature Genetics</i> , 2016, 48, 336-341.	9.4	113

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37	A Multi-Functional Tubulovesicular Network as the Ancestral Eukaryotic Endomembrane System. <i>Biology</i> , 2015, 4, 264-281.	1.3	3
38	Ten Simple Rules for Organizing an Unconference. <i>PLoS Computational Biology</i> , 2015, 11, e1003905.	1.5	69
39	A bacterial tubulovesicular network. <i>Journal of Cell Science</i> , 2014, 127, 277-80.	1.2	40
40	Subtle Changes in Motif Positioning Cause Tissue-Specific Effects on Robustness of an Enhancer's Activity. <i>PLoS Genetics</i> , 2014, 10, e1004060.	1.5	59
41	The nucleoporin MEL-28 promotes RanGTP-dependent $\hat{1}^3$ -tubulin recruitment and microtubule nucleation in mitotic spindle formation. <i>Nature Communications</i> , 2014, 5, 3270.	5.8	56
42	Evolution of the nucleus. <i>Current Opinion in Cell Biology</i> , 2014, 28, 8-15.	2.6	49
43	Mind the PVCs. <i>Environmental Microbiology</i> , 2014, 16, 1217-1221.	1.8	24
44	Re-interpretation of the evidence for the PVC cell plan supports a Gram-negative origin. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 271-274.	0.7	37
45	PVC bacteria: variation of, but not exception to, the Gram-negative cell plan. <i>Trends in Microbiology</i> , 2014, 22, 14-20.	3.5	69
46	Gemmata obscuriglobus. <i>Current Biology</i> , 2013, 23, R705-R707.	1.8	17
47	Three-Dimensional Reconstruction of Bacteria with a Complex Endomembrane System. <i>PLoS Biology</i> , 2013, 11, e1001565.	2.6	116
48	Structural Aspects of MC Proteins of PVC Superphylum Members. , 2013, , 77-87.		0
49	Analysis of the yeast nucleoporin Nup188 reveals a conserved S-like structure with similarity to karyopherins. <i>Journal of Structural Biology</i> , 2012, 177, 99-105.	1.3	30
50	Evaluating the Evolutionary Origins of Unexpected Character Distributions within the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum. <i>Frontiers in Microbiology</i> , 2012, 3, 401.	1.5	10
51	Regarding the presence of membrane coat proteins in bacteria: Confusion? What confusion?. <i>BioEssays</i> , 2012, 34, 38-39.	1.2	20
52	Insight into Structure and Assembly of the Nuclear Pore Complex by Utilizing the Genome of a Eukaryotic Thermophile. <i>Cell</i> , 2011, 146, 277-289.	13.5	232
53	Transitional forms between the three domains of life and evolutionary implications. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 3321-3328.	1.2	40
54	A Conserved Coatomer-related Complex Containing Sec13 and Seh1 Dynamically Associates With the Vacuole in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006478.	2.5	115

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55	The three-dimensional molecular structure of the desmosomal plaque. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6480-6485.	3.3	71
56	Conformational flexibility of RNA polymerase III during transcriptional elongation. EMBO Journal, 2010, 29, 3762-3772.	3.5	64
57	Endocytosis-like protein uptake in the bacterium <i>Gemmata obscuriglobus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12883-12888.	3.3	210
58	The Compartmentalized Bacteria of the Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum Have Membrane Coat-Like Proteins. PLoS Biology, 2010, 8, e1000281.	2.6	133
59	Intermediate Steps. Science, 2010, 330, 1187-1188.	6.0	68
60	A Functional Proteomic Study of the Trypanosoma brucei Nuclear Pore Complex: An Informatic Strategy. Methods in Molecular Biology, 2010, 673, 231-238.	0.4	11
61	Evidence for a Shared Nuclear Pore Complex Architecture That Is Conserved from the Last Common Eukaryotic Ancestor. Molecular and Cellular Proteomics, 2009, 8, 2119-2130.	2.5	200
62	Proteome Organization in a Genome-Reduced Bacterium. Science, 2009, 326, 1235-1240.	6.0	440
63	Conservation of Helical Bundle Structure between the Exocyst Subunits. PLoS ONE, 2009, 4, e4443.	1.1	27
64	À la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. Molecular Microbiology, 2008, 42, 47-59.	1.2	72
65	RAWUL: A new ubiquitin-like domain in PRC1 Ring finger proteins that unveils putative plant and worm PRC1 orthologs. BMC Genomics, 2008, 9, 308.	1.2	112
66	Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. Accounts of Chemical Research, 2008, 41, 617-627.	7.6	123
67	A more complete, complexed and structured interactome. Current Opinion in Structural Biology, 2007, 17, 370-377.	2.6	53
68	Determining the architectures of macromolecular assemblies. Nature, 2007, 450, 683-694.	13.7	499
69	The molecular architecture of the nuclear pore complex. Nature, 2007, 450, 695-701.	13.7	947
70	A composite score for predicting errors in protein structure models. Protein Science, 2006, 15, 1653-1666.	3.1	160
71	Protease Accessibility Laddering: A Proteomic Tool for Probing Protein Structure. Structure, 2006, 14, 653-660.	1.6	30
72	Simple fold composition and modular architecture of the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2172-2177.	3.3	243

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73	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. <i>PLoS Biology</i> , 2004, 2, e380.	2.6	357
74	POTRA: a conserved domain in the FtsQ family and a class of $\beta$ -barrel outer membrane proteins. <i>Trends in Biochemical Sciences</i> , 2003, 28, 523-526.	3.7	195
75	The single tryptophan of the PsbQ protein of photosystem II is at the end of a 4- $\beta$ -helical bundle domain. <i>FEBS Journal</i> , 2003, 270, 3916-3927.	0.2	10
76	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	1.8	65
77	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265.	2.0	312
78	BRICHOS: a conserved domain in proteins associated with dementia, respiratory distress and cancer. <i>Trends in Biochemical Sciences</i> , 2002, 27, 329-332.	3.7	192
79	Deciphering the action of aromatic effectors on the prokaryotic enhancer-binding protein XylR: a structural model of its N-terminal domain. <i>Environmental Microbiology</i> , 2002, 4, 29-41.	1.8	40
80	Intrinsic errors in genome annotation. <i>Trends in Genetics</i> , 2001, 17, 429-431.	2.9	265
81	Practical limits of function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 98-107.	1.5	306