

Damien Devos

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6918799/publications.pdf>

Version: 2024-02-01

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	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007, 450, 695-701.	13.7	947
2	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007, 450, 683-694.	13.7	499
3	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	6.0	440
4	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. <i>PLoS Biology</i> , 2004, 2, e380.	2.6	357
5	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
6	Practical limits of function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 98-107.	1.5	306
7	Intrinsic errors in genome annotation. <i>Trends in Genetics</i> , 2001, 17, 429-431.	2.9	265
8	Simple fold composition and modular architecture of the nuclear pore complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2172-2177.	3.3	243
9	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
10	Endocytosis-like protein uptake in the bacterium <i>Gemmata obscuriglobus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12883-12888.	3.3	210
11	Evidence for a Shared Nuclear Pore Complex Architecture That Is Conserved from the Last Common Eukaryotic Ancestor. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2119-2130.	2.5	200
12	POTRA: a conserved domain in the FtsQ family and a class of β -barrel outer membrane proteins. <i>Trends in Biochemical Sciences</i> , 2003, 28, 523-526.	3.7	195
13	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
14	Determining the bacterial cell biology of Planctomycetes. <i>Nature Communications</i> , 2017, 8, 14853.	5.8	175
15	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
16	A composite score for predicting errors in protein structure models. <i>Protein Science</i> , 2006, 15, 1653-1666.	3.1	160
17	The Compartmentalized Bacteria of the Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum Have Membrane Coat-Like Proteins. <i>PLoS Biology</i> , 2010, 8, e1000281.	2.6	133
18	Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. <i>Accounts of Chemical Research</i> , 2008, 41, 617-627.	7.6	123

#	ARTICLE	IF	CITATIONS
19	Three-Dimensional Reconstruction of Bacteria with a Complex Endomembrane System. <i>PLoS Biology</i> , 2013, 11, e1001565.	2.6	116
20	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
21	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
22	RAWUL: A new ubiquitin-like domain in PRC1 Ring finger proteins that unveils putative plant and worm PRC1 orthologs. <i>BMC Genomics</i> , 2008, 9, 308.	1.2	112
23	Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.	1.7	98
24	The In Vivo Architecture of the Exocyst Provides Structural Basis for Exocytosis. <i>Cell</i> , 2017, 168, 400-412.e18.	13.5	89
25	The changing view of eukaryogenesis – fossils, cells, lineages and how they all come together. <i>Journal of Cell Science</i> , 2016, 129, 3695-3703.	1.2	77
26	À la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. <i>Molecular Microbiology</i> , 2008, 42, 47-59.	1.2	72
27	The three-dimensional molecular structure of the desmosomal plaque. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6480-6485.	3.3	71
28	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
29	Ten Simple Rules for Organizing an Unconference. <i>PLoS Computational Biology</i> , 2015, 11, e1003905.	1.5	69
30	Intermediate Steps. <i>Science</i> , 2010, 330, 1187-1188.	6.0	68
31	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	1.8	65
32	Conformational flexibility of RNA polymerase III during transcriptional elongation. <i>EMBO Journal</i> , 2010, 29, 3762-3772.	3.5	64
33	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
34	The nucleoporin MEL-28 promotes RanGTP-dependent β -tubulin recruitment and microtubule nucleation in mitotic spindle formation. <i>Nature Communications</i> , 2014, 5, 3270.	5.8	56
35	A more complete, complexed and structured interactome. <i>Current Opinion in Structural Biology</i> , 2007, 17, 370-377.	2.6	53
36	Evolution of the nucleus. <i>Current Opinion in Cell Biology</i> , 2014, 28, 8-15.	2.6	49

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Evolutionary Cell Biology of Division Mode in the Bacterial Planctomycetes-Verrucomicrobia-Chlamydiae Superphylum. <i>Frontiers in Microbiology</i> , 2016, 7, 1964.	1.5	45
40	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
41	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
42	A bacterial tubulovesicular network. <i>Journal of Cell Science</i> , 2014, 127, 277-80.	1.2	40
43	Planctomycetes attached to algal surfaces: Insight into their genomes. <i>Genomics</i> , 2018, 110, 231-238.	1.3	39
44	Development of Genetic Tools for the Manipulation of the Planctomycetes. <i>Frontiers in Microbiology</i> , 2016, 7, 914.	1.5	38
45	Origin and Evolution of Polycyclic Triterpene Synthesis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1925-1941.	3.5	38
46	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
47	Protease Accessibility Laddering: A Proteomic Tool for Probing Protein Structure. <i>Structure</i> , 2006, 14, 653-660.	1.6	30
48	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
49	Editorial: Planctomycetes-Verrucomicrobia-Chlamydiae Bacterial Superphylum: New Model Organisms for Evolutionary Cell Biology. <i>Frontiers in Microbiology</i> , 2017, 8, 1458.	1.5	28
50	Conservation of Helical Bundle Structure between the Exocyst Subunits. <i>PLoS ONE</i> , 2009, 4, e4443.	1.1	27
51	Non-essentiality of canonical cell division genes in the planctomycete <i>Planctopirus limnophila</i> . <i>Scientific Reports</i> , 2020, 10, 66.	1.6	26
52	Mind the PVCs. <i>Environmental Microbiology</i> , 2014, 16, 1217-1221.	1.8	24
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	Regarding the presence of membrane coat proteins in bacteria: Confusion? What confusion?. <i>BioEssays</i> , 2012, 34, 38-39.	1.2	20
56	Nuclear Pore Complex Components in the Malaria Parasite <i>Plasmodium berghei</i> . <i>Scientific Reports</i> , 2018, 8, 11249.	1.6	19
57	Essentiality of sterol synthesis genes in the planctomycete bacterium <i>Gemmata obscuriglobus</i> . <i>Nature Communications</i> , 2019, 10, 2916.	5.8	19
58	<i>Gemmata obscuriglobus</i> . <i>Current Biology</i> , 2013, 23, R705-R707.	1.8	17
59	<i>Maoricimonas 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
60	<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
61	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
62	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
63	Functional diversity of isoprenoid lipids in <i>Methylobacterium extorquens</i> PA1. <i>Molecular Microbiology</i> , 2021, 116, 1064-1078.	1.2	12
64	Peroxisome retention involves Inp1-dependent peroxisome-plasma membrane contact sites in yeast. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	12
65	<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
66	A Functional Proteomic Study of the <i>Trypanosoma brucei</i> Nuclear Pore Complex: An Informatic Strategy. <i>Methods in Molecular Biology</i> , 2010, 673, 231-238.	0.4	11
67	The single tryptophan of the PsbQ protein of photosystem II is at the end of a 4- α -helical bundle domain. <i>FEBS Journal</i> , 2003, 270, 3916-3927.	0.2	10
68	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
69	Planctomycetes. , 2019, , 614-614.		10
70	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
71	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
72	Commentary: Manifold Routes to a Nucleus. <i>Frontiers in Microbiology</i> , 2019, 10, 1198.	1.5	4

#	ARTICLE	IF	CITATIONS
73	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
74	A Multi-Functional Tubulovesicular Network as the Ancestral Eukaryotic Endomembrane System. <i>Biology</i> , 2015, 4, 264-281.	1.3	3
75	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
76	Live-Cell Structural Biology to Solve Biological Mechanisms: The Case of the Exocyst. <i>Structure</i> , 2019, 27, 886-892.	1.6	3
77	Structural, Evolutionary, and Functional Analysis of the Protein O-Mannosyltransferase Family in Pathogenic Fungi. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 328.	1.5	3
78	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
79	ICBdocker: a Docker image for proteome annotation and visualization. <i>Bioinformatics</i> , 2018, 34, 3937-3938.	1.8	1
80	Complementary Tendencies in the Use of Regulatory Elements (Transcription Factors, Sigma Factors,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	1
81	Structural Aspects of MC Proteins of PVC Superphylum Members. , 2013, , 77-87.		0