

Pascal Braun

List of Publications by Year in descending order

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53
papers

10,500
citations

145106

33
h-index

182931

54
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62
all docs

62
docs citations

62
times ranked

16096
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemokine-like MDL proteins modulate flowering time and innate immunity in plants. <i>Journal of Biological Chemistry</i> , 2021, 296, 100611.	1.6	10
2	ARMADILLO REPEAT ONLY proteins confine Rho GTPase signalling to polar growth sites. <i>Nature Plants</i> , 2020, 6, 1275-1288.	4.7	24
3	TRIPP Is a Plant-Specific Component of the Arabidopsis TRAPP II Membrane Trafficking Complex with Important Roles in Plant Development. <i>Plant Cell</i> , 2020, 32, 2424-2443.	3.1	24
4	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11836-11842.	3.3	16
5	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	13.7	328
6	Extensive signal integration by the phytohormone protein network. <i>Nature</i> , 2020, 583, 271-276.	13.7	104
7	GROWTH-REGULATING FACTORS Interact with DELLAs and Regulate Growth in Cold Stress. <i>Plant Cell</i> , 2020, 32, 1018-1034.	3.1	108
8	Interactions between Transport Protein Particle (TRAPP) complexes and Rab GTPases in Arabidopsis. <i>Plant Journal</i> , 2019, 100, 279-297.	2.8	27
9	Systems Biology of Plant-Microbiome Interactions. <i>Molecular Plant</i> , 2019, 12, 804-821.	3.9	299
10	iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community. <i>Molecular Plant</i> , 2019, 12, 727-730.	3.9	5
11	Drought resistance is mediated by divergent strategies in closely related Brassicaceae. <i>New Phytologist</i> , 2019, 223, 783-797.	3.5	34
12	Independent yet overlapping pathways ensure the robustness and responsiveness of trans-Golgi network functions in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2018, 145, .	1.2	28
13	High-Quality Yeast-Hybrid Interaction Network Mapping. <i>Current Protocols in Plant Biology</i> , 2018, 3, e20067.	2.8	13
14	Big data biology – Just the next big hype?. <i>Current Opinion in Systems Biology</i> , 2017, 4, iv-vi.	1.3	0
15	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	2.3	11
16	LSU network hubs integrate abiotic and biotic stress responses via interaction with the superoxide dismutase FSD2. <i>Journal of Experimental Botany</i> , 2017, 68, 1185-1197.	2.4	39
17	Pooled-matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	3.2	102
18	Cell cycle-regulated PLEIADE/AtMAP65 links membrane and microtubule dynamics during plant cytokinesis. <i>Plant Journal</i> , 2016, 88, 531-541.	2.8	29

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19	Mapping transcription factor interactome networks using HaloTag protein arrays. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4238-47.	3.3	67
20	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189.	2.9	22
21	FYVE1 Is Essential for Vacuole Biogenesis and Intracellular Trafficking in Arabidopsis. Plant Physiology, 2015, 167, 1361-1373.	2.3	110
22	<i>Arabidopsis</i> ALIX is required for the endosomal localization of the deubiquitinating enzyme AMSH3. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5543-51.	3.3	56
23	Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and Diverse Microdomains in <i>Arabidopsis</i> and <i>Nicotiana benthamiana</i>. Plant Cell, 2014, 26, 1698-1711.	3.1	180
24	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	13.5	1,199
25	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. Cell Host and Microbe, 2014, 16, 364-375.	5.1	367
26	Plant Protein Interactomes. Annual Review of Plant Biology, 2013, 64, 161-187.	8.6	135
27	Reproducibility restoredâ€”on toward the human interactome. Nature Methods, 2013, 10, 301-303.	9.0	6
28	Viral Perturbations of Host Networks Reflect Disease Etiology. PLoS Computational Biology, 2012, 8, e1002531.	1.5	102
29	History of proteinâ€“protein interactions: From eggâ€“white to complex networks. Proteomics, 2012, 12, 1478-1498.	1.3	214
30	Interactome mapping for analysis of complex phenotypes: Insights from benchmarking binary interaction assays. Proteomics, 2012, 12, 1499-1518.	1.3	52
31	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	6.0	838
32	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	6.0	776
33	Next-generation sequencing to generate interactome datasets. Nature Methods, 2011, 8, 478-480.	9.0	258
34	A Systematic Screen for CDK4/6 Substrates Links FOXM1 Phosphorylation to Senescence Suppression in Cancer Cells. Cancer Cell, 2011, 20, 620-634.	7.7	449
35	MODELING HOST-PATHOGEN INTERACTIONS: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS FOR INFECTIOUS DISEASE RESEARCH. , 2011, , .		0
36	Reply to "Exhaustive benchmarking of the yeast two-hybrid system". Nature Methods, 2010, 7, 668-668.	9.0	3

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37	An International Bioinformatics Infrastructure to Underpin the <i>Arabidopsis</i> Community. <i>Plant Cell</i> , 2010, 22, 2530-2536.	3.1	23
38	High-Quality Binary Interactome Mapping. <i>Methods in Enzymology</i> , 2010, 470, 281-315.	0.4	126
39	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	9.0	260
40	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	9.0	800
41	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 91-97.	9.0	397
42	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	9.0	288
43	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	6.0	1,297
44	Networking metabolites and diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9849-9850.	3.3	36
45	QUICKstep and GS-TAP: new moves for protein-interaction analysis. <i>Nature Methods</i> , 2006, 3, 975-976.	9.0	5
46	High throughput protein production for functional proteomics. <i>Drug Discovery Today</i> , 2004, 9, S1-7.	3.2	1
47	High throughput protein production for functional proteomics. <i>Trends in Biotechnology</i> , 2003, 21, 383-388.	4.9	162
48	Molecular characterization of lymphatic endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16069-16074.	3.3	436
49	Proteome-scale purification of human proteins from bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2654-2659.	3.3	256
50	Cloning of a catalytic subunit of cAMP-dependent protein kinase from the honeybee (<i>Apis mellifera</i>) and its localization in the brain. <i>Insect Molecular Biology</i> , 2001, 10, 173-181.	1.0	23
51	FLEXGene repository: from sequenced genomes to gene repositories for high-throughput functional biology and proteomics. <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 155-165.	0.5	49
52	Combinatorial roles for pRB, p107, and p130 in E2F-mediated cell cycle control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10820-10825.	3.3	105
53	Genetic characterization of a mammalian protein-protein interaction domain by using a yeast reverse two-hybrid system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10321-10326.	3.3	165