Pascal Braun

List of Publications by Year
in descending order

53 papers	10,500 citations	126907 33 h-index	161849 54 g-index
62 all docs	62 docs citations	62 times ranked	14319 citing authors

#	Article	IF	Citations
1	Chemokine-like MDL proteins modulate flowering time and innate immunity in plants. Journal of Biological Chemistry, 2021, 296, 100611.	3.4	10
2	ARMADILLO REPEAT ONLY proteins confine Rho GTPase signalling to polar growth sites. Nature Plants, 2020, 6, 1275-1288.	9.3	24
3	TRIPP Is a Plant-Specific Component of the Arabidopsis TRAPPII Membrane Trafficking Complex with Important Roles in Plant Development. Plant Cell, 2020, 32, 2424-2443.	6.6	24
4	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11836-11842.	7.1	16
5	Mass-spectrometry-based draft of the Arabidopsis proteome. Nature, 2020, 579, 409-414.	27.8	328
6	Extensive signal integration by the phytohormone protein network. Nature, 2020, 583, 271-276.	27.8	104
7	GROWTH-REGULATING FACTORS Interact with DELLAs and Regulate Growth in Cold Stress. Plant Cell, 2020, 32, 1018-1034.	6.6	108
8	Interactions between Transport Protein Particle (TRAPP) complexes and Rab <scp>GTP</scp>ases in Arabidopsis. Plant Journal, 2019, 100, 279-297.	5.7	27
9	Systems Biology of Plant-Microbiome Interactions. Molecular Plant, 2019, 12, 804-821.	8.3	299
10	iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community. Molecular Plant, 2019, 12, 727-730.	8.3	5
11	Drought resistance is mediated by divergent strategies in closely related Brassicaceae. New Phytologist, 2019, 223, 783-797.	7.3	34
12	Independent yet overlapping pathways ensure the robustness and responsiveness of trans-Golgi network functions in <i>Arabidopsis</i>. Development (Cambridge), 2018, 145, .	2.5	28
13	Highâ€Quality Yeastâ€2â€Hybrid Interaction Network Mapping. Current Protocols in Plant Biology, 2018, 3, e20067.	2.8	13
14	Big data biology â€" Just the next big hype?. Current Opinion in Systems Biology, 2017, 4, iv-vi.	2.6	0
15	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. Plant Physiology, 2017, 175, 1499-1509.	4.8	11
16	LSU network hubs integrate abiotic and biotic stress responses via interaction with the superoxide dismutase FSD2. Journal of Experimental Botany, 2017, 68, 1185-1197.	4.8	39
17	Pooledâ€matrix protein interaction screens using Barcode Fusion Genetics. Molecular Systems Biology, 2016, 12, 863.	7.2	102
18	Cell cycleâ€regulated <scp>PLEIADE</scp>/At<scp>MAP</scp>65â€3 links membrane and microtubule dynamics during plant cytokinesis. Plant Journal, 2016, 88, 531-541.	5.7	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.	7.1	67
20	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189.	6.4	22
21	FYVE1 Is Essential for Vacuole Biogenesis and Intracellular Trafficking in Arabidopsis. Plant Physiology, 2015, 167, 1361-1373.	4.8	110
22	*Arabidopsis* 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.	7.1	56
23	Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and Diverse Microdomains in *Arabidopsis* and *Nicotiana benthamiana* . Plant Cell, 2014, 26, 1698-1711.	6.6	180
24	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	28.9	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.	11.0	367
26	Plant Protein Interactomes. Annual Review of Plant Biology, 2013, 64, 161-187.	18.7	135
27	Reproducibility restored—on toward the human interactome. Nature Methods, 2013, 10, 301-303.	19.0	6
28	Viral Perturbations of Host Networks Reflect Disease Etiology. PLoS Computational Biology, 2012, 8, e1002531.	3.2	102
29	History of protein—protein interactions: From egg–white to complex networks. Proteomics, 2012, 12, 1478-1498.	2.2	214
30	Interactome mapping for analysis of complex phenotypes: Insights from benchmarking binary interaction assays. Proteomics, 2012, 12, 1499-1518.	2.2	52
31	Evidence for Network Evolution in an *Arabidopsis* Interactome Map. Science, 2011, 333, 601-607.	12.6	838
32	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	12.6	776
33	Next-generation sequencing to generate interactome datasets. Nature Methods, 2011, 8, 478-480.	19.0	258
34	A Systematic Screen for CDK4/6 Substrates Links FOXM1 Phosphorylation to Senescence Suppression in Cancer Cells. Cancer Cell, 2011, 20, 620-634.	16.8	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.	19.0	3

#	ARTICLE	IF	CITATIONS
37	An International Bioinformatics Infrastructure to Underpin the <i>Arabidopsis</i> Community. Plant Cell, 2010, 22, 2530-2536.	6.6	23
38	High-Quality Binary Interactome Mapping. Methods in Enzymology, 2010, 470, 281-315.	1.0	126
39	Empirically controlled mapping of the Caenorhabditis elegans protein-protein interactome network. Nature Methods, 2009, 6, 47-54.	19.0	260
40	An empirical framework for binary interactome mapping. Nature Methods, 2009, 6, 83-90.	19.0	800
41	An experimentally derived confidence score for binary protein-protein interactions. Nature Methods, 2009, 6, 91-97.	19.0	397
42	Literature-curated protein interaction datasets. Nature Methods, 2009, 6, 39-46.	19.0	288
43	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. Science, 2008, 322, 104-110.	12.6	1,297
44	Networking metabolites and diseases. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9849-9850.	7.1	36
45	QUICKstep and GS-TAP: new moves for protein-interaction analysis. Nature Methods, 2006, 3, 975-976.	19.0	5
46	High throughput protein production for functional proteomics. Drug Discovery Today, 2004, 9, S1-7.	6.4	1
47	High throughput protein production for functional proteomics. Trends in Biotechnology, 2003, 21, 383-388.	9.3	162
48	Molecular characterization of lymphatic endothelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16069-16074.	7.1	436
49	Proteome-scale purification of human proteins from bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2654-2659.	7.1	256
50	Cloning of a catalytic subunit of cAMP-dependent protein kinase from the honeybee (Apis mellifera) and its localization in the brain. Insect Molecular Biology, 2001, 10, 173-181.	2.0	23
51	FLEXGene repository: from sequenced genomes to gene repositories for high-throughput functional biology and proteomics. Molecular and Biochemical Parasitology, 2001, 118, 155-165.	1.1	49
52	Combinatorial roles for pRB, p107, and p130 in E2F-mediated cell cycle control. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10820-10825.	7.1	105
53	Genetic characterization of a mammalian protein-protein interaction domain by using a yeast reverse two-hybrid system.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 10321-10326.	7.1	165