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	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. Science, 2008, 322, 104-110.	12.6	1,297
2	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	28.9	1,199
3	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	12.6	838
4	An empirical framework for binary interactome mapping. Nature Methods, 2009, 6, 83-90.	19.0	800
5	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	12.6	776
6	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
7	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
8	An experimentally derived confidence score for binary protein-protein interactions. Nature Methods, 2009, 6, 91-97.	19.0	397
9	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
10	Mass-spectrometry-based draft of the Arabidopsis proteome. Nature, 2020, 579, 409-414.	27.8	328
11	Systems Biology of Plant-Microbiome Interactions. Molecular Plant, 2019, 12, 804-821.	8.3	299
12	Literature-curated protein interaction datasets. Nature Methods, 2009, 6, 39-46.	19.0	288
13	Empirically controlled mapping of the Caenorhabditis elegans protein-protein interactome network. Nature Methods, 2009, 6, 47-54.	19.0	260
14	Next-generation sequencing to generate interactome datasets. Nature Methods, 2011, 8, 478-480.	19.0	258
15	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
16	History of protein–protein interactions: From egg‑white to complex networks. Proteomics, 2012, 12, 1478-1498.	2.2	214
17	Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and Diverse Microdomains in<i>Arabidopsis</i>and<i>Nicotiana benthamiana</i>Â Â. Plant Cell, 2014, 26, 1698-1711.	6.6	180
18	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

#	Article	IF	Citations
19	High throughput protein production for functional proteomics. Trends in Biotechnology, 2003, 21, 383-388.	9.3	162
20	Plant Protein Interactomes. Annual Review of Plant Biology, 2013, 64, 161-187.	18.7	135
21	High-Quality Binary Interactome Mapping. Methods in Enzymology, 2010, 470, 281-315.	1.0	126
22	FYVE1 Is Essential for Vacuole Biogenesis and Intracellular Trafficking in Arabidopsis. Plant Physiology, 2015, 167, 1361-1373.	4.8	110
23	GROWTH-REGULATING FACTORS Interact with DELLAs and Regulate Growth in Cold Stress. Plant Cell, 2020, 32, 1018-1034.	6.6	108
24	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
25	Extensive signal integration by the phytohormone protein network. Nature, 2020, 583, 271-276.	27.8	104
26	Viral Perturbations of Host Networks Reflect Disease Etiology. PLoS Computational Biology, 2012, 8, e1002531.	3.2	102
27	Pooled‐matrix protein interaction screens using Barcode Fusion Genetics. Molecular Systems Biology, 2016, 12, 863.	7.2	102
28	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
29	*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
30	Interactome mapping for analysis of complex phenotypes: Insights from benchmarking binary interaction assays. Proteomics, 2012, 12, 1499-1518.	2.2	52
31	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
32	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
33	Networking metabolites and diseases. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9849-9850.	7.1	36
34	Drought resistance is mediated by divergent strategies in closely related Brassicaceae. New Phytologist, 2019, 223, 783-797.	7.3	34
35	Cell cycle‐regulated PLEIADE/AtMAP65‐3 links membrane and microtubule dynamics during plant cytokinesis. Plant Journal, 2016, 88, 531-541.	5.7	29
36	Independent yet overlapping pathways ensure the robustness and responsiveness of trans-Golgi network functions in *Arabidopsis*. Development (Cambridge), 2018, 145, .	2.5	28

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37	Interactions between Transport Protein Particle (TRAPP) complexes and Rab <scp>GTP</scp>ases in Arabidopsis. Plant Journal, 2019, 100, 279-297.	5.7	27
38	ARMADILLO REPEAT ONLY proteins confine Rho GTPase signalling to polar growth sites. Nature Plants, 2020, 6, 1275-1288.	9.3	24
39	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
40	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
41	An International Bioinformatics Infrastructure to Underpin the <i>Arabidopsis</i> Community. Plant Cell, 2010, 22, 2530-2536.	6.6	23
42	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. Cell Reports, 2015, 12, 183-189.	6.4	22
43	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
44	High‐Quality Yeast‐2‐Hybrid Interaction Network Mapping. Current Protocols in Plant Biology, 2018, 3, e20067.	2.8	13
45	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. Plant Physiology, 2017, 175, 1499-1509.	4.8	11
46	Chemokine-like MDL proteins modulate flowering time and innate immunity in plants. Journal of Biological Chemistry, 2021, 296, 100611.	3.4	10
47	Reproducibility restored—on toward the human interactome. Nature Methods, 2013, 10, 301-303.	19.0	6
48	QUICKstep and GS-TAP: new moves for protein-interaction analysis. Nature Methods, 2006, 3, 975-976.	19.0	5
49	iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community. Molecular Plant, 2019, 12, 727-730.	8.3	5
50	Reply to "Exhaustive benchmarking of the yeast two-hybrid system". Nature Methods, 2010, 7, 668-668.	19.0	3
51	High throughput protein production for functional proteomics. Drug Discovery Today, 2004, 9, S1-7.	6.4	1
52	MODELING HOST-PATHOGEN INTERACTIONS: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS FOR INFECTIOUS DISEASE RESEARCH. , 2011, , .		0
53	Big data biology â€" Just the next big hype?. Current Opinion in Systems Biology, 2017, 4, iv-vi.	2.6	0