

Anne-Claude Gavin

List of Publications by Year in descending order

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85
papers

16,385
citations

53751

45
h-index

58549

82
g-index

95
all docs

95
docs citations

95
times ranked

18676
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional organization of the yeast proteome by systematic analysis of protein complexes. <i>Nature</i> , 2002, 415, 141-147.	13.7	4,509
2	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006, 440, 631-636.	13.7	2,347
3	Drug Target Identification Using Side-Effect Similarity. <i>Science</i> , 2008, 321, 263-266.	6.0	1,097
4	A physical and functional map of the human TNF- α /NF- κ B signal transduction pathway. <i>Nature Cell Biology</i> , 2004, 6, 97-105.	4.6	970
5	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010, 7, S56-S68.	9.0	548
6	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	6.0	440
7	90S Pre-Ribosomes Include the 35S Pre-rRNA, the U3 snoRNP, and 40S Subunit Processing Factors but Predominantly Lack 60S Synthesis Factors. <i>Molecular Cell</i> , 2002, 10, 105-115.	4.5	427
8	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	6.0	394
9	Structure-Based Assembly of Protein Complexes in Yeast. <i>Science</i> , 2004, 303, 2026-2029.	6.0	367
10	Interactome map uncovers phosphatidylserine transport by oxysterol-binding proteins. <i>Nature</i> , 2013, 501, 257-261.	13.7	279
11	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
12	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	6.0	267
13	Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011, 7, 511.	3.2	267
14	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	3.2	216
15	A Conserved Circular Network of Coregulated Lipids Modulates Innate Immune Responses. <i>Cell</i> , 2015, 162, 170-183.	13.5	181
16	Crosstalk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	3.2	169
17	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014, 6, 82.	3.6	169
18	Impact of spliceosome mutations on RNA splicing in myelodysplasia: dysregulated genes/pathways and clinical associations. <i>Blood</i> , 2018, 132, 1225-1240.	0.6	168

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19	A MAP kinase docking site is required for phosphorylation and activation of p90 ^{rsk} /MAPKAP kinase-1. <i>Current Biology</i> , 1999, 9, 281-286.	1.8	163
20	The systematic analysis of protein-lipid interactions comes of age. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 753-761.	16.1	148
21	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	3.2	146
22	Defining a minimal cell: essentiality of small ORFs and ncRNAs in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2015, 11, 780.	3.2	133
23	Protein complexes and proteome organization from yeast to man. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 21-27.	2.8	125
24	Visualizing biological data—now and in the future. <i>Nature Methods</i> , 2010, 7, S2-S4.	9.0	115
25	In-Vivo Profiling and Visualization of Cellular Protein-Lipid Interactions Using Bifunctional Fatty Acids. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4033-4038.	7.2	114
26	Recent advances in charting protein-protein interaction: mass spectrometry-based approaches. <i>Current Opinion in Biotechnology</i> , 2011, 22, 42-49.	3.3	113
27	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013, 9, 662.	3.2	110
28	Systematic identification of proteins that elicit drug side effects. <i>Molecular Systems Biology</i> , 2013, 9, 663.	3.2	110
29	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017, 13, 936.	3.2	108
30	Bifunctional Sphingosine for Cell-Based Analysis of Protein-Sphingolipid Interactions. <i>ACS Chemical Biology</i> , 2016, 11, 222-230.	1.6	99
31	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. <i>Nucleic Acids Research</i> , 2015, 43, e10-e10.	6.5	95
32	Cell type-specific chromatin immunoprecipitation from multicellular complex samples using BiTS-ChIP. <i>Nature Protocols</i> , 2012, 7, 978-994.	5.5	90
33	A complex prediction: three-dimensional model of the yeast exosome. <i>EMBO Reports</i> , 2002, 3, 628-635.	2.0	89
34	SIGNAL TRANSDUCTION:Cell Survival Demands Some Rsk. <i>Science</i> , 1999, 286, 1309-1310.	6.0	87
35	The orchestra of lipid-transfer proteins at the crossroads between metabolism and signaling. <i>Progress in Lipid Research</i> , 2016, 61, 30-39.	5.3	85
36	The social network of a cell: Recent advances in interactome mapping. <i>Biotechnology Annual Review</i> , 2008, 14, 1-28.	2.1	84

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37	A quantitative liposome microarray to systematically characterize protein-lipid interactions. <i>Nature Methods</i> , 2014, 11, 47-50.	9.0	77
38	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline. <i>Nature Communications</i> , 2018, 9, 4004.	5.8	71
39	Interaction networks for systems biology. <i>FEBS Letters</i> , 2008, 582, 1220-1224.	1.3	64
40	The deca-GX3 proteins Yae1-Lto1 function as adaptors recruiting the ABC protein Rli1 for iron-sulfur cluster insertion. <i>ELife</i> , 2015, 4, e08231.	2.8	62
41	Casein kinase 2-dependent serine phosphorylation of MuSK regulates acetylcholine receptor aggregation at the neuromuscular junction. <i>Genes and Development</i> , 2006, 20, 1800-1816.	2.7	60
42	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015, 12, 1519-1530.	2.9	59
43	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	6.5	55
44	SnapShot: Protein-Protein Interaction Networks. <i>Cell</i> , 2011, 144, 1000-1000.e1.	13.5	51
45	Mass Spectrometry Reveals Stable Modules in holo and apo RNA Polymerases I and III. <i>Structure</i> , 2011, 19, 90-100.	1.6	47
46	A p90 ^{rsk} Mutant Constitutively Interacting with MAP Kinase Uncouples MAP Kinase from p34 ^{cdc2} /Cyclin B Activation in <i>Xenopus</i> Oocytes. <i>Molecular Biology of the Cell</i> , 1999, 10, 2971-2986.	0.9	44
47	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017, 13, e1005462.	1.5	44
48	Transcription start site associated RNAs in bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 585.	3.2	40
49	Enzymatic complexes across scales. <i>Essays in Biochemistry</i> , 2018, 62, 501-514.	2.1	40
50	APOE2, E3, and E4 differentially modulate cellular homeostasis, cholesterol metabolism, and inflammatory response in isogenic iPSC-derived astrocytes. <i>Stem Cell Reports</i> , 2022, 17, 110-126.	2.3	40
51	Structure of the Kti11/Kti13 Heterodimer and Its Double Role in Modifications of tRNA and Eukaryotic Elongation Factor 2. <i>Structure</i> , 2015, 23, 149-160.	1.6	36
52	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202.	6.5	35
53	Isoform- and cell-state-specific lipidation of ApoE in astrocytes. <i>Cell Reports</i> , 2022, 38, 110435.	2.9	35
54	Phosphatase of regenerating liver (PRL)-3 disrupts epithelial architecture by altering the post-mitotic midbody position. <i>Journal of Cell Science</i> , 2016, 129, 4130-4142.	1.2	33

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55	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. <i>Nature Communications</i> , 2017, 8, 2101.	5.8	33
56	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features. <i>Bioinformatics</i> , 2020, 36, 1213-1218.	1.8	31
57	Structural insights and activating mutations in diverse pathologies define mechanisms of deregulation for phospholipase C gamma enzymes. <i>EBioMedicine</i> , 2020, 51, 102607.	2.7	31
58	Quantitative mass spectrometry of posttranslational modifications: Keys to confidence. <i>Science Signaling</i> , 2015, 8, re5.	1.6	30
59	Cell metabolism regulates integrin mechanosensing via an SLC3A2-dependent sphingolipid biosynthesis pathway. <i>Nature Communications</i> , 2018, 9, 4862.	5.8	28
60	Detection and Characterization of Protein Interactions In Vivo by a Simple Live-Cell Imaging Method. <i>PLoS ONE</i> , 2013, 8, e62195.	1.1	28
61	Dynamic Buffering of Extracellular Chemokine by a Dedicated Scavenger Pathway Enables Robust Adaptation during Directed Tissue Migration. <i>Developmental Cell</i> , 2020, 52, 492-508.e10.	3.1	25
62	A protocol for the systematic and quantitative measurement of protein-lipid interactions using the liposome-microarray-based assay. <i>Nature Protocols</i> , 2016, 11, 1021-1038.	5.5	24
63	Structural Analyses of the Slm1-PH Domain Demonstrate Ligand Binding in the Non-Canonical Site. <i>PLoS ONE</i> , 2012, 7, e36526.	1.1	21
64	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats. <i>PLoS ONE</i> , 2020, 15, e0242677.	1.1	18
65	A generic protocol for the purification and characterization of water-soluble complexes of affinity-tagged proteins and lipids. <i>Nature Protocols</i> , 2014, 9, 2256-2266.	5.5	16
66	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2387-2401.	2.5	14
67	Structural and Functional Characterization of a Phosphatase Domain within Yeast General Transcription Factor IIIC. <i>Journal of Biological Chemistry</i> , 2013, 288, 15110-15120.	1.6	13
68	Glycogen accumulation, central carbon metabolism, and aging of hematopoietic stem and progenitor cells. <i>Scientific Reports</i> , 2020, 10, 11597.	1.6	12
69	Protein co-membership and biochemical affinity purifications. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 325-330.	4.0	6
70	Towards quantitative analysis of proteome dynamics. <i>Nature Biotechnology</i> , 2007, 25, 298-300.	9.4	6
71	CLICK-enabled analogues reveal pregnenolone interactomes in cancer and immune cells. <i>IScience</i> , 2021, 24, 102485.	1.9	6
72	Glucose Metabolism and Aging of Hematopoietic Stem and Progenitor Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3028.	1.8	6

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73	Coupling proteomics and metabolomics for the unsupervised identification of proteinâ€“metabolite interactions in <i>Chaetomium thermophilum</i> . PLoS ONE, 2021, 16, e0254429.	1.1	5
74	Network Biology editorial 2013. Molecular BioSystems, 2013, 9, 1557.	2.9	1
75	Proteomics Analysis of Cellular Network in Human Bone Marrow Reveals Lineage Skewing Towards Megakaryocytes and Decrease in Lymphoid Development upon Aging. Blood, 2016, 128, 2658-2658.	0.6	1
76	Elevated Central Carbon Metabolism - a Hallmark for Senescent Cells in Aging Human Hematopoietic Stem Cell Compartment. Blood, 2021, 138, 1088-1088.	0.6	1
77	The Ribomethylome Landscape of Hematopoietic System. Blood, 2020, 136, 41-42.	0.6	1
78	Expanding the frontiers in proteomics. Drug Discovery Today: Technologies, 2006, 3, 315-316.	4.0	0
79	Systemsâ€“wide analysis of protein complexes in <i>Saccharomyces cerevisiae</i> . FASEB Journal, 2007, 21, A211.	0.2	0
80	Proteome Analyses and Single-Cell RNA Sequencing Reveal Age-Dependent Re-Wiring of Central Carbon Metabolism in Myeloid-Biased Subsets of Human Hematopoietic Stem Cells. Blood, 2018, 132, 873-873.	0.6	0
81	Title is missing!. , 2020, 15, e0242677.		0
82	Title is missing!. , 2020, 15, e0242677.		0
83	Title is missing!. , 2020, 15, e0242677.		0
84	Title is missing!. , 2020, 15, e0242677.		0
85	Title is missing!. , 2020, 15, e0242677.		0