

Anne-Claude Gavin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

86
papers

13,836
citations

42
h-index

95
g-index

95
ext. papers

15,474
ext. citations

15.5
avg, IF

5.57
L-index

#	Paper	IF	Citations
86	Isoform- and cell-state-specific lipidation of ApoE in astrocytes.. <i>Cell Reports</i> , 2022 , 38, 110435	10.6	1
85	Glucose Metabolism and Aging of Hematopoietic Stem and Progenitor Cells.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	1
84	APOE2, E3, and E4 differentially modulate cellular homeostasis, cholesterol metabolism, and inflammatory response in isogenic iPSC-derived astrocytes.. <i>Stem Cell Reports</i> , 2021 ,	8	4
83	Elevated Central Carbon Metabolism - a Hallmark for Senescent Cells in Aging Human Hematopoietic Stem Cell Compartment. <i>Blood</i> , 2021 , 138, 1088-1088	2.2	1
82	CLICK-enabled analogues reveal pregnenolone interactomes in cancer and immune cells. <i>IScience</i> , 2021 , 24, 102485	6.1	1
81	Coupling proteomics and metabolomics for the unsupervised identification of protein-metabolite interactions in <i>Chaetomium thermophilum</i> . <i>PLoS ONE</i> , 2021 , 16, e0254429	3.7	3
80	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	10.2	10
79	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features. <i>Bioinformatics</i> , 2020 , 36, 1213-1218	7.2	10
78	The Ribomethylome Landscape of Hematopoietic System. <i>Blood</i> , 2020 , 136, 41-42	2.2	
77	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	3.7	10
76	Structural insights and activating mutations in diverse pathologies define mechanisms of deregulation for phospholipase C gamma enzymes. <i>EBioMedicine</i> , 2020 , 51, 102607	8.8	17
75	Glycogen accumulation, central carbon metabolism, and aging of hematopoietic stem and progenitor cells. <i>Scientific Reports</i> , 2020 , 10, 11597	4.9	3
74	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
73	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
72	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
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70	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		

69	Impact of spliceosome mutations on RNA splicing in myelodysplasia: dysregulated genes/pathways and clinical associations. <i>Blood</i> , 2018 , 132, 1225-1240	2.2	90
68	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. <i>Blood</i> , 2018 , 132, 873-873	2.2	
67	Cell metabolism regulates integrin mechanosensing via an SLC3A2-dependent sphingolipid biosynthesis pathway. <i>Nature Communications</i> , 2018 , 9, 4862	17.4	17
66	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline. <i>Nature Communications</i> , 2018 , 9, 4004	17.4	38
65	Enzymatic complexes across scales. <i>Essays in Biochemistry</i> , 2018 , 62, 501-514	7.6	22
64	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2387-2401	7.6	10
63	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017 , 13, 936	12.2	79
62	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. <i>Nature Communications</i> , 2017 , 8, 2101	17.4	21
61	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017 , 13, e1005462	5	31
60	The orchestra of lipid-transfer proteins at the crossroads between metabolism and signaling. <i>Progress in Lipid Research</i> , 2016 , 61, 30-9	14.3	64
59	Bifunctional Sphingosine for Cell-Based Analysis of Protein-Sphingolipid Interactions. <i>ACS Chemical Biology</i> , 2016 , 11, 222-30	4.9	68
58	Proteomics Analysis of Cellular Network in Human Bone Marrow Reveals Lineage Skewing Towards Megakaryocytes and Decrease in Lymphoid Development upon Aging. <i>Blood</i> , 2016 , 128, 2658-2658	2.2	
57	PRL-3 disrupts epithelial architecture by altering the post-mitotic midbody position. <i>Journal of Cell Science</i> , 2016 , 129, 4130-4142	5.3	17
56	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, 1192-202	20.1	25
55	A protocol for the systematic and quantitative measurement of protein-lipid interactions using the liposome-microarray-based assay. <i>Nature Protocols</i> , 2016 , 11, 1021-38	18.8	18
54	A Conserved Circular Network of Coregulated Lipids Modulates Innate Immune Responses. <i>Cell</i> , 2015 , 162, 170-83	56.2	123
53	The systematic analysis of protein-lipid interactions comes of age. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 753-61	48.7	119
52	Defining a minimal cell: essentiality of small ORFs and ncRNAs in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2015 , 11, 780	12.2	90

51	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015 , 12, 1519-30	10.6	44
50	Quantitative mass spectrometry of posttranslational modifications: keys to confidence. <i>Science Signaling</i> , 2015 , 8, re5	8.8	27
49	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	5.2	31
48	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. <i>Nucleic Acids Research</i> , 2015 , 43, e10	20.1	57
47	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	8.9	42
46	A quantitative liposome microarray to systematically characterize protein-lipid interactions. <i>Nature Methods</i> , 2014 , 11, 47-50	21.6	66
45	A generic protocol for the purification and characterization of water-soluble complexes of affinity-tagged proteins and lipids. <i>Nature Protocols</i> , 2014 , 9, 2256-66	18.8	15
44	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014 , 6, 82	14.4	126
43	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014 , 42, 13525-33	20.1	40
42	Interactome map uncovers phosphatidylserine transport by oxysterol-binding proteins. <i>Nature</i> , 2013 , 501, 257-61	50.4	235
41	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013 , 9, 662	12.2	86
40	In vivo profiling and visualization of cellular protein-lipid interactions using bifunctional fatty acids. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 4033-8	16.4	86
39	Bifunktionalisierte Fettsäuren zur Visualisierung und Identifizierung von Protein-Lipid-Interaktionen in lebenden Zellen. <i>Angewandte Chemie</i> , 2013 , 125, 4125-4130	3.6	14
38	Systematic identification of proteins that elicit drug side effects. <i>Molecular Systems Biology</i> , 2013 , 9, 663	12.2	91
37	Structural and functional characterization of a phosphatase domain within yeast general transcription factor IIIc. <i>Journal of Biological Chemistry</i> , 2013 , 288, 15110-20	5.4	7
36	Detection and characterization of protein interactions in vivo by a simple live-cell imaging method. <i>PLoS ONE</i> , 2013 , 8, e62195	3.7	18
35	Cell type-specific chromatin immunoprecipitation from multicellular complex samples using BiTS-ChIP. <i>Nature Protocols</i> , 2012 , 7, 978-94	18.8	73
34	Structural analyses of the Slm1-PH domain demonstrate ligand binding in the non-canonical site. <i>PLoS ONE</i> , 2012 , 7, e36526	3.7	16

33	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012 , 8, 599	12.2	171
32	Transcription start site associated RNAs in bacteria. <i>Molecular Systems Biology</i> , 2012 , 8, 585	12.2	35
31	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012 , 8, 571	12.2	144
30	SnapShot: Protein-protein interaction networks. <i>Cell</i> , 2011 , 144, 1000, 1000.e1	56.2	45
29	Mass spectrometry reveals stable modules in holo and apo RNA polymerases I and III. <i>Structure</i> , 2011 , 19, 90-100	5.2	44
28	Recent advances in charting protein-protein interaction: mass spectrometry-based approaches. <i>Current Opinion in Biotechnology</i> , 2011 , 22, 42-9	11.4	96
27	Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011 , 7, 511	12.2	207
26	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010 , 7, S56-68	21.6	459
25	Visualizing biological data-now and in the future. <i>Nature Methods</i> , 2010 , 7, S2-4	21.6	85
24	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010 , 6, 430	12.2	132
23	Impact of genome reduction on bacterial metabolism and its regulation. <i>Science</i> , 2009 , 326, 1263-8	33.3	229
22	Proteome organization in a genome-reduced bacterium. <i>Science</i> , 2009 , 326, 1235-40	33.3	383
21	Transcriptome complexity in a genome-reduced bacterium. <i>Science</i> , 2009 , 326, 1268-71	33.3	341
20	Interaction networks for systems biology. <i>FEBS Letters</i> , 2008 , 582, 1220-4	3.8	55
19	The social network of a cell: recent advances in interactome mapping. <i>Biotechnology Annual Review</i> , 2008 , 14, 1-28		72
18	Drug target identification using side-effect similarity. <i>Science</i> , 2008 , 321, 263-6	33.3	937
17	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007 , 25, 894-8	44.5	229
16	Systems-wide analysis of protein complexes in <i>Saccharomyces cerevisiae</i> . <i>FASEB Journal</i> , 2007 , 21, A2110.9		

15	Casein kinase 2-dependent serine phosphorylation of MuSK regulates acetylcholine receptor aggregation at the neuromuscular junction. <i>Genes and Development</i> , 2006 , 20, 1800-16	12.6	48
14	Protein co-membership and biochemical affinity purifications. <i>Drug Discovery Today: Technologies</i> , 2006 , 3, 325-30	7.1	6
13	Expanding the frontiers in proteomics. <i>Drug Discovery Today: Technologies</i> , 2006 , 3, 315-6	7.1	
12	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006 , 440, 631-6	50.4	2096
11	Structure-based assembly of protein complexes in yeast. <i>Science</i> , 2004 , 303, 2026-9	33.3	308
10	A physical and functional map of the human TNF-alpha/NF-kappa B signal transduction pathway. <i>Nature Cell Biology</i> , 2004 , 6, 97-105	23.4	847
9	Protein complexes and proteome organization from yeast to man. <i>Current Opinion in Chemical Biology</i> , 2003 , 7, 21-7	9.7	115
8	Functional organization of the yeast proteome by systematic analysis of protein complexes. <i>Nature</i> , 2002 , 415, 141-7	50.4	4018
7	A complex prediction: three-dimensional model of the yeast exosome. <i>EMBO Reports</i> , 2002 , 3, 628-35	6.5	84
6	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, 105-15	17.6	395
5	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, 2971-86	3.5	38
4	A MAP kinase docking site is required for phosphorylation and activation of p90(rsk)/MAPKAP kinase-1. <i>Current Biology</i> , 1999 , 9, 281-4	6.3	153
3	Perspectives: signal transduction. Cell survival demands some Rsk. <i>Science</i> , 1999 , 286, 1309-10	33.3	79
2	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features		1
1	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats		3