

# Anne Gonzalez de Peredo

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

2,006  
citations

279798

23  
h-index

377865

34  
g-index

36  
all docs

36  
docs citations

36  
times ranked

3589  
citing authors

#	ARTICLE	IF	CITATIONS
1	Urine in Clinical Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1850-1862.	3.8	368
2	Proline: an efficient and user-friendly software suite for large-scale proteomics. <i>Bioinformatics</i> , 2020, 36, 3148-3155.	4.1	155
3	General Repression of RNA Polymerase III Transcription Is Triggered by Protein Phosphatase Type 2A-Mediated Dephosphorylation of Maf1. <i>Molecular Cell</i> , 2006, 22, 623-632.	9.7	150
4	In-depth Exploration of Cerebrospinal Fluid by Combining Peptide Ligand Library Treatment and Label-free Protein Quantification. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1006-1021.	3.8	116
5	C-Mannosylation and O-Fucosylation of Thrombospondin Type 1 Repeats. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 11-18.	3.8	106
6	Resistance of melanoma to immune checkpoint inhibitors is overcome by targeting the sphingosine kinase-1. <i>Nature Communications</i> , 2020, 11, 437.	12.8	89
7	Quantitative interactomics in primary T cells unveils TCR signal diversification extent and dynamics. <i>Nature Immunology</i> , 2019, 20, 1530-1541.	14.5	78
8	Spectroscopic and Saturation Magnetization Properties of the Manganese- and Cobalt-Substituted Ferric Uptake Regulation (Fur) Protein from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 6248-6260.	2.5	76
9	Extracellular IL-33 cytokine, but not endogenous nuclear IL-33, regulates protein expression in endothelial cells. <i>Scientific Reports</i> , 2016, 6, 34255.	3.3	74
10	Lamellar Bodies of Human Epidermis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2151-2175.	3.8	72
11	Identification of the Two Zinc-Bound Cysteines in the Ferric Uptake Regulation Protein from <i>Escherichia coli</i> : Chemical Modification and Mass Spectrometry Analysis. <i>Biochemistry</i> , 1999, 38, 8582-8589.	2.5	68
12	Benchmarking quantitative label-free LC-MS data processing workflows using a complex spiked proteomic standard dataset. <i>Journal of Proteomics</i> , 2016, 132, 51-62.	2.4	68
13	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. <i>Journal of Proteome Research</i> , 2016, 15, 3998-4019.	3.7	66
14	Conformational changes of the ferric uptake regulation protein upon metal activation and DNA binding; first evidence of structural homologies with the diphtheria toxin repressor. Edited by G. v. Heijne. <i>Journal of Molecular Biology</i> , 2001, 310, 83-91.	4.2	54
15	Co-recruitment analysis of the CBL and CBLB signalosomes in primary T cells identifies CD5 as a key regulator of TCR-induced ubiquitylation. <i>Molecular Systems Biology</i> , 2016, 12, 876.	7.2	41
16	Reversible Redox- and Zinc-Dependent Dimerization of the <i>Escherichia coli</i> Fur Protein. <i>Biochemistry</i> , 2007, 46, 1329-1342.	2.5	40
17	The T cell CD6 receptor operates a multitask signalosome with opposite functions in T cell activation. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	35
18	The costimulatory molecule CD226 signals through VAV1 to amplify TCR signals and promote IL-17 production by CD4 <sup>+</sup> T cells. <i>Science Signaling</i> , 2018, 11, .	3.6	33

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19	Structural studies on protein O-fucosylation by electron capture dissociation. International Journal of Mass Spectrometry, 2004, 234, 11-21.	1.5	32
20	An Optimized Strategy for ICAT Quantification of Membrane Proteins. Molecular and Cellular Proteomics, 2006, 5, 68-78.	3.8	30
21	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data in Brief, 2016, 6, 286-294.	1.0	30
22	Themis1 enhances T cell receptor signaling during thymocyte development by promoting Vav1 activity and Grb2 stability. Science Signaling, 2016, 9, ra51.	3.6	29
23	Asb21±â€œFilamin A Axis Is Essential for Actin Cytoskeleton Remodeling During Heart Development. Circulation Research, 2018, 122, e34-e48.	4.5	29
24	mzDB: A File Format Using Multiple Indexing Strategies for the Efficient Analysis of Large LC-MS/MS and SWATH-MS Data Sets*. Molecular and Cellular Proteomics, 2015, 14, 771-781.	3.8	27
25	Label-free quantitative proteomic analysis of human plasma-derived microvesicles to find protein signatures of abdominal aortic aneurysms. Proteomics - Clinical Applications, 2014, 8, 620-625.	1.6	26
26	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. Scientific Data, 2022, 9, 126.	5.3	20
27	Opposing regulatory functions of the TIM3 (HAVCR2) signalosome in primary effector T cells as revealed by quantitative interactomics. Cellular and Molecular Immunology, 2021, 18, 1581-1583.	10.5	17
28	CD5 signalosome coordinates antagonist TCR signals to control the generation of Treg cells induced by foreign antigens. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12969-12979.	7.1	15
29	Revisiting the Timing of Action of the PAC Adaptor Using Quantitative Proteomics Analysis of Primary T Cells. Journal of Immunology, 2015, 195, 5472-5481.	0.8	14
30	LymphoAtlas: a dynamic and integrated phosphoproteomic resource of <scp>TCR</scp> signaling in primary T cells reveals <scp>ITSN</scp> 2 as a regulator of effector functions. Molecular Systems Biology, 2020, 16, e9524.	7.2	13
31	Synthesis and Biological Evaluation of Flavanones and Flavones Related to Podophyllotoxin.. Chemical and Pharmaceutical Bulletin, 1998, 46, 79-83.	1.3	12
32	IL-33 acts as a costimulatory signal to generate alloreactive Th1 cells in graft-versus-host disease. Journal of Clinical Investigation, 2022, 132, .	8.2	10
33	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. Scientific Data, 2021, 8, 311.	5.3	6
34	Systems-level conservation of the proximal TCR signaling network of mice and humans. Journal of Experimental Medicine, 2022, 219, .	8.5	6
35	The EuPA Standardization Initiative. EuPA Open Proteomics, 2016, 11, 31-32.	2.5	0