Anne Gonzalez de Peredo

List of Publications by Year
in descending order

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	Systems-level conservation of the proximal TCR signaling network of mice and humans. Journal of Experimental Medicine, 2022, 219, .	8.5	6
2	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. Scientific Data, 2022, 9, 126.	5.3	20
3	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
4	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
5	The T cell CD6 receptor operates a multitask signalosome with opposite functions in T cell activation. Journal of Experimental Medicine, 2021, 218, .	8.5	35
6	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. Scientific Data, 2021, 8, 311.	5.3	6
7	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
8	Proline: an efficient and user-friendly software suite for large-scale proteomics. Bioinformatics, 2020, 36, 3148-3155.	4.1	155
9	Resistance of melanoma to immune checkpoint inhibitors is overcome by targeting the sphingosine kinase-1. Nature Communications, 2020, 11, 437.	12.8	89
10	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
11	Quantitative interactomics in primary T cells unveils TCR signal diversification extent and dynamics. Nature Immunology, 2019, 20, 1530-1541.	14.5	78
12	Asb2Î±â€“Filamin A Axis Is Essential for Actin Cytoskeleton Remodeling During Heart Development. Circulation Research, 2018, 122, e34-e48.	4.5	29
13	The costimulatory molecule CD226 signals through VAV1 to amplify TCR signals and promote IL-17 production by CD4 ⁺ T cells. Science Signaling, 2018, 11, .	3.6	33
14	Themis1 enhances T cell receptor signaling during thymocyte development by promoting Vav1 activity and Grb2 stability. Science Signaling, 2016, 9, ra51.	3.6	29
15	Extracellular IL-33 cytokine, but not endogenous nuclear IL-33, regulates protein expression in endothelial cells. Scientific Reports, 2016, 6, 34255.	3.3	74
16	The EuPA Standardization Initiative. EuPA Open Proteomics, 2016, 11, 31-32.	2.5	0
17	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. Journal of Proteome Research, 2016, 15, 3998-4019.	3.7	66
18	Coâ€recruitment analysis of the <scp>CBL</scp> and <scp>CBLB</scp> signalosomes in primary T cells identifies <scp>CD</scp> 5 as a key regulator of <scp>TCR</scp> â€induced ubiquitylation. Molecular Systems Biology, 2016, 12, 876.	7.2	41

#	Article	IF	Citations
19	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data in Brief, 2016, 6, 286-294.	1.0	30
20	Benchmarking quantitative label-free LCâ€"MS data processing workflows using a complex spiked proteomic standard dataset. Journal of Proteomics, 2016, 132, 51-62.	2.4	68
21	Revisiting the Timing of Action of the PAG Adaptor Using Quantitative Proteomics Analysis of Primary T Cells. Journal of Immunology, 2015, 195, 5472-5481.	0.8	14
22	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
23	Labelâ€free quantitative proteomic analysis of human plasmaâ€derived microvesicles to find protein signatures of abdominal aortic aneurysms. Proteomics - Clinical Applications, 2014, 8, 620-625.	1.6	26
24	In-depth Exploration of Cerebrospinal Fluid by Combining Peptide Ligand Library Treatment and Label-free Protein Quantification. Molecular and Cellular Proteomics, 2010, 9, 1006-1021.	3.8	116
25	Urine in Clinical Proteomics. Molecular and Cellular Proteomics, 2008, 7, 1850-1862.	3.8	368
26	Lamellar Bodies of Human Epidermis. Molecular and Cellular Proteomics, 2008, 7, 2151-2175.	3.8	72
27	Reversible Redox- and Zinc-Dependent Dimerization of theEscherichia coliFur Protein. Biochemistry, 2007, 46, 1329-1342.	2.5	40
28	General Repression of RNA Polymerase III Transcription Is Triggered by Protein Phosphatase Type 2A-Mediated Dephosphorylation of Maf1. Molecular Cell, 2006, 22, 623-632.	9.7	150
29	An Optimized Strategy for ICAT Quantification of Membrane Proteins. Molecular and Cellular Proteomics, 2006, 5, 68-78.	3.8	30
30	Structural studies on protein O-fucosylation by electron capture dissociation. International Journal of Mass Spectrometry, 2004, 234, 11-21.	1.5	32
31	C-Mannosylation and O-Fucosylation of Thrombospondin Type 1 Repeats. Molecular and Cellular Proteomics, 2002, 1, 11-18.	3.8	106
32	Conformational changes of the ferric uptake regulation protein upon metal activation and DNA binding; first evidence of structural homologies with the diphtheria toxin repressor11Edited by G. v. Heijne. Journal of Molecular Biology, 2001, 310, 83-91.	4.2	54
33	Identification of the Two Zinc-Bound Cysteines in the Ferric Uptake Regulation Protein from <i>Escherichia coli</i>:â€‰ Chemical Modification and Mass Spectrometry Analysis. Biochemistry, 1999, 38, 8582-8589.	2.5	68
34	Spectroscopic and Saturation Magnetization Properties of the Manganese- and Cobalt-Substituted Fur (Ferric Uptake Regulation) Protein fromEscherichia coliâ€. Biochemistry, 1999, 38, 6248-6260.	2.5	76
35	Synthesis and Biological Evaluation of Flavanones and Flavones Related to Podophyllotoxin.. Chemical and Pharmaceutical Bulletin, 1998, 46, 79-83.	1.3	12