Jerome Garin

List of Publications by Year in descending order

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50276 82547 11,379 72 46 72 citations h-index g-index papers 73 73 73 14447 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Proteomic Analysis of Dendritic Cell-Derived Exosomes: A Secreted Subcellular Compartment Distinct from Apoptotic Vesicles. Journal of Immunology, 2001, 166, 7309-7318.	0.8	1,360
2	Molecular Characterization of Dendritic Cell-Derived Exosomes. Journal of Cell Biology, 1999, 147, 599-610.	5.2	950
3	The Phagosome Proteome. Journal of Cell Biology, 2001, 152, 165-180.	5. 2	665
4	Yap1 and Skn7 Control Two Specialized Oxidative Stress Response Regulons in Yeast. Journal of Biological Chemistry, 1999, 274, 16040-16046.	3.4	489
5	AT_CHLORO, a Comprehensive Chloroplast Proteome Database with Subplastidial Localization and Curated Information on Envelope Proteins. Molecular and Cellular Proteomics, 2010, 9, 1063-1084.	3.8	425
6	Isotope-labeled Protein Standards. Molecular and Cellular Proteomics, 2007, 6, 2139-2149.	3.8	409
7	Proteomics of the Chloroplast Envelope Membranes from Arabidopsis thaliana. Molecular and Cellular Proteomics, 2003, 2, 325-345.	3.8	405
8	The early responses of Arabidopsis thaliana cells to cadmium exposure explored by protein and metabolite profiling analyses. Proteomics, 2006, 6, 2180-2198.	2.2	348
9	New zwitterionic detergents improve the analysis of membrane proteins by two-dimensional electrophoresis. Electrophoresis, 1998, 19, 1901-1909.	2.4	344
10	A Proteomics Dissection of Arabidopsis thaliana Vacuoles Isolated from Cell Culture. Molecular and Cellular Proteomics, 2007, 6, 394-412.	3.8	294
11	Isotope dilution strategies for absolute quantitative proteomics. Journal of Proteomics, 2009, 72, 740-749.	2.4	292
12	Flotillin-1-enriched Lipid Raft Domains Accumulate on Maturing Phagosomes. Journal of Biological Chemistry, 2001, 276, 18507-18512.	3.4	275
13	Pericentric heterochromatin reprogramming by new histone variants during mouse spermiogenesis. Journal of Cell Biology, 2007, 176, 283-294.	5.2	261
14	Integral membrane proteins of the chloroplast envelope: Identification and subcellular localization of new transporters. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11487-11492.	7.1	241
15	Identification of New Intrinsic Proteins in Arabidopsis Plasma Membrane Proteome. Molecular and Cellular Proteomics, 2004, 3, 675-691.	3.8	233
16	Two-dimensional electrophoresis of human placental mitochondria and protein identification by mass spectrometry: Toward a human mitochondrial proteome. Electrophoresis, 1998, 19, 1006-1014.	2.4	218
17	Chloroplast Proteomics and the Compartmentation of Plastidial Isoprenoid Biosynthetic Pathways. Molecular Plant, 2009, 2, 1154-1180.	8.3	199
18	Histone-Modifying Complexes Regulate Gene Expression Pertinent to the Differentiation of the Protozoan Parasite Toxoplasma gondii. Molecular and Cellular Biology, 2005, 25, 10301-10314.	2.3	172

#	Article	IF	CITATIONS
19	A Proteomic Survey of Chlamydomonas reinhardtii Mitochondria Sheds New Light on the Metabolic Plasticity of the Organelle and on the Nature of the Â-Proteobacterial Mitochondrial Ancestor. Molecular Biology and Evolution, 2009, 26, 1533-1548.	8.9	172
20	An Extended Proteome Map of the Lysosomal Membrane Reveals Novel Potential Transporters. Molecular and Cellular Proteomics, 2013, 12, 1572-1588.	3.8	172
21	Regulation of the V-ATPase along the Endocytic Pathway Occurs through Reversible Subunit Association and Membrane Localization. PLoS ONE, 2008, 3, e2758.	2.5	168
22	Investigating the plant response to cadmium exposure by proteomic and metabolomic approaches. Proteomics, $2011,11,1650\text{-}1663$.	2,2	168
23	Non-canonical Transit Peptide for Import into the Chloroplast. Journal of Biological Chemistry, 2002, 277, 47770-47778.	3.4	154
24	Towards the recovery of hydrophobic proteins on two-dimensional electrophoresis gels. Electrophoresis, 1999, 20, 705-711.	2.4	153
25	Chloroplast proteomics highlights the subcellular compartmentation of lipid metabolism. Progress in Lipid Research, 2010, 49, 128-158.	11.6	153
26	Organic solvent extraction as a versatile procedure to identify hydrophobic chloroplast membrane proteins. Electrophoresis, 2000, 21, 3517-3526.	2.4	152
27	A survey of the plant mitochondrial proteome in relation to development. Proteomics, 2002, 2, 880.	2.2	152
28	Analysis of the proteins targeted by CDSP32, a plastidic thioredoxin participating in oxidative stress responses. Plant Journal, 2004, 41, 31-42.	5.7	143
29	The hydrophobic proteome of mitochondrial membranes from Arabidopsis cell suspensions. Phytochemistry, 2004, 65, 1693-1707.	2.9	135
30	A High Content in Lipid-modified Peripheral Proteins and Integral Receptor Kinases Features in the Arabidopsis Plasma Membrane Proteome. Molecular and Cellular Proteomics, 2007, 6, 1980-1996.	3.8	128
31	The Mammalian Passenger Protein TD-60 Is an RCC1 Family Member with an Essential Role in Prometaphase to Metaphase Progression. Developmental Cell, 2003, 5, 295-307.	7.0	122
32	Protein Standard Absolute Quantification (PSAQ) for improved investigation of staphylococcal food poisoning outbreaks. Proteomics, 2008, 8, 4633-4636.	2.2	121
33	Pyruvate Formate-lyase and a Novel Route of Eukaryotic ATP Synthesis in Chlamydomonas Mitochondria*. Journal of Biological Chemistry, 2006, 281, 9909-9918.	3.4	118
34	Dendritic cell derived-exosomes: biology and clinical implementations. Journal of Leukocyte Biology, 2006, 80, 471-478.	3.3	117
35	Calcium-dependent secretion in human neutrophils: A proteomic approach. Electrophoresis, 2000, 21, 665-672.	2.4	111
36	Differential extraction of hydrophobic proteins from chloroplast envelope membranes: a subcellular-specific proteomic approach to identify rare intrinsic membrane proteins. Plant Journal, 1999, 19, 217-228.	5.7	100

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37	Proteomic analysis of human lysosomes: Application to monocytic and breast cancer cells. Proteomics, 2002, 2, 1026.	2.2	97
38	Distinct protein patterns associated with Listeria monocytogenes InlA- or InlB-phagosomes. Cellular Microbiology, 2002, 4, 101-115.	2.1	85
39	Accurate Quantification of Cardiovascular Biomarkers in Serum Using Protein Standard Absolute Quantification (PSAQâ,,¢) and Selected Reaction Monitoring. Molecular and Cellular Proteomics, 2012, 11, M111.008235.	3.8	71
40	15N-Metabolic labeling for comparative plasma membrane proteomics in Arabidopsis cells. Proteomics, 2007, 7, 750-754.	2.2	68
41	PSAQâ,,¢ standards for accurate MS–based quantification of proteins: from the concept to biomedical applications. Journal of Mass Spectrometry, 2012, 47, 1353-1363.	1.6	68
42	Proteomics of chloroplast envelope membranes. Photosynthesis Research, 2003, 78, 205-230.	2.9	63
43	Toward a standardized urine proteome analysis methodology. Proteomics, 2011, 11, 1160-1171.	2.2	56
44	Peptide Storage: Are You Getting the Best Return on Your Investment? Defining Optimal Storage Conditions for Proteomics Samples. Journal of Proteome Research, 2009, 8, 3778-3785.	3.7	50
45	Purification of Toxoplasma dense granule proteins reveals that they are in complexes throughout the secretory pathway. Molecular and Biochemical Parasitology, 2008, 157, 13-21.	1.1	49
46	Proteomic analysis of the eukaryotic parasiteEncephalitozoon cuniculi (microsporidia): a reference map for proteins expressed in late sporogonial stages. Proteomics, 2006, 6, 3625-3635.	2.2	47
47	Proteomic Analysis of S-Acylated Proteins in Human B Cells Reveals Palmitoylation of the Immune Regulators CD20 and CD23. PLoS ONE, 2012, 7, e37187.	2.5	47
48	Production and Use of Stable Isotope-Labeled Proteins for Absolute Quantitative Proteomics. Methods in Molecular Biology, 2011, 753, 93-115.	0.9	43
49	\hat{l}^3 -Secretase-Dependent Proteolysis of CD44 Promotes Neoplastic Transformation of Rat Fibroblastic Cells. Cancer Research, 2006, 66, 3681-3687.	0.9	40
50	Development of a Protein Standard Absolute Quantification (PSAQâ,,¢) assay for the quantification of Staphylococcus aureus enterotoxin A in serum. Journal of Proteomics, 2012, 75, 3041-3049.	2.4	39
51	A versatile method for deciphering plant membrane proteomes. Journal of Experimental Botany, 2006, 57, 1579-1589.	4.8	33
52	An Optimized Strategy for ICAT Quantification of Membrane Proteins. Molecular and Cellular Proteomics, 2006, 5, 68-78.	3.8	30
53	PepLine: A Software Pipeline for High-Throughput Direct Mapping of Tandem Mass Spectrometry Data on Genomic Sequences. Journal of Proteome Research, 2008, 7, 1873-1883.	3.7	28
54	Mass spectrometryâ€based absolute protein quantification: <scp>PSAQ</scp> â,,¢ strategy makes use of "noncanonical―proteotypic peptides. Proteomics, 2012, 12, 1217-1221.	2.2	28

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55	Protein Arginylation in Rat Brain Cytosol: A Proteomic Analysis. Neurochemical Research, 2006, 31, 401-409.	3.3	27
56	Large-Scale SRM Screen of Urothelial Bladder Cancer Candidate Biomarkers in Urine. Journal of Proteome Research, 2017, 16, 1617-1631.	3.7	25
57	Identification of proteins binding the native tubulin dimer. Biochemical and Biophysical Research Communications, 2005, 327, 35-42.	2.1	24
58	Dynamics of Arabidopsis thaliana soluble proteome in response to different nutrient culture conditions. Electrophoresis, 2006, 27, 495-507.	2.4	24
59	<i>DIGESTIF</i> : A Universal Quality Standard for the Control of Bottom-Up Proteomics Experiments. Journal of Proteome Research, 2015, 14, 787-803.	3.7	24
60	Multiplex and accurate quantification of acute kidney injury biomarker candidates in urine using Protein Standard Absolute Quantification (PSAQ) and targeted proteomics. Talanta, 2017, 164, 77-84.	5.5	24
61	Identification in Saccharomyces cerevisiae of a New Stable Variant of Alkyl Hydroperoxide Reductase 1 (Ahp1) Induced by Oxidative Stress. Journal of Biological Chemistry, 2002, 277, 4823-4830.	3.4	21
62	Proteomic strategy for the identification of critical actors in reorganization of the post-meiotic male genome. Molecular Human Reproduction, 2012, 18, 1-13.	2.8	21
63	Expression profiling of genes and proteins in HaCaT keratinocytes: Proliferating versus differentiated state. Journal of Cellular Biochemistry, 2004, 93, 1048-1062.	2.6	20
64	Introducing AAA-MS, a Rapid and Sensitive Method for Amino Acid Analysis Using Isotope Dilution and High-Resolution Mass Spectrometry. Journal of Proteome Research, 2012, 11, 3929-3936.	3.7	20
65	Intracellular localization of p40, a protein identified in a preparation of lysosomal membranes. Biochemical Journal, 2006, 395, 39-47.	3.7	16
66	Prospects for monolithic nano-LC columns in shotgun proteomics. Analytical and Bioanalytical Chemistry, 2008, 392, 1291-1297.	3.7	16
67	Activated leukocyte cell adhesion molecule modulates neurotrophin signaling. Journal of Neurochemistry, 2012, 121, 575-586.	3.9	14
68	Mass Spectrometry-based Workflow for Accurate Quantification of Escherichia coli Enzymes: How Proteomics Can Play a Key Role in Metabolic Engineering. Molecular and Cellular Proteomics, 2014, 13, 954-968.	3.8	14
69	Influence of mass resolution on species matching in accurate mass and retention time (AMT) tag proteomics experiments. Rapid Communications in Mass Spectrometry, 2008, 22, 986-992.	1.5	13
70	High-density rafts preferentially host the complement activator measles virus F glycoprotein but not the regulators of complement activation. Molecular Immunology, 2008, 45, 3036-3044.	2.2	7
71	Introducing plasma/serum glycodepletion for the targeted proteomics analysis of cytolysis biomarkers. Talanta, 2017, 170, 473-480.	5.5	7
72	Mass Spectrometry-Based Proteomics Reveal Alcohol Dehydrogenase 1B as a Blood Biomarker Candidate to Monitor Acetaminophen-Induced Liver Injury. International Journal of Molecular Sciences, 2021, 22, 11071.	4.1	1