## Chiara D'ambrosio

## List of Publications by Year in descending order

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93 papers 4,359 citations

38 h-index 63 g-index

94 all docs 94
docs citations

94 times ranked 5834 citing authors

#	Article	IF	CITATIONS
1	APE1/Ref-1 Interacts with NPM1 within Nucleoli and Plays a Role in the rRNA Quality Control Process. Molecular and Cellular Biology, 2009, 29, 1834-1854.	2.3	209
2	Biochemical characterization and bacterial expression of an odorant-binding protein from Locusta migratoria. Cellular and Molecular Life Sciences, 2003, 60, 390-400.	5.4	174
3	Soluble proteins of chemical communication in the social wasp Polistes dominulus. Cellular and Molecular Life Sciences, 2003, 60, 1933-1943.	5.4	154
4	Proteins from bovine tissues and biological fluids: Defining a reference electrophoresis map for liver, kidney, muscle, plasma and red blood cells. Proteomics, 2003, 3, 440-460.	2.2	152
5	Exploring the Chicken Egg White Proteome with Combinatorial Peptide Ligand Libraries. Journal of Proteome Research, 2008, 7, 3461-3474.	3.7	150
6	Proteomic analysis of tomato fruits from two ecotypes during ripening. Proteomics, 2006, 6, 3781-3791.	2.2	148
7	The Structure of Rigidoporus lignosus Laccase Containing a Full Complement of Copper lons, Reveals an Asymmetrical Arrangement for the T3 Copper Pair. Journal of Molecular Biology, 2004, 342, 1519-1531.	4.2	140
8	Glomerular Autoimmune Multicomponents of Human Lupus Nephritis In Vivo. Journal of the American Society of Nephrology: JASN, 2014, 25, 2483-2498.	6.1	112
9	Mammalian APE1 controls miRNA processing and its interactome is linked to cancer RNA metabolism. Nature Communications, 2017, 8, 797.	12.8	107
10	Critical lysine residues within the overlooked N-terminal domain of human APE1 regulate its biological functions. Nucleic Acids Research, 2010, 38, 8239-8256.	14.5	105
11	Transcriptomic and proteomic analysis of a compatible tomato-aphid interaction reveals a predominant salicylic acid-dependent plant response. BMC Genomics, 2013, 14, 515.	2.8	103
12	Nucleolar accumulation of APE1 depends on charged lysine residues that undergo acetylation upon genotoxic stress and modulate its BER activity in cells. Molecular Biology of the Cell, 2012, 23, 4079-4096.	2.1	99
13	A proteomic characterization of water buffalo milk fractions describing PTM of major species and the identification of minor components involved in nutrient delivery and defense against pathogens. Proteomics, 2008, 8, 3657-3666.	2.2	94
14	Dairy products and the Maillard reaction: A promising future for extensive food characterization by integrated proteomics studies. Food Chemistry, 2017, 219, 477-489.	8.2	92
15	A proteomic approach to identify early molecular targets of oxidative stress in human epithelial lens cells. Biochemical Journal, 2004, 378, 929-937.	3.7	91
16	Genomeâ€wide analysis and proteomic studies reveal APE1/Refâ€1 multifunctional role in mammalian cells. Proteomics, 2009, 9, 1058-1074.	2.2	90
17	Structure, conformation and biological activity of a novel lipodepsipeptide from Pseudomonas corrugata: cormycin A1. Biochemical Journal, 2004, 384, 25-36.	3.7	86
18	Transcription regulation by the adaptor protein Fe65 and the nucleosome assembly factor SET. EMBO Reports, 2005, 6, 77-82.	4.5	86

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19	Proteomic analysis of apricot fruit during ripening. Journal of Proteomics, 2013, 78, 39-57.	2.4	76
20	SIRT1 gene expression upon genotoxic damage is regulated by APE1 through nCaRE-promoter elements. Molecular Biology of the Cell, 2014, 25, 532-547.	2.1	74
21	Nonâ€enzymatic glycation and glycoxidation protein products in foods and diseases: An interconnected, complex scenario fully open to innovative proteomic studies. Mass Spectrometry Reviews, 2014, 33, 49-77.	5.4	71
22	Cooperative activity of Ref-1/APE and ERp57 in reductive activation of transcription factors. Free Radical Biology and Medicine, 2006, 41, 1113-1123.	2.9	69
23	Oxidized Transthyretin in Amniotic Fluid as an Early Marker of Preeclampsia. Journal of Proteome Research, 2007, 6, 160-170.	3.7	65
24	Proteomic analysis of the major soluble components in Annurca apple flesh. Molecular Nutrition and Food Research, 2007, 51, 255-262.	3.3	62
25	Knock-in reconstitution studies reveal an unexpected role of Cys-65 in regulating APE1/Ref-1 subcellular trafficking and function. Molecular Biology of the Cell, 2011, 22, 3887-3901.	2.1	62
26	The expression of tomato prosystemin gene in tobacco plants highly affects host proteomic repertoire. Journal of Proteomics, 2008, 71, 176-185.	2.4	59
27	New role for leucyl aminopeptidase in glutathione turnover. Biochemical Journal, 2004, 378, 35-44.	3.7	58
28	Overoxidation of peroxiredoxins as an immediate and sensitive marker of oxidative stress in HepG2 cells and its application to the redox effects induced by ischemia/reperfusion in human liver. Free Radical Research, 2005, 39, 255-268.	3.3	58
29	Proteome analysis ofNeisseria meningitidis serogroup A. Proteomics, 2004, 4, 2893-2926.	2.2	57
30	Hyperphosphorylation of JNK-interacting Protein 1, a Protein Associated with Alzheimer Disease. Molecular and Cellular Proteomics, 2006, 5, 97-113.	3.8	57
31	A proteomic study on human osteoblastic cells proliferation and differentiation. Proteomics, 2006, 6, 3520-3532.	2.2	55
32	Proteomic analysis of liver tissues subjected to early ischemia/reperfusion injury during human orthotopic liver transplantation. Proteomics, 2006, 6, 3455-3465.	2.2	53
33	Antimicrobial peptide induction in the haemolymph of the Mexican scorpion Centruroides limpidus limpidus in response to septic injury. Cellular and Molecular Life Sciences, 2004, 61, 1507-1519.	5.4	51
34	A study of Streptococcus thermophilus proteome by integrated analytical procedures and differential expression investigations. Proteomics, 2006, 6, 181-192.	2.2	51
35	Growth Factor Receptor-bound Protein 2 Interaction with the Tyrosine-phosphorylated Tail of Amyloid $\hat{l}^2$ Precursor Protein Is Mediated by Its Src Homology 2 Domain. Journal of Biological Chemistry, 2004, 279, 25374-25380.	3.4	50
36	Probing the Dimeric Structure of Porcine Aminoacylase 1 by Mass Spectrometric and Modeling Procedures. Biochemistry, 2003, 42, 4430-4443.	2.5	47

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37	Overexpression of 14-3-3 proteins enhances cold tolerance and increases levels of stress-responsive proteins of Arabidopsis plants. Plant Science, 2019, 289, 110215.	3.6	47
38	Comparative proteomic analysis of mammalian animal tissues and body fluids: bovine proteome database. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 815, 157-168.	2.3	44
39	Integrated analytical approach in veal calves administered the anabolic androgenic steroids boldenone and boldione: urine and plasma kinetic profile and changes in plasma protein expression. Proteomics, 2007, 7, 3184-3193.	2.2	39
40	Gambling on putative biomarkers of osteoarthritis and osteochondrosis by equine synovial fluid proteomics. Journal of Proteomics, 2012, 75, 4478-4493.	2.4	37
41	Aurora-A recruitment and centrosomal maturation are regulated by a Golgi-activated pool of Src during G2. Nature Communications, 2016, 7, 11727.	12.8	37
42	Helicobacter pyloriimmunoproteomes in case reports of rosacea and chronic urticaria. Proteomics, 2005, 5, 777-787.	2.2	34
43	An Odorant-Binding Protein Is Abundantly Expressed in the Nose and in the Seminal Fluid of the Rabbit. PLoS ONE, 2014, 9, e111932.	2.5	34
44	Identification of miRâ€494 direct targets involved in senescence of human diploid fibroblasts. FASEB Journal, 2014, 28, 3720-3733.	0.5	34
45	Identification of a microRNA (miR-663a) induced by ER stress and its target gene PLOD3 by a combined microRNome and proteome approach. Cell Biology and Toxicology, 2016, 32, 285-303.	5.3	33
46	The cytosolic chaperone α-Crystallin B rescues appropriate folding and compartmentalization of misfolded multispan transmembrane proteins. Journal of Cell Science, 2013, 126, 4160-72.	2.0	31
47	Differential representation of albumins and globulins during grain development in durum wheat and its possible functional consequences. Journal of Proteomics, 2017, 162, 86-98.	2.4	31
48	Identification of the Ligands of Protein Interaction Domains through a Functional Approach. Molecular and Cellular Proteomics, 2007, 6, 333-345.	3.8	30
49	Analytical methodologies for the detection and structural characterization of phosphorylated proteins. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 849, 163-180.	2.3	30
50	BRCA1 modulates the expression of hnRNPA2B1 and KHSRP. Cell Cycle, 2010, 9, 4666-4673.	2.6	30
51	Identification of Early Represented Gluten Proteins during Durum Wheat Grain Development. Journal of Agricultural and Food Chemistry, 2017, 65, 3242-3250.	5.2	28
52	Multiple plasma proteins control atrial natriuretic peptide (ANP) aggregation. Journal of Molecular Endocrinology, 2004, 33, 335-341.	2.5	27
53	Proteomic evaluation of core biopsy specimens from breast lesions. Cancer Letters, 2004, 204, 79-86.	7.2	27
54	"Cheek-to-cheek―urinary proteome profiling via combinatorial peptide ligand libraries: A novel, unexpected elution system. Journal of Proteomics, 2012, 75, 796-805.	2.4	27

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55	APE1 polymorphic variants cause persistent genomic stress and affect cancer cell proliferation. Oncotarget, 2016, 7, 26293-26306.	1.8	27
56	Secretory Proteins as Potential Semiochemical Carriers in the Horse. Biochemistry, 2006, 45, 13418-13428.	2.5	25
57	Proteomic Signatures in Thapsigargin-Treated Hepatoma Cells. Chemical Research in Toxicology, 2011, 24, 1215-1222.	3.3	25
58	Mechanistic studies on bovine cytosolic 5'-nucleotidase II, an enzyme belonging to the HAD superfamily. FEBS Journal, 2004, 271, 4881-4891.	0.2	24
59	A widespread picture of the Streptococcus thermophilus proteome by cell lysate fractionation and gel-based/gel-free approaches. Proteomics, 2007, 7, 1420-1433.	2.2	24
60	Combinatorial peptide ligand libraries for the analysis of lowâ€expression proteins: Validation for normal urine and definition of a first protein MAP. Proteomics, 2012, 12, 509-515.	2.2	22
61	Architecture of The Human Ape1 Interactome Defines Novel Cancers Signatures. Scientific Reports, 2020, 10, 28.	3.3	22
62	Increased anaerobic metabolism is a distinctive signature in a colorectal cancer cellular model of resistance to antiepidermal growth factor receptor antibody. Proteomics, 2013, 13, 866-877.	2.2	21
63	A differential proteomic approach to identify proteins associated with thyroid cell transformation. Journal of Molecular Endocrinology, 2005, 34, 199-207.	2.5	20
64	DNA-binding Activity of the ERp57 C-terminal Domain Is Related to a Redox-dependent Conformational Change. Journal of Biological Chemistry, 2007, 282, 10299-10310.	3.4	20
65	Small HDL form via apo A-I a complex with atrial natriuretic peptide. Biochemical and Biophysical Research Communications, 2004, 315, 16-21.	2.1	18
66	Fibromodulin Gene Transcription Is Induced by Ultraviolet Irradiation, and Its Regulation Is Impaired in Senescent Human Fibroblasts. Journal of Biological Chemistry, 2005, 280, 31809-31817.	3.4	18
67	Low-protein/high-carbohydrate diet induces AMPK-dependent canonical and non-canonical thermogenesis in subcutaneous adipose tissue. Redox Biology, 2020, 36, 101633.	9.0	18
68	Nucleotide receptors stimulation by extracellular ATP controls Hsp90 expression through APE1/Ref-1 in thyroid cancer cells: A novel tumorigenic pathway. Journal of Cellular Physiology, 2006, 209, 44-55.	4.1	17
69	A combined ANXA2-NDRG1-STAT1 gene signature predicts response to chemoradiotherapy in cervical cancer. Journal of Experimental and Clinical Cancer Research, 2019, 38, 279.	8.6	16
70	Proteomic analysis reveals novel common genes modulated in both replicative and stress-induced senescence. Journal of Proteomics, 2015, 128, 18-29.	2.4	15
71	Tuberomics: a molecular profiling for the adaption of edible fungi (Tuber magnatum Pico) to different natural environments. BMC Genomics, 2020, 21, 90.	2.8	15
72	Mass Spectrometric Characterization of Proteins Modified by Nitric Oxideâ€Derived Species. Methods in Enzymology, 2008, 440, 3-15.	1.0	11

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73	Mass Spectrometry-Based Approaches for Structural Studies on Protein Complexes at Low-Resolution. Current Proteomics, 2007, 4, 1-16.	0.3	10
74	Mapping phosphoproteins in <i>Neisseria meningitidis</i> serogroup A. Proteomics, 2011, 11, 1351-1358.	2.2	10
75	DNAJC17 is localized in nuclear speckles and interacts with splicing machinery components. Scientific Reports, 2018, 8, 7794.	3.3	10
76	Identification of RNA-binding proteins that partner with Lin28a to regulate Dnmt3a expression. Scientific Reports, 2021, 11, 2345.	3.3	10
77	Selective Ion Tracing and MSnAnalysis of Peptide Digests from FSBA-Treated Kinases for the Analysis of Protein ATP-Binding Sites. Journal of Proteome Research, 2006, 5, 2019-2024.	3.7	9
78	Urine proteome analysis in Dent's disease shows high selective changes potentially involved in chronic renal damage. Journal of Proteomics, 2016, 130, 26-32.	2.4	9
79	AMOTL2 interaction with TAZ causes the inhibition of surfactant proteins expression in lung cells. Gene, 2013, 529, 300-306.	2.2	8
80	Combinatorial Peptide Ligand Library and two dimensional electrophoresis: New frontiers in the study of peritoneal dialysis effluent in pediatric patients. Journal of Proteomics, 2015, 116, 68-80.	2.4	8
81	An αB-Crystallin Peptide Rescues Compartmentalization and Trafficking Response to Cu Overload of ATP7B-H1069Q, the Most Frequent Cause of Wilson Disease in the Caucasian Population. International Journal of Molecular Sciences, 2018, 19, 1892.	4.1	8
82	Study on prevalence and bacterial etiology of mastitis, and effects of subclinical mastitis and stage of lactation on SCC in dairy goats in Egypt. Tropical Animal Health and Production, 2020, 52, 3091-3097.	1.4	8
83	A comparative study of carbonic anhydrase activity in lymphocytes from colorectal cancer tissues and adjacent healthy counterparts. Journal of Enzyme Inhibition and Medicinal Chemistry, 2022, 37, 1651-1655.	5.2	8
84	Poly(ADP-ribose) polymerase 1 binds to Pax8 and inhibits its transcriptional activity. Journal of Molecular Endocrinology, 2008, 41, 379-388.	2.5	7
85	Effect of short-term water restriction on oxidative and inflammatory status of sheep ( Ovis aries ) reared in Southern Italy. Small Ruminant Research, 2018, 162, 77-84.	1.2	6
86	Cleavage of the APE1 N-Terminal Domain in Acute Myeloid Leukemia Cells Is Associated with Proteasomal Activity. Biomolecules, 2020, 10, 531.	4.0	6
87	A Differential Proteomic Approach Reveals an Evolutionary Conserved Regulation of Nme Proteins by Fe65 in C.Âelegans and Mouse. Neurochemical Research, 2008, 33, 2547-2555.	3.3	5
88	Proteomic Analysis of Sera from Common Variable Immunodeficiency Patients Undergoing Replacement Intravenous Immunoglobulin Therapy. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-10.	3.0	4
89	Novel Biomarkers of Mastitis in Goat Milk Revealed by MALDI-TOF-MS-Based Peptide Profiling. Biology, 2020, 9, 193.	2.8	4
90	Inhibition of <i>PID1/NYGGF4/PCLI1</i> gene expression highlights its role in the early events of the cell cycle in NIH3T3 fibroblasts. Journal of Enzyme Inhibition and Medicinal Chemistry, 2016, 31, 45-53.	5.2	2

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91	A Proteomic Approach to Study Escherichia coli. Acetyl Esterase Interactors Unveil a Sequence Motif Involved in Protein-Protein Interaction. Protein and Peptide Letters, 2008, 15, 333-340.	0.9	1
92	Proteomic Characterization of Nonenzymatic Modifications Induced in Bovine Milk Following Thermal Treatments., 2017,, 241-260.		1
93	Bovine hemoglobin polymorphism: a novel alpha-globin variant identified in the Agerolese breed from southern Italy. Czech Journal of Animal Science, 2015, 60, 145-151.	1.3	O