

Carmela Giglione

List of Publications by Year in descending order

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79
papers

4,620
citations

101543

36
h-index

106344

65
g-index

81
all docs

81
docs citations

81
times ranked

5018
citing authors

#	ARTICLE	IF	CITATIONS
1	The Proteomics of N-terminal Methionine Cleavage. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2336-2349.	3.8	326
2	Paternal Control of Embryonic Patterning in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2009, 323, 1485-1488.	12.6	298
3	The Host Antimicrobial Peptide Bac71-35 Binds to Bacterial Ribosomal Proteins and Inhibits Protein Synthesis. <i>Chemistry and Biology</i> , 2014, 21, 1639-1647.	6.0	191
4	The Scope, Functions, and Dynamics of Posttranslational Protein Modifications. <i>Annual Review of Plant Biology</i> , 2019, 70, 119-151.	18.7	158
5	Peptide deformylase as a target for new generation, broad spectrum antimicrobial agents. <i>Molecular Microbiology</i> , 2002, 36, 1197-1205.	2.5	157
6	N-terminal protein modifications: Bringing back into play the ribosome. <i>Biochimie</i> , 2015, 114, 134-146.	2.6	150
7	Unexpected Protein Families Including Cell Defense Components Feature in the N-Myristoylome of a Higher Eukaryote. <i>Journal of Biological Chemistry</i> , 2003, 278, 43418-43429.	3.4	145
8	Comparative Large Scale Characterization of Plant versus Mammal Proteins Reveals Similar and Idiosyncratic N-terminal Acetylation Features. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015131.	3.8	143
9	Extent of N-terminal modifications in cytosolic proteins from eukaryotes. <i>Proteomics</i> , 2008, 8, 2809-2831.	2.2	136
10	Comparative metagenomics of microbial traits within oceanic viral communities. <i>ISME Journal</i> , 2011, 5, 1178-1190.	9.8	135
11	Control of protein life-span by N-terminal methionine excision. <i>EMBO Journal</i> , 2003, 22, 13-23.	7.8	134
12	An Unusual Peptide Deformylase Features in the Human Mitochondrial N-terminal Methionine Excision Pathway. <i>Journal of Biological Chemistry</i> , 2003, 278, 52953-52963.	3.4	119
13	Downregulation of N-terminal acetylation triggers ABA-mediated drought responses in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2015, 6, 7640.	12.8	119
14	The Crystal Structures of Four Peptide Deformylases Bound to the Antibiotic Actinonin Reveal Two Distinct Types: A Platform for the Structure-based Design of Antibacterial Agents. <i>Journal of Molecular Biology</i> , 2002, 320, 951-962.	4.2	118
15	Two N-Terminal Acetyltransferases Antagonistically Regulate the Stability of a Nod-Like Receptor in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 1547-1562.	6.6	102
16	Organellar peptide deformylases: universality of the N-terminal methionine cleavage mechanism. <i>Trends in Plant Science</i> , 2001, 6, 566-572.	8.8	100
17	Molecular identification and functional characterization of the first N-terminal acetyltransferase in plastids by global acetylome profiling. <i>Proteomics</i> , 2015, 15, 2426-2435.	2.2	92
18	N-Myristoylation Regulates the SnRK1 Pathway in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 2804-2821.	6.6	91

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19	Distinctive features of the two classes of eukaryotic peptide deformylases 1 Edited by G. von Heijne. Journal of Molecular Biology, 2001, 314, 695-708.	4.2	76
20	Tools for analyzing and predicting N-terminal protein modifications. Proteomics, 2008, 8, 626-649.	2.2	74
21	Functional and Developmental Impact of Cytosolic Protein N-Terminal Methionine Excision in Arabidopsis. Plant Physiology, 2005, 137, 623-637.	4.8	72
22	Roles of N-Terminal Fatty Acid Acylations in Membrane Compartment Partitioning: Arabidopsis h-Type Thioredoxins as a Case Study. Plant Cell, 2013, 25, 1056-1077.	6.6	70
23	Processed N-termini of mature proteins in higher eukaryotes and their major contribution to dynamic proteomics. Biochimie, 2005, 87, 701-712.	2.6	67
24	Myristoylation, an Ancient Protein Modification Mirroring Eukaryogenesis and Evolution. Trends in Biochemical Sciences, 2020, 45, 619-632.	7.5	66
25	Impact of the N-terminal amino acid on targeted protein degradation. Biological Chemistry, 2006, 387, 839-51.	2.5	62
26	Structural and genomic decoding of human and plant myristoylomes reveals a definitive recognition pattern. Nature Chemical Biology, 2018, 14, 671-679.	8.0	62
27	Discovery and Refinement of a New Structural Class of Potent Peptide Deformylase Inhibitors. Journal of Medicinal Chemistry, 2007, 50, 10-20.	6.4	60
28	Proteome-wide analysis of the amino terminal status of Escherichia coli proteins at the steady-state and upon deformylation inhibition. Proteomics, 2015, 15, 2503-2518.	2.2	58
29	High-resolution snapshots of human N-myristoyltransferase in action illuminate a mechanism promoting N-terminal Lys and Gly myristoylation. Nature Communications, 2020, 11, 1132.	12.8	58
30	Targeted Profiling of Arabidopsis thaliana Subproteomes Illuminates Co- and Posttranslationally N-Terminal Myristoylated Proteins. Plant Cell, 2018, 30, 543-562.	6.6	54
31	Dual lysine and N-terminal acetyltransferases reveal the complexity underpinning protein acetylation. Molecular Systems Biology, 2020, 16, e9464.	7.2	53
32	Dynamics of posttranslational modifications and protein stability in the stroma of Chlamydomonas reinhardtii chloroplasts. Proteomics, 2011, 11, 1734-1750.	2.2	51
33	Interplay Between N-Terminal Methionine Excision and FtsH Protease Is Essential for Normal Chloroplast Development and Function in Arabidopsis. Plant Cell, 2011, 23, 3745-3760.	6.6	46
34	NatB-Mediated N-Terminal Acetylation Affects Growth and Biotic Stress Responses. Plant Physiology, 2020, 182, 792-806.	4.8	44
35	New peptide deformylase inhibitors and cooperative interaction: a combination to improve antibacterial activity. Journal of Antimicrobial Chemotherapy, 2012, 67, 1392-1400.	3.0	42
36	Cotranslational processing mechanisms: towards a dynamic 3D model. Trends in Biochemical Sciences, 2009, 34, 417-426.	7.5	41

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37	Structure-Activity Relationship Analysis of the Peptide Deformylase Inhibitor 5-Bromo-L-tryptophan-tryptophan-acetohydroxamic Acid. <i>ChemMedChem</i> , 2009, 4, 261-275.	3.2	41
38	Golgi Traffic and Integrity Depend on N-Myristoyl Transferase-1 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 1756-1773.	6.6	39
39	Cotranslational Proteolysis Dominates Glutathione Homeostasis to Support Proper Growth and Development. <i>Plant Cell</i> , 2009, 21, 3296-3314.	6.6	38
40	The Crystal Structure of Mitochondrial (Type 1A) Peptide Deformylase Provides Clear Guidelines for the Design of Inhibitors Specific for the Bacterial Forms*. <i>Journal of Biological Chemistry</i> , 2005, 280, 42315-42324.	3.4	35
41	New Antibiotic Molecules: Bypassing the Membrane Barrier of Gram Negative Bacteria Increases the Activity of Peptide Deformylase Inhibitors. <i>PLoS ONE</i> , 2009, 4, e6443.	2.5	35
42	Expanded impact of protein N-myristoylation in plants. <i>Plant Signaling and Behavior</i> , 2008, 3, 501-502.	2.4	32
43	Ion mobility coupled to native mass spectrometry as a relevant tool to investigate extremely small ligand-induced conformational changes. <i>Analyst</i> , 2015, 140, 7234-7245.	3.5	32
44	MetAP1 and MetAP2 drive cell selectivity for a potent anti-cancer agent in synergy, by controlling glutathione redox state. <i>Oncotarget</i> , 2016, 7, 63306-63323.	1.8	32
45	Trapping Conformational States Along Ligand-Binding Dynamics of Peptide Deformylase: The Impact of Induced Fit on Enzyme Catalysis. <i>PLoS Biology</i> , 2011, 9, e1001066.	5.6	30
46	Rice Peptide Deformylase PDF1B is Crucial for Development of Chloroplasts. <i>Plant and Cell Physiology</i> , 2008, 49, 1536-1546.	3.1	28
47	High-throughput profiling of N-myristoylation substrate specificity across species including pathogens. <i>Proteomics</i> , 2013, 13, 25-36.	2.2	28
48	A unique peptide deformylase platform to rationally design and challenge novel active compounds. <i>Scientific Reports</i> , 2016, 6, 35429.	3.3	28
49	Alternative and effective proteomic analysis in <i>Arabidopsis</i> . <i>Proteomics</i> , 2007, 7, 3788-3799.	2.2	27
50	Evolution-Driven Versatility of N Terminal Acetylation in Photoautotrophs. <i>Trends in Plant Science</i> , 2021, 26, 375-391.	8.8	27
51	Protein lipidation meets proteomics. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 6326.	3.0	25
52	The <i>Arabidopsis</i> N-acetyltransferase NAA60 locates to the plasma membrane and is vital for the high salt stress response. <i>New Phytologist</i> , 2020, 228, 554-569.	7.3	25
53	SILProNAQ: A Convenient Approach for Proteome-Wide Analysis of Protein N-Termini and N-Terminal Acetylation Quantitation. <i>Methods in Molecular Biology</i> , 2017, 1574, 17-34.	0.9	24
54	Peptide deformylase as an emerging target for antiparasitic agents. <i>Expert Opinion on Therapeutic Targets</i> , 2001, 5, 41-57.	1.0	23

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55	NAA50 Is an Enzymatically Active N^{\pm} -Acetyltransferase That Is Crucial for Development and Regulation of Stress Responses. <i>Plant Physiology</i> , 2020, 183, 1502-1516.	4.8	23
56	The Ras GDP/GTP cycle is regulated by oxidizing agents at the level of Ras regulators and effectors. <i>FEBS Letters</i> , 2001, 492, 139-145.	2.8	22
57	The intriguing realm of protein biogenesis: Facing the green co-translational protein maturation networks. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 531-550.	2.3	22
58	Differential actions of p60c-Src and Lck kinases on the Ras regulators p120-GAP and GDP/GTP exchange factor CDC25Mm. <i>FEBS Journal</i> , 2001, 268, 3275-3283.	0.2	21
59	Synthesis and evaluation of 1-(1H-indol-3-yl)ethanamine derivatives as new antibacterial agents. <i>Biorganic and Medicinal Chemistry</i> , 2011, 19, 3204-3215.	3.0	20
60	Mapping the myristoylome through a complete understanding of protein myristoylation biochemistry. <i>Progress in Lipid Research</i> , 2022, 85, 101139.	11.6	19
61	Resistance to anti-peptide deformylase drugs. <i>Expert Opinion on Therapeutic Targets</i> , 2001, 5, 415-418.	3.4	16
62	Mutations in Three Distinct Loci Cause Resistance to Peptide Deformylase Inhibitors in <i>Bacillus subtilis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 1673-1678.	3.2	16
63	A New Function of p120-GTPase-activating Protein. <i>Journal of Biological Chemistry</i> , 1997, 272, 25128-25134.	3.4	14
64	High yield production of myristoylated Arf6 small GTPase by recombinant N-myristoyl transferase. <i>Small GTPases</i> , 2013, 4, 3-8.	1.6	14
65	EnCOUNTER: a parsing tool to uncover the mature N-terminus of organelle-targeted proteins in complex samples. <i>BMC Bioinformatics</i> , 2017, 18, 182.	2.6	14
66	Raf-1 Is Involved in the Regulation of the Interaction between Guanine Nucleotide Exchange Factor and Ha-Ras. <i>Journal of Biological Chemistry</i> , 1998, 273, 34737-34744.	3.4	12
67	Type 3 peptide deformylases are required for oxidative phosphorylation in <i>Trypanosoma brucei</i> . <i>Molecular Microbiology</i> , 2007, 65, 1218-1228.	2.5	12
68	Structure-activity relationship analysis and therapeutic potential of peptide deformylase inhibitors. <i>Current Opinion in Investigational Drugs</i> , 2004, 5, 809-22.	2.3	11
69	HYPK promotes the activity of the N^{\pm} -acetyltransferase A complex to determine proteostasis of nonAc-X N^{\pm} -degron-containing proteins. <i>Science Advances</i> , 2022, 8, .	10.3	11
70	N-myristoyltransferases inhibitory activity of ellagitannins from <i>Terminalia bentzo</i> (L.) L. f. subsp. <i>bentzo</i> . <i>FÄ-toterapÄ-Äç</i> , 2018, 131, 91-95.	2.2	9
71	N-acetylation of secreted proteins in Apicomplexa is widespread and is independent of the ER acetyl-CoA transporter AT1. <i>Journal of Cell Science</i> , 2022, 135, .	2.0	7
72	The C-terminal residue of phage Vp16 PDF, the smallest peptide deformylase, acts as an offset element locking the active conformation. <i>Scientific Reports</i> , 2017, 7, 11041.	3.3	6

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73	A Continuous Assay Set to Screen and Characterize Novel Protein N-Acetyltransferases Unveils Rice General Control Non-repressible 5-Related N-Acetyltransferase2 Activity. <i>Frontiers in Plant Science</i> , 2022, 13, 832144.	3.6	6
74	Understanding the highly efficient catalysis of prokaryotic peptide deformylases by shedding light on the determinants specifying the low activity of the human counterpart. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 242-252.	2.5	5
75	N-terminal modifications contribute to flowering time and immune response regulations. <i>Plant Signaling and Behavior</i> , 2015, 10, e1073874.	2.4	5
76	Influence of various endogenous and artefact modifications on large-scale proteomics analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 443-450.	1.5	4
77	Peptide deformylases from <i>Vibrio parahaemolyticus</i> phage and bacteria display similar deformylase activity and inhibitor binding clefts. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 348-355.	2.3	4
78	Seeking new targets for antiparasitic agents. <i>Trends in Parasitology</i> , 2001, 17, 7-8.	3.3	3
79	Chemical Modification of <i>Bacillus thuringiensis</i> Subsp. <i>aizawai</i> Î-Endotoxin : Implication of Arginine Residues in <i>Bombyx mori</i> Toxicity. <i>Pesticide Biochemistry and Physiology</i> , 1994, 50, 15-22.	3.6	0