

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	Mapping the myristoylome through a complete understanding of protein myristoylation biochemistry. <i>Progress in Lipid Research</i> , 2022, 85, 101139.	11.6	19
2	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
3	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
4	HYPK promotes the activity of the N ^ε -acetyltransferase A complex to determine proteostasis of nonAc-X ² /N-degron ^ε containing proteins. <i>Science Advances</i> , 2022, 8, .	10.3	11
5	Evolution-Driven Versatility of N Terminal Acetylation in Photoautotrophs. <i>Trends in Plant Science</i> , 2021, 26, 375-391.	8.8	27
6	NatB-Mediated N-Terminal Acetylation Affects Growth and Biotic Stress Responses. <i>Plant Physiology</i> , 2020, 182, 792-806.	4.8	44
7	NAA50 Is an Enzymatically Active N ^ε -Acetyltransferase That Is Crucial for Development and Regulation of Stress Responses. <i>Plant Physiology</i> , 2020, 183, 1502-1516.	4.8	23
8	The Arabidopsis N ^ε -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
9	High-resolution snapshots of human N-myristoyltransferase in action illuminate a mechanism promoting N-terminal Lys and Gly myristoylation. <i>Nature Communications</i> , 2020, 11, 1132.	12.8	58
10	Myristoylation, an Ancient Protein Modification Mirroring Eukaryogenesis and Evolution. <i>Trends in Biochemical Sciences</i> , 2020, 45, 619-632.	7.5	66
11	Dual lysine and N ^ε -terminal acetyltransferases reveal the complexity underpinning protein acetylation. <i>Molecular Systems Biology</i> , 2020, 16, e9464.	7.2	53
12	The Scope, Functions, and Dynamics of Posttranslational Protein Modifications. <i>Annual Review of Plant Biology</i> , 2019, 70, 119-151.	18.7	158
13	Targeted Profiling of <i>Arabidopsis thaliana</i> Subproteomes Illuminates Co- and Posttranslationally N-Terminal Myristoylated Proteins. <i>Plant Cell</i> , 2018, 30, 543-562.	6.6	54
14	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
15	N-myristoyltransferases inhibitory activity of ellagitannins from <i>Terminalia bitorquata</i> (L.) L. f. subsp. <i>bentzo</i> . <i>FÄ-toterapÄ-Äç</i> , 2018, 131, 91-95.	2.2	9
16	Structural and genomic decoding of human and plant myristoylomes reveals a definitive recognition pattern. <i>Nature Chemical Biology</i> , 2018, 14, 671-679.	8.0	62
17	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
18	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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19	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
20	A unique peptide deformylase platform to rationally design and challenge novel active compounds. <i>Scientific Reports</i> , 2016, 6, 35429.	3.3	28
21	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
22	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
23	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
24	Proteome-wide analysis of the amino terminal status of <i>Escherichia coli</i> proteins at the steady-state and upon deformylation inhibition. <i>Proteomics</i> , 2015, 15, 2503-2518.	2.2	58
25	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
26	Downregulation of N-terminal acetylation triggers ABA-mediated drought responses in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2015, 6, 7640.	12.8	119
27	Ion mobility coupled to native mass spectrometry as a relevant tool to investigate extremely small ligand-induced conformational changes. <i>Analyst, The</i> , 2015, 140, 7234-7245.	3.5	32
28	N-terminal modifications contribute to flowering time and immune response regulations. <i>Plant Signaling and Behavior</i> , 2015, 10, e1073874.	2.4	5
29	N-terminal protein modifications: Bringing back into play the ribosome. <i>Biochimie</i> , 2015, 114, 134-146.	2.6	150
30	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
31	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
32	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
33	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
34	High-throughput profiling of N-myristoylation substrate specificity across species including pathogens. <i>Proteomics</i> , 2013, 13, 25-36.	2.2	28
35	Roles of N-Terminal Fatty Acid Acylations in Membrane Compartment Partitioning: <i>Arabidopsis</i> h-Type Thioredoxins as a Case Study. <i>Plant Cell</i> , 2013, 25, 1056-1077.	6.6	70
36	High yield production of myristoylated Arf6 small GTPase by recombinant N-myristoyl transferase. <i>Small GTPases</i> , 2013, 4, 3-8.	1.6	14

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37	Comparative Large Scale Characterization of Plant versus Mammal Proteins Reveals Similar and Idiosyncratic N- \pm -Acetylation Features. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015131.	3.8	143
38	New peptide deformylase inhibitors and cooperative interaction: a combination to improve antibacterial activity. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1392-1400.	3.0	42
39	Comparative metagenomics of microbial traits within oceanic viral communities. <i>ISME Journal</i> , 2011, 5, 1178-1190.	9.8	135
40	Dynamics of post-translational modifications and protein stability in the stroma of <i>Chlamydomonas reinhardtii</i> chloroplasts. <i>Proteomics</i> , 2011, 11, 1734-1750.	2.2	51
41	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
42	Interplay Between N-Terminal Methionine Excision and FtsH Protease Is Essential for Normal Chloroplast Development and Function in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011, 23, 3745-3760.	6.6	46
43	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
44	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
45	Cotranslational Proteolysis Dominates Glutathione Homeostasis to Support Proper Growth and Development. <i>Plant Cell</i> , 2009, 21, 3296-3314.	6.6	38
46	Cotranslational processing mechanisms: towards a dynamic 3D model. <i>Trends in Biochemical Sciences</i> , 2009, 34, 417-426.	7.5	41
47	Structure-Activity Relationship Analysis of the Peptide Deformylase Inhibitor 5-Bromo-1-H-indole-3-acetohydroxamic Acid. <i>ChemMedChem</i> , 2009, 4, 261-275.	3.2	41
48	Paternal Control of Embryonic Patterning in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2009, 323, 1485-1488.	12.6	298
49	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
50	Tools for analyzing and predicting N-terminal protein modifications. <i>Proteomics</i> , 2008, 8, 626-649.	2.2	74
51	Extent of N-terminal modifications in cytosolic proteins from eukaryotes. <i>Proteomics</i> , 2008, 8, 2809-2831.	2.2	136
52	Expanded impact of protein N-myristoylation in plants. <i>Plant Signaling and Behavior</i> , 2008, 3, 501-502.	2.4	32
53	Rice Peptide Deformylase PDF1B is Crucial for Development of Chloroplasts. <i>Plant and Cell Physiology</i> , 2008, 49, 1536-1546.	3.1	28
54	Protein lipidation meets proteomics. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 6326.	3.0	25

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55	<i>N</i> -Myristoylation Regulates the SnRK1 Pathway in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 2804-2821.	6.6	91
56	Discovery and Refinement of a New Structural Class of Potent Peptide Deformylase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2007, 50, 10-20.	6.4	60
57	Alternative and effective proteomic analysis in <i>Arabidopsis</i> . <i>Proteomics</i> , 2007, 7, 3788-3799.	2.2	27
58	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
59	The Proteomics of N-terminal Methionine Cleavage. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2336-2349.	3.8	326
60	Impact of the N-terminal amino acid on targeted protein degradation. <i>Biological Chemistry</i> , 2006, 387, 839-51.	2.5	62
61	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
62	Functional and Developmental Impact of Cytosolic Protein N-Terminal Methionine Excision in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 137, 623-637.	4.8	72
63	Processed N-termini of mature proteins in higher eukaryotes and their major contribution to dynamic proteomics. <i>Biochimie</i> , 2005, 87, 701-712.	2.6	67
64	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
65	Control of protein life-span by N-terminal methionine excision. <i>EMBO Journal</i> , 2003, 22, 13-23.	7.8	134
66	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
67	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
68	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
69	Peptide deformylase as a target for new generation, broad spectrum antimicrobial agents. <i>Molecular Microbiology</i> , 2002, 36, 1197-1205.	2.5	157
70	Peptide deformylase as an emerging target for antiparasitic agents. <i>Expert Opinion on Therapeutic Targets</i> , 2001, 5, 41-57.	1.0	23
71	Distinctive features of the two classes of eukaryotic peptide deformylases 1 Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 2001, 314, 695-708.	4.2	76
72	Organellar peptide deformylases: universality of the N-terminal methionine cleavage mechanism. <i>Trends in Plant Science</i> , 2001, 6, 566-572.	8.8	100

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73	The Ras GDP/GTP cycle is regulated by oxidizing agents at the level of Ras regulators and effectors. FEBS Letters, 2001, 492, 139-145.	2.8	22
74	Resistance to anti-peptide deformylase drugs. Expert Opinion on Therapeutic Targets, 2001, 5, 415-418.	3.4	16
75	Differential actions of p60c-Src and Lck kinases on the Ras regulators p120-GAP and GDP/GTP exchange factor CDC25Mm. FEBS Journal, 2001, 268, 3275-3283.	0.2	21
76	Seeking new targets for antiparasitic agents. Trends in Parasitology, 2001, 17, 7-8.	3.3	3
77	Raf-1 Is Involved in the Regulation of the Interaction between Guanine Nucleotide Exchange Factor and Ha-Ras. Journal of Biological Chemistry, 1998, 273, 34737-34744.	3.4	12
78	A New Function of p120-GTPase-activating Protein. Journal of Biological Chemistry, 1997, 272, 25128-25134.	3.4	14
79	Chemical Modification of Bacillus thuringiensis Subsp. aizawai $\hat{\text{I}}$ -Endotoxin : Implication of Arginine Residues in Bombyx mori Toxicity. Pesticide Biochemistry and Physiology, 1994, 50, 15-22.	3.6	0