Natalie G Ahn

List of Publications by Year
in descending order

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77 papers	9,255 citations	101384 36 h-index	88477 70 g-index
88 all docs	88 docs citations	88 times ranked	12463 citing authors

#	Article	IF	Citations
1	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.	9.4	1,710
2	Signal Transduction through MAP Kinase Cascades. Advances in Cancer Research, 1998, 74, 49-139.	1.9	1,551
3	Comparison of Label-free Methods for Quantifying Human Proteins by Shotgun Proteomics. Molecular and Cellular Proteomics, 2005, 4, 1487-1502.	2.5	1,063
4	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	9.0	452
5	Protein Analysis by Hydrogen Exchange Mass Spectrometry. Annual Review of Biophysics and Biomolecular Structure, 2003, 32, 1-25.	18.3	354
6	Docking Motif Interactions in MAP Kinases Revealed by Hydrogen Exchange Mass Spectrometry. Molecular Cell, 2004, 14, 43-55.	4.5	278
7	Identification of Novel MAP Kinase Pathway Signaling Targets by Functional Proteomics and Mass Spectrometry. Molecular Cell, 2000, 6, 1343-1354.	4.5	246
8	Wnt5a Control of Cell Polarity and Directional Movement by Polarized Redistribution of Adhesion Receptors. Science, 2008, 320, 365-369.	6.0	229
9	Improving Reproducibility and Sensitivity in Identifying Human Proteins by Shotgun Proteomics. Analytical Chemistry, 2004, 76, 3556-3568.	3.2	225
10	Activation of the MKK/ERK Pathway during Somatic Cell Mitosis: Direct Interactions of Active ERK with Kinetochores and Regulation of the Mitotic 3F3/2 Phosphoantigen. Journal of Cell Biology, 1998, 142, 1533-1545.	2.3	217
11	Structure of histone-based chromatin in Archaea. Science, 2017, 357, 609-612.	6.0	149
12	Thermal-activated protein mobility and its correlation with catalysis in thermophilic alcohol dehydrogenase. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9556-9561.	3.3	134
13	Interdependent Domains Controlling the Enzymatic Activity of Mitogen-Activated Protein Kinase Kinase 1â€. Biochemistry, 1996, 35, 15529-15536.	1.2	131
14	Distinct Cell Cycle Timing Requirements for Extracellular Signal-Regulated Kinase and Phosphoinositide 3-Kinase Signaling Pathways in Somatic Cell Mitosis. Molecular and Cellular Biology, 2002, 22, 7226-7241.	1.1	130
15	Identification of Novel Phosphorylation Sites on Xenopus laevis Aurora A and Analysis of Phosphopeptide Enrichment by Immobilized Metal-affinity Chromatography. Molecular and Cellular Proteomics, 2003, 2, 1055-1067.	2.5	127
16	Functional Proteomics Identifies Targets of Phosphorylation by B-Raf Signaling in Melanoma. Molecular Cell, 2009, 34, 115-131.	4.5	127
17	Mitotic Phosphorylation of Golgi Reassembly Stacking Protein 55 by Mitogen-activated Protein Kinase ERK2. Molecular Biology of the Cell, 2001, 12, 1811-1817.	0.9	106
18	The gatekeeper residue controls autoactivation of ERK2 via a pathway of intramolecular connectivity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18101-18106.	3.3	97

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19	A Phosphoproteomic Comparison of B-RAFV600E and MKK1/2 Inhibitors in Melanoma Cells*. Molecular and Cellular Proteomics, 2015, 14, 1599-1615.	2.5	94
20	Proteomics and genomics: perspectives on drug and target discovery. Current Opinion in Chemical Biology, 2008, 12, 1-3.	2.8	92
21	Proteomics strategies for protein identification. FEBS Letters, 2005, 579, 885-889.	1.3	80
22	Deuterium Exchange Mass Spectrometry as a Probe of Protein Kinase Activation. Analysis of Wild-Type and Constitutively Active Mutants of MAP Kinase Kinase-1â€. Biochemistry, 1998, 37, 463-475.	1.2	78
23	Networks for the allosteric control of protein kinases. Current Opinion in Structural Biology, 2006, 16, 686-692.	2.6	74
24	Modeling deuterium exchange behavior of ERK2 using pepsin mapping to probe secondary structure. Journal of the American Society for Mass Spectrometry, 1999, 10, 685-702.	1.2	71
25	Side Population Cells from Human Melanoma Tumors Reveal Diverse Mechanisms for Chemoresistance. Journal of Investigative Dermatology, 2012, 132, 2440-2450.	0.3	68
26	Phosphorylation releases constraints to domain motion in ERK2. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2506-2511.	3.3	67
27	Protein phosphorylation analysis by electrospray ionization-mass spectrometry. Methods in Enzymology, 1997, 283, 29-44.	0.4	57
28	Mass Spectrometric Analysis of 40 S Ribosomal Proteins from Rat-1 Fibroblasts. Journal of Biological Chemistry, 1996, 271, 28189-28198.	1.6	55
29	Wnt5a Directs Polarized Calcium Gradients by Recruiting Cortical Endoplasmic Reticulum to the Cell Trailing Edge. Developmental Cell, 2013, 26, 645-657.	3.1	55
30	Achieving In-Depth Proteomics Profiling by Mass Spectrometry. ACS Chemical Biology, 2007, 2, 39-52.	1.6	54
31	The Cac1 subunit of histone chaperone CAF-1 organizes CAF-1-H3/H4 architecture and tetramerizes histones. ELife, 2016, 5, .	2.8	51
32	Improved Validation of Peptide MS/MS Assignments Using Spectral Intensity Prediction. Molecular and Cellular Proteomics, 2007, 6, 1-17.	2.5	46
33	Centromere protein F includes two sites that couple efficiently to depolymerizing microtubules. Journal of Cell Biology, 2015, 209, 813-828.	2.3	46
34	Hydrogen Exchange Solvent Protection by an ATP Analogue Reveals Conformational Changes in ERK2 upon Activation. Journal of Molecular Biology, 2005, 353, 600-612.	2.0	45
35	Global Gene Expression Analysis of ERK5 and ERK1/2 Signaling Reveals a Role for HIF-1 in ERK5-mediated Responses. Journal of Biological Chemistry, 2006, 281, 20993-21003.	1.6	45
36	Hydrogen-Exchange Mass Spectrometry Reveals Activation-Induced Changes in the Conformational Mobility of p38Î± MAP Kinase. Journal of Molecular Biology, 2008, 379, 1075-1093.	2.0	44

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37	The p38Î² Mitogen-activated Protein Kinase Possesses an Intrinsic Autophosphorylation Activity, Generated by a Short Region Composed of the Î±-G Helix and MAPK Insert. Journal of Biological Chemistry, 2014, 289, 23546-23556.	1.6	39
38	Temperature dependence of protein motions in a thermophilic dihydrofolate reductase and its relationship to catalytic efficiency. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10074-10079.	3.3	37
39	Protein mass analysis of histones. Methods, 2003, 31, 3-11.	1.9	36
40	Structural and mechanistic insights into Mps1 kinase activation. Journal of Cellular and Molecular Medicine, 2009, 13, 1679-1694.	1.6	35
41	Slow Inhibition and Conformation Selective Properties of Extracellular Signal-Regulated Kinase 1 and 2 Inhibitors. Biochemistry, 2015, 54, 22-31.	1.2	35
42	Dynamics of Protein Kinases: Insights from Nuclear Magnetic Resonance. Accounts of Chemical Research, 2015, 48, 1106-1114.	7.6	34
43	Applying proteomics to signaling networks. Current Opinion in Genetics and Development, 2004, 14, 492-498.	1.5	33
44	Intrinsically active variants of Erk oncogenically transform cells and disclose unexpected autophosphorylation capability that is independent of TEY phosphorylation. Molecular Biology of the Cell, 2016, 27, 1026-1039.	0.9	32
45	A Quantitative Comparison of Human HT-1080 Fibrosarcoma Cells and Primary Human Dermal Fibroblasts Identifies a 3D Migration Mechanism with Properties Unique to the Transformed Phenotype. PLoS ONE, 2013, 8, e81689.	1.1	32
46	Identification of a Family of Fatty-Acid-Speciated Sonic Hedgehog Proteins, Whose Members Display Differential Biological Properties. Cell Reports, 2015, 10, 1280-1287.	2.9	30
47	The Cac2 subunit is essential for productive histone binding and nucleosome assembly in CAF-1. Scientific Reports, 2017, 7, 46274.	1.6	30
48	Introduction:Â Protein Phosphorylation and Signaling. Chemical Reviews, 2001, 101, 2207-2208.	23.0	28
49	Activation loop dynamics are controlled by conformation-selective inhibitors of ERK2. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15463-15468.	3.3	28
50	Specificity of Phosphorylation Responses to Mitogen Activated Protein (MAP) Kinase Pathway Inhibitors in Melanoma Cells. Molecular and Cellular Proteomics, 2018, 17, 550-564.	2.5	27
51	Extracellular-Regulated Kinase 2 Is Activated by the Enhancement of Hinge Flexibility. Journal of Molecular Biology, 2014, 426, 1925-1935.	2.0	25
52	Practical Methods for Deuterium Exchange/Mass Spectrometry. , 2004, 250, 283-298.		24
53	Comparative Hydrogenâ€“Deuterium Exchange for a Mesophilic vs Thermophilic Dihydrofolate Reductase at 25 Â°C: Identification of a Single Active Site Region with Enhanced Flexibility in the Mesophilic Protein. Biochemistry, 2011, 50, 8251-8260.	1.2	24
54	Phosphorylation-Dependent Changes in Structure and Dynamics in ERK2 Detected by SDSL and EPR. Biophysical Journal, 2004, 86, 395-403.	0.2	22

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55	Identification of G2/M targets for the MAP kinase pathway by functional proteomics. Proteomics, 2006, 6, 4541-4553.	1.3	22
56	Phosphorylation and subcellular redistribution of high mobility group proteins 14 and 17, analyzed by mass spectrometry. Protein Science, 2000, 9, 170-179.	3.1	20
57	Intermittent treatment of BRAF ^{V600E} melanoma cells delays resistance by adaptive resensitization to drug rechallenge. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2113535119.	3.3	20
58	Distinct patterns of activation-dependent changes in conformational mobility between ERK1 and ERK2. International Journal of Mass Spectrometry, 2011, 302, 101-109.	0.7	19
59	Structure-Based Assignment of Ile, Leu, and Val Methyl Groups in the Active and Inactive Forms of the Mitogen-Activated Protein Kinase Extracellular Signal-Regulated Kinase 2. Biochemistry, 2015, 54, 4307-4319.	1.2	19
60	Hydrogen deuterium exchange defines catalytically linked regions of protein flexibility in the catechol O -methyltransferase reaction. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10797-10805.	3.3	19
61	CELL BIOLOGY: Lessons in Rational Drug Design for Protein Kinases. Science, 2005, 308, 1266-1267.	6.0	17
62	Functional Proteomics Identifies Protein-tyrosine Phosphatase 1B as a Target of RhoA Signaling. Molecular and Cellular Proteomics, 2006, 5, 1359-1367.	2.5	15
63	p38Î² Mitogen-Activated Protein Kinase Modulates Its Own Basal Activity by Autophosphorylation of the Activating Residue Thr180 and the Inhibitory Residues Thr241 and Ser261. Molecular and Cellular Biology, 2016, 36, 1540-1554.	1.1	15
64	Rear-polarized Wnt5a-receptor-actin-myosin-polarity (WRAMP) structures promote the speed and persistence of directional cell migration. Molecular Biology of the Cell, 2017, 28, 1924-1936.	0.9	15
65	Kinase Activation by Small Conformational Changes. Journal of Chemical Information and Modeling, 2020, 60, 821-832.	2.5	15
66	Activation Loop Dynamics Are Coupled to Core Motions in Extracellular Signal-Regulated Kinase-2. Biochemistry, 2020, 59, 2698-2706.	1.2	15
67	Structural characterization of the membraneâ€associated regulatory subunit of type I cAMPâ€dependent protein kinase by mass spectrometry: Identification of Ser81 as the in vivo phosphorylation site of RIÎ±. Protein Science, 1999, 8, 1515-1522.	3.1	13
68	Dosage and Temporal Thresholds in microRNA Proteomics*. Molecular and Cellular Proteomics, 2015, 14, 289-302.	2.5	10
69	Variants of the yeast MAPK Mpk1 are fully functional independently of activation loop phosphorylation. Molecular Biology of the Cell, 2016, 27, 2771-2783.	0.9	9
70	Dynamic equilibria in protein kinases. Current Opinion in Structural Biology, 2021, 71, 215-222.	2.6	6
71	Analysis of MAP Kinases by Hydrogen Exchange Mass Spectrometry. Methods in Molecular Biology, 2010, 661, 239-255.	0.4	5
72	Protein Identification by In-Gel Digestion and Mass Spectrometry. , 2004, , 163-182.		2

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73	Hydrogen Exchange Measurements in Proteins. , 0, , 1361-1391.		0
74	Targets of Signal Transduction Pathways in Melanoma. FASEB Journal, 2006, 20, A852.	0.2	0
75	The gatekeeper residue controls autoactivation of ERK2 via a pathway of intramolecular connectivity. FASEB Journal, 2007, 21, A646.	0.2	0
76	Defining the Role of Protein Interactions at WRAMP Structures in Directional Migration. FASEB Journal, 2018, 32, 667.4.	0.2	0
77	Microtubule Involvement with the WRAMP Structure, a Mechanism for Rear Membrane Retraction in Mammalian Cells. FASEB Journal, 2018, 32, 667.11.	0.2	0