

Florian Gnad

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

18,979
citations

57719

44
h-index

123376

61
g-index

63
all docs

63
docs citations

63
times ranked

29292
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct resistance mechanisms arise to allosteric vs. ATP-competitive AKT inhibitors. <i>Nature Communications</i> , 2022, 13, 2057.	5.8	12
2	NRF2 Activation Promotes Aggressive Lung Cancer and Associates with Poor Clinical Outcomes. <i>Clinical Cancer Research</i> , 2021, 27, 877-888.	3.2	84
3	Applying graph database technology for analyzing perturbed co-expression networks in cancer. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	2
4	Systematic analysis of the intersection of disease mutations with protein modifications. <i>BMC Medical Genomics</i> , 2019, 12, 109.	0.7	16
5	iProteinDB: An Integrative Database of <i>Drosophila</i> Post-translational Modifications. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1-11.	0.8	24
6	The Case for Proteomics and Phospho-Proteomics in Personalized Cancer Medicine. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800113.	0.8	88
7	ERBB3 and IGF1R Signaling Are Required for Nrf2-Dependent Growth in KEAP1-Mutant Lung Cancer. <i>Cancer Research</i> , 2019, 79, 4828-4839.	0.4	15
8	15 years of PhosphoSitePlus®: integrating post-translationally modified sites, disease variants and isoforms. <i>Nucleic Acids Research</i> , 2019, 47, D433-D441.	6.5	208
9	USP7 small-molecule inhibitors interfere with ubiquitin binding. <i>Nature</i> , 2017, 550, 534-538.	13.7	258
10	<i>Kras</i> mutant genetically engineered mouse models of human cancers are genomically heterogeneous. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10947-E10955.	3.3	58
11	Role of the E3 ubiquitin ligase RNF157 as a novel downstream effector linking PI3K and MAPK signaling pathways to the cell cycle. <i>Journal of Biological Chemistry</i> , 2017, 292, 14311-14324.	1.6	14
12	Cellular Interrogation: Exploiting Cell-to-Cell Variability to Discriminate Regulatory Mechanisms in Oscillatory Signalling. <i>PLoS Computational Biology</i> , 2016, 12, e1004995.	1.5	5
13	Phosphoproteome analysis of the MAPK pathway reveals previously undetected feedback mechanisms. <i>Proteomics</i> , 2016, 16, 1998-2004.	1.3	6
14	Quantitative phosphoproteomic analysis of the PI3K-regulated signaling network. <i>Proteomics</i> , 2016, 16, 1992-1997.	1.3	4
15	Uncovering a Dual Regulatory Role for Caspases During Endoplasmic Reticulum Stress-induced Cell Death. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2293-2307.	2.5	7
16	Recurrent Loss of NFE2L2 Exon 2 Is a Mechanism for Nrf2 Pathway Activation in Human Cancers. <i>Cell Reports</i> , 2016, 16, 2605-2617.	2.9	155
17	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. <i>Nature Genetics</i> , 2016, 48, 407-416.	9.4	730
18	CCAT1 is an enhancer-templated RNA that predicts BET sensitivity in colorectal cancer. <i>Journal of Clinical Investigation</i> , 2016, 126, 639-652.	3.9	185

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19	Bioinformatics analysis of thousands of TCGA tumors to determine the involvement of epigenetic regulators in human cancer. <i>BMC Genomics</i> , 2015, 16, S5.	1.2	29
20	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015, 33, 306-312.	9.4	556
21	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014, 5, 3830.	5.8	77
22	<scp>PAK1</scp> mediates pancreatic cancer cell migration and resistance to <scp>MET</scp> inhibition. <i>Journal of Pathology</i> , 2014, 234, 502-513.	2.1	44
23	Integrative analysis of two cell lines derived from a non-small-lung cancer patient—a panomics approach. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014, , 75-86.	0.7	4
24	Assessment of computational methods for predicting the effects of missense mutations in human cancers. <i>BMC Genomics</i> , 2013, 14, S7.	1.2	153
25	Systems-wide Analysis of K-Ras, Cdc42, and PAK4 Signaling by Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2070-2080.	2.5	43
26	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012, 22, 2315-2327.	2.4	177
27	Phosphoproteome of <i>Pristionchus pacificus</i> Provides Insights into Architecture of Signaling Networks in Nematode Models. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1631-1639.	2.5	30
28	Proteus: a web-based, context-specific modelling tool for molecular networks. <i>Bioinformatics</i> , 2012, 28, 1284-1286.	1.8	3
29	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. <i>Molecular Systems Biology</i> , 2012, 8, 611.	3.2	221
30	Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012, 488, 660-664.	13.7	862
31	Mapping N-Glycosylation Sites across Seven Evolutionarily Distant Species Reveals a Divergent Substrate Proteome Despite a Common Core Machinery. <i>Molecular Cell</i> , 2012, 46, 542-548.	4.5	238
32	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1111-1116.	9.4	906
33	C2 Domain-Containing Phosphoprotein CDP138 Regulates GLUT4 Insertion into the Plasma Membrane. <i>Cell Metabolism</i> , 2011, 14, 378-389.	7.2	64
34	Systems-wide Proteomic Analysis in Mammalian Cells Reveals Conserved, Functional Protein Turnover. <i>Journal of Proteome Research</i> , 2011, 10, 5275-5284.	1.8	235
35	PHOSIDA 2011: the posttranslational modification database. <i>Nucleic Acids Research</i> , 2011, 39, D253-D260.	6.5	366
36	Profiling the <i>Trypanosoma cruzi</i> Phosphoproteome. <i>PLoS ONE</i> , 2011, 6, e25381.	1.1	68

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37	Predicting post-translational lysine acetylation using support vector machines. <i>Bioinformatics</i> , 2010, 26, 1666-1668.	1.8	61
38	Evolutionary Constraints of Phosphorylation in Eukaryotes, Prokaryotes, and Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2642-2653.	2.5	83
39	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. <i>Journal of Proteome Research</i> , 2010, 9, 3280-3289.	1.8	253
40	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
41	Site-Specific Identification of SUMO-2 Targets in Cells Reveals an Inverted SUMOylation Motif and a Hydrophobic Cluster SUMOylation Motif. <i>Molecular Cell</i> , 2010, 39, 641-652.	4.5	255
42	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	13.5	789
43	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Applied to Quantitative Proteomics of <i>Bacillus subtilis</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3638-3646.	1.8	108
44	Ser/Thr/Tyr Protein Phosphorylation in the Archaeon <i>Halobacterium salinarum</i> —A Representative of the Third Domain of Life. <i>PLoS ONE</i> , 2009, 4, e4777.	1.1	84
45	Systems-wide Analysis of a Phosphatase Knock-down by Quantitative Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1908-1920.	2.5	94
46	Large-scale Proteomics Analysis of the Human Kinome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1751-1764.	2.5	257
47	MAPU 2.0: high-accuracy proteomes mapped to genomes. <i>Nucleic Acids Research</i> , 2009, 37, D902-D906.	6.5	18
48	High-accuracy identification and bioinformatic analysis of <i>in vivo</i> protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009, 9, 4642-4652.	1.3	132
49	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	6.0	3,883
50	<i>Caenorhabditis elegans</i> Has a Phosphoproteome Atypical for Metazoans That Is Enriched in Developmental and Sex Determination Proteins. <i>Journal of Proteome Research</i> , 2009, 8, 4039-4049.	1.8	66
51	The Ser/Thr/Tyr phosphoproteome of <i>Lactococcus lactis</i> IL1403 reveals multiply phosphorylated proteins. <i>Proteomics</i> , 2008, 8, 3486-3493.	1.3	145
52	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008, 8, 4534-4546.	1.3	93
53	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
54	Solid Tumor Proteome and Phosphoproteome Analysis by High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 5314-5326.	1.8	132

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55	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. <i>Molecular Cell</i> , 2008, 31, 438-448.	4.5	548
56	Phosphoproteome Analysis of <i>E. coli</i> Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 299-307.	2.5	385
57	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 697-707.	2.5	359
58	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	13.9	410
59	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007, 7, 106-115.	1.3	102
60	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. <i>Cell</i> , 2006, 127, 635-648.	13.5	3,201
61	Sebida: a database for the functional and evolutionary analysis of genes with sex-biased expression. <i>Bioinformatics</i> , 2006, 22, 2577-2579.	1.8	96