

Florian Gnad

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

15,771

citations

42

h-index

63

g-index

63

ext. papers

17,855

ext. citations

13.9

avg, IF

6.11

L-index

#	Paper	IF	Citations
62	Distinct resistance mechanisms arise to allosteric vs. ATP-competitive AKT inhibitors.. <i>Nature Communications</i> , 2022 , 13, 2057	17.4	1
61	NRF2 Activation Promotes Aggressive Lung Cancer and Associates with Poor Clinical Outcomes. <i>Clinical Cancer Research</i> , 2021 , 27, 877-888	12.9	33
60	Applying graph database technology for analyzing perturbed co-expression networks in cancer. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	1
59	iProteinDB: An Integrative Database of Post-translational Modifications. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1-11	3.2	10
58	The Case for Proteomics and Phospho-Proteomics in Personalized Cancer Medicine. <i>Proteomics - Clinical Applications</i> , 2019 , 13, e1800113	3.1	56
57	Systematic analysis of the intersection of disease mutations with protein modifications. <i>BMC Medical Genomics</i> , 2019 , 12, 109	3.7	4
56	ERBB3 and IGF1R Signaling Are Required for Nrf2-Dependent Growth in KEAP1-Mutant Lung Cancer. <i>Cancer Research</i> , 2019 , 79, 4828-4839	10.1	9
55	15 years of PhosphoSitePlus [®] : integrating post-translationally modified sites, disease variants and isoforms. <i>Nucleic Acids Research</i> , 2019 , 47, D433-D441	20.1	96
54	USP7 small-molecule inhibitors interfere with ubiquitin binding. <i>Nature</i> , 2017 , 550, 534-538	50.4	165
53	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	11.5	35
52	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	5.4	9
51	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. <i>Nature Genetics</i> , 2016 , 48, 407-16	36.3	497
50	CCAT1 is an enhancer-templated RNA that predicts BET sensitivity in colorectal cancer. <i>Journal of Clinical Investigation</i> , 2016 , 126, 639-52	15.9	147
49	Cellular Interrogation: Exploiting Cell-to-Cell Variability to Discriminate Regulatory Mechanisms in Oscillatory Signalling. <i>PLoS Computational Biology</i> , 2016 , 12, e1004995	5	3
48	Phosphoproteome analysis of the MAPK pathway reveals previously undetected feedback mechanisms. <i>Proteomics</i> , 2016 , 16, 1998-2004	4.8	6
47	Quantitative phosphoproteomic analysis of the PI3K-regulated signaling network. <i>Proteomics</i> , 2016 , 16, 1992-7	4.8	4
46	Uncovering a Dual Regulatory Role for Caspases During Endoplasmic Reticulum Stress-induced Cell Death. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2293-307	7.6	6

45	Recurrent Loss of NFE2L2 Exon 2 Is a Mechanism for Nrf2 Pathway Activation in Human Cancers. <i>Cell Reports</i> , 2016 , 16, 2605-2617	10.6	108
44	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015 , 33, 306-312	11.5	407
43	Bioinformatics analysis of thousands of TCGA tumors to determine the involvement of epigenetic regulators in human cancer. <i>BMC Genomics</i> , 2015 , 16 Suppl 8, S5	4.5	22
42	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014 , 5, 3830	17.4	66
41	PAK1 mediates pancreatic cancer cell migration and resistance to MET inhibition. <i>Journal of Pathology</i> , 2014 , 234, 502-13	9.4	34
40	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	1.3	4
39	Assessment of computational methods for predicting the effects of missense mutations in human cancers. <i>BMC Genomics</i> , 2013 , 14 Suppl 3, S7	4.5	120
38	Systems-wide analysis of K-Ras, Cdc42, and PAK4 signaling by quantitative phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2070-80	7.6	38
37	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. <i>Molecular Systems Biology</i> , 2012 , 8, 611	12.2	174
36	Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012 , 488, 660-4	50.4	711
35	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, 542-8	17.6	199
34	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. <i>Nature Genetics</i> , 2012 , 44, 1111-6	36.3	712
33	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012 , 22, 2315-27	9.7	158
32	Phosphoproteome of <i>Pristionchus pacificus</i> provides insights into architecture of signaling networks in nematode models. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1631-9	7.6	11
31	Proteus: a web-based, context-specific modelling tool for molecular networks. <i>Bioinformatics</i> , 2012 , 28, 1284-6	7.2	3
30	C2 domain-containing phosphoprotein CDP138 regulates GLUT4 insertion into the plasma membrane. <i>Cell Metabolism</i> , 2011 , 14, 378-89	24.6	50
29	Systems-wide proteomic analysis in mammalian cells reveals conserved, functional protein turnover. <i>Journal of Proteome Research</i> , 2011 , 10, 5275-84	5.6	179
28	PHOSIDA 2011: the posttranslational modification database. <i>Nucleic Acids Research</i> , 2011 , 39, D253-60	20.1	321

27	Profiling the Trypanosoma cruzi phosphoproteome. <i>PLoS ONE</i> , 2011 , 6, e25381	3.7	56
26	Predicting post-translational lysine acetylation using support vector machines. <i>Bioinformatics</i> , 2010 , 26, 1666-8	7.2	52
25	Evolutionary constraints of phosphorylation in eukaryotes, prokaryotes, and mitochondria. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2642-53	7.6	70
24	Brain phosphoproteome obtained by a FASP-based method reveals plasma membrane protein topology. <i>Journal of Proteome Research</i> , 2010 , 9, 3280-9	5.6	221
23	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106
22	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, 641-52	17.6	215
21	Precision mapping of an in vivo N-glycoproteome reveals rigid topological and sequence constraints. <i>Cell</i> , 2010 , 141, 897-907	56.2	700
20	Stable isotope labeling by amino acids in cell culture (SILAC) applied to quantitative proteomics of Bacillus subtilis. <i>Journal of Proteome Research</i> , 2010 , 9, 3638-46	5.6	91
19	Ser/Thr/Tyr protein phosphorylation in the archaeon Halobacterium salinarum--a representative of the third domain of life. <i>PLoS ONE</i> , 2009 , 4, e4777	3.7	69
18	Systems-wide analysis of a phosphatase knock-down by quantitative proteomics and phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 1908-20	7.6	88
17	Large-scale proteomics analysis of the human kinome. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 1751-646	6.4	236
16	MAPU 2.0: high-accuracy proteomes mapped to genomes. <i>Nucleic Acids Research</i> , 2009 , 37, D902-6	20.1	17
15	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009 , 9, 4642-52	4.8	103
14	Lysine acetylation targets protein complexes and co-regulates major cellular functions. <i>Science</i> , 2009 , 325, 834-40	33.3	3316
13	Caenorhabditis elegans has a phosphoproteome atypical for metazoans that is enriched in developmental and sex determination proteins. <i>Journal of Proteome Research</i> , 2009 , 8, 4039-49	5.6	59
12	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
11	Solid tumor proteome and phosphoproteome analysis by high resolution mass spectrometry. <i>Journal of Proteome Research</i> , 2008 , 7, 5314-26	5.6	119
10	Kinase-selective enrichment enables quantitative phosphoproteomics of the kinome across the cell cycle. <i>Molecular Cell</i> , 2008 , 31, 438-48	17.6	495

9	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	7.6	334
8	The Ser/Thr/Tyr phosphoproteome of <i>Lactococcus lactis</i> IL1403 reveals multiply phosphorylated proteins. <i>Proteomics</i> , 2008 , 8, 3486-93	4.8	128
7	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008 , 8, 4534-46	4.8	89
6	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007 , 7, 106-15	4.8	95
5	The serine/threonine/tyrosine phosphoproteome of the model bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 697-707	7.6	309
4	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007 , 8, R250	18.3	376
3	Sebida: a database for the functional and evolutionary analysis of genes with sex-biased expression. <i>Bioinformatics</i> , 2006 , 22, 2577-9	7.2	90
2	Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. <i>Cell</i> , 2006 , 127, 635-48	56.2	2797
1	iProteinDB: an integrative database of <i>Drosophila</i> post-translational modifications		2