Judit Villen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2876331/publications.pdf

Version: 2024-02-01

86 papers	23,869 citations	34105 52 h-index	53230 85 g-index
103 all docs	103 docs citations	103 times ranked	31695 citing authors

#	Article	IF	Citations
1	The impact of microRNAs on protein output. Nature, 2008, 455, 64-71.	27.8	3,270
2	Global Survey of Phosphotyrosine Signaling Identifies Oncogenic Kinases in Lung Cancer. Cell, 2007, 131, 1190-1203.	28.9	2,139
3	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. Cell, 2010, 143, 1174-1189.	28.9	1,564
4	A probability-based approach for high-throughput protein phosphorylation analysis and site localization. Nature Biotechnology, 2006, 24, 1285-1292.	17.5	1,482
5	A quantitative atlas of mitotic phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10762-10767.	7.1	1,435
6	Large-scale characterization of HeLa cell nuclear phosphoproteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12130-12135.	7.1	1,434
7	Global Analysis of Cdk1 Substrate Phosphorylation Sites Provides Insights into Evolution. Science, 2009, 325, 1682-1686.	12.6	821
8	Angiogenin-Induced tRNA Fragments Inhibit Translation Initiation. Molecular Cell, 2011, 43, 613-623.	9.7	776
9	Phosphoproteomic Analysis Identifies Grb10 as an mTORC1 Substrate That Negatively Regulates Insulin Signaling. Science, 2011, 332, 1322-1326.	12.6	772
10	A Conserved MST-FOXO Signaling Pathway Mediates Oxidative-Stress Responses and Extends Life Span. Cell, 2006, 125, 987-1001.	28.9	758
11	An AMPK-FOXO Pathway Mediates Longevity Induced by a Novel Method of Dietary Restriction in C. elegans. Current Biology, 2007, 17, 1646-1656.	3.9	701
12	Large-scale phosphorylation analysis of mouse liver. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1488-1493.	7.1	691
13	The SCX/IMAC enrichment approach for global phosphorylation analysis by mass spectrometry. Nature Protocols, 2008, 3, 1630-1638.	12.0	566
14	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nature Methods, 2013, 10, 676-682.	19.0	520
15	Signaling networks assembled by oncogenic EGFR and c-Met. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 692-697.	7.1	480
16	mRNA Destabilization Is the Dominant Effect of Mammalian MicroRNAs by the Time Substantial Repression Ensues. Molecular Cell, 2014, 56, 104-115.	9.7	424
17	Systematic Functional Prioritization of Protein Posttranslational Modifications. Cell, 2012, 150, 413-425.	28.9	375
18	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. Nature Communications, 2018, 9, 5128.	12.8	337

#	ARTICLE	IF	CITATIONS
19	Phosphoproteomic Analysis of the Developing Mouse Brain. Molecular and Cellular Proteomics, 2004, 3, 1093-1101.	3.8	322
20	Large-Scale Phosphorylation Analysis of Î±-Factor-Arrested Saccharomyces cerevisiae. Journal of Proteome Research, 2007, 6, 1190-1197.	3.7	276
21	Aktâ€"RSKâ€"S6 Kinase Signaling Networks Activated by Oncogenic Receptor Tyrosine Kinases. Science Signaling, 2010, 3, ra64.	3.6	263
22	Optimization and Use of Peptide Mass Measurement Accuracy in Shotgun Proteomics. Molecular and Cellular Proteomics, 2006, 5, 1326-1337.	3.8	253
23	Phosphoproteome Analysis of <i>Drosophila melanogaster</i> Embryos. Journal of Proteome Research, 2008, 7, 1675-1682.	3.7	250
24	Chemical Genetic Screen for AMPKÎ±2 Substrates Uncovers a Network of Proteins Involved in Mitosis. Molecular Cell, 2011, 44, 878-892.	9.7	232
25	Global phosphorylation analysis of Î²-arrestinâ€"mediated signaling downstream of a seven transmembrane receptor (7TMR). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15299-15304.	7.1	182
26	Phosphoproteome Analysis of Fission Yeast. Journal of Proteome Research, 2008, 7, 1088-1097.	3.7	173
27	Proteomic Profiling of ClpXP Substrates after DNA Damage Reveals Extensive Instability within SOS Regulon. Molecular Cell, 2006, 22, 193-204.	9.7	172
28	Regulation of Neuronal Cell Death by MST1-FOXO1 Signaling. Journal of Biological Chemistry, 2009, 284, 11285-11292.	3.4	153
29	A Cullin E3 Ubiquitin Ligase Complex Associates with Rik1 and the Clr4 Histone H3-K9 Methyltransferase and is Required for RNAi-Mediated Heterochromatin Formation. RNA Biology, 2005, 2, 106-111.	3.1	149
30	Inhibition of homologous recombination by a cohesin-associated clamp complex recruited to the rDNA recombination enhancer. Genes and Development, 2006, 20, 2887-2901.	5.9	144
31	The histone H3 Lys 27 demethylase JMJD3 regulates gene expression by impacting transcriptional elongation. Genes and Development, 2012, 26, 1364-1375.	5.9	141
32	The Impact of Peptide Abundance and Dynamic Range on Stable-Isotope-Based Quantitative Proteomic Analyses. Journal of Proteome Research, 2008, 7, 4756-4765.	3.7	111
33	Hypomorphic Notch 3 alleles link Notch signaling to ischemic cerebral small-vessel disease. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E128-35.	7.1	106
34	Plug-and-play analysis of the human phosphoproteome by targeted high-resolution mass spectrometry. Nature Methods, 2016, 13, 431-434.	19.0	106
35	Two different Argonaute complexes are required for siRNA generation and heterochromatin assembly in fission yeast. Nature Structural and Molecular Biology, 2007, 14, 200-207.	8.2	105
36	S. pombe LSD1 Homologs Regulate Heterochromatin Propagation and Euchromatic Gene Transcription. Molecular Cell, 2007, 26, 89-101.	9.7	102

#	ARTICLE	IF	CITATIONS
37	R2â€P2 rapidâ€robotic phosphoproteomics enables multidimensional cell signaling studies. Molecular Systems Biology, 2019, 15, e9021.	7.2	102
38	Sensitive multiplexed analysis of kinase activities and activity-based kinase identification. Nature Biotechnology, 2009, 27, 933-940.	17.5	99
39	An atlas of human kinase regulation. Molecular Systems Biology, 2016, 12, 888.	7.2	98
40	Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast. Nature Structural and Molecular Biology, 2008, 15, 873-880.	8.2	97
41	mTORC2-AKT signaling to ATP-citrate lyase drives brown adipogenesis and de novo lipogenesis. Nature Communications, 2020, 11, 575.	12.8	97
42	Evolution of protein phosphorylation across 18 fungal species. Science, 2016, 354, 229-232.	12.6	93
43	Decoding Post-Translational Modification Crosstalk With Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100129.	3.8	92
44	Genetic inhibition of hepatic acetyl-CoA carboxylase activity increases liver fat and alters global protein acetylation. Molecular Metabolism, 2014, 3, 419-431.	6.5	87
45	Evaluation of the utility of neutralâ€lossâ€dependent MS3 strategies in largeâ€scale phosphorylation analysis. Proteomics, 2008, 8, 4444-4452.	2.2	85
46	Determinants and Regulation of Protein Turnover in Yeast. Cell Systems, 2017, 5, 283-294.e5.	6.2	85
47	The <i>S. pombe</i> SAGA complex controls the switch from proliferation to sexual differentiation through the opposing roles of its subunits Gcn5 and Spt8. Genes and Development, 2008, 22, 3184-3195.	5.9	81
48	A site-specific, multiplexed kinase activity assay using stable-isotope dilution and high-resolution mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11606-11611.	7.1	78
49	Targeting of AMSH to Endosomes Is Required for Epidermal Growth Factor Receptor Degradation. Journal of Biological Chemistry, 2007, 282, 9805-9812.	3.4	75
50	Unphosphorylated SR-Like Protein Npl3 Stimulates RNA Polymerase II Elongation. PLoS ONE, 2008, 3, e3273.	2.5	64
51	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. EMBO Journal, 2011, 30, 2843-2852.	7.8	63
52	Phosphorylation of ubiquitin at Ser65 affects its polymerization, targets, and proteomeâ€wide turnover. EMBO Reports, 2015, 16, 1131-1144.	4.5	63
53	Survey of Activated FLT3 Signaling in Leukemia. PLoS ONE, 2011, 6, e19169.	2.5	53
54	E2~Ub conjugates regulate the kinase activity ofShigellaeffector OspG during pathogenesis. EMBO Journal, 2014, 33, n/a-n/a.	7.8	53

#	ARTICLE	IF	CITATIONS
55	Affinity-Based Probes Based on Type II Kinase Inhibitors. Journal of the American Chemical Society, 2012, 134, 19017-19025.	13.7	47
56	Thesaurus: quantifying phosphopeptide positional isomers. Nature Methods, 2019, 16, 703-706.	19.0	44
57	The Septins Function in G1 Pathways that Influence the Pattern of Cell Growth in Budding Yeast. PLoS ONE, 2008, 3, e2022.	2.5	41
58	Studies on the Mechanism of RNAi-dependent Heterochromatin Assembly. Cold Spring Harbor Symposia on Quantitative Biology, 2006, 71, 461-471.	1.1	40
59	TORC1 and TORC2 converge to regulate the SAGA coâ€activator in response to nutrient availability. EMBO Reports, 2017, 18, 2197-2218.	4.5	39
60	Identification of phosphosites that alter protein thermal stability. Nature Methods, 2021, 18, 760-762.	19.0	36
61	Synthetic Approaches to Multivalent Lipopeptide Dendrimers Containing Cyclic Disulfide Epitopes of Foot-and-Mouth Disease Virus. Bioconjugate Chemistry, 2003, 14, 144-152.	3.6	31
62	Lipin 2 Binds Phosphatidic Acid by the Electrostatic Hydrogen Bond Switch Mechanism Independent of Phosphorylation. Journal of Biological Chemistry, 2014, 289, 18055-18066.	3.4	28
63	The phosphatidic acidâ€“binding, polybasic domain is responsible for the differences in the phosphoregulation of lipins 1 and 3. Journal of Biological Chemistry, 2017, 292, 20481-20493.	3.4	27
64	Altered CSNK1E, FABP4 and NEFH protein levels in the dorsolateral prefrontal cortex in schizophrenia. Schizophrenia Research, 2016, 177, 88-97.	2.0	26
65	PKC downregulation upon rapamycin treatment attenuates mitochondrial disease. Nature Metabolism, 2020, 2, 1472-1481.	11.9	26
66	Modulating Mistranslation Potential of tRNASer in Saccharomyces cerevisiae. Genetics, 2019, 213, 849-863.	2.9	21
67	Functional Mimicry of a Discontinuous Antigenic Site by a Designed Synthetic Peptide. ChemBioChem, 2002, 3, 175-182.	2.6	20
68	Elamipretide (SS-31) treatment attenuates age-associated post-translational modifications of heart proteins. GeroScience, 2021, 43, 2395-2412.	4.6	17
69	Calcium-binding proteins are altered in the cerebellum in schizophrenia. PLoS ONE, 2020, 15, e0230400.	2.5	16
70	Towards a multi-site synthetic vaccine to foot-and-mouth disease: addition of discontinuous site peptide mimic increases the neutralization response in immunized animals. Vaccine, 2004, 22, 3523-3529.	3.8	15
71	Feasibility of Protein Turnover Studies in Prototroph <i>Saccharomyces cerevisiae</i> Strains. Analytical Chemistry, 2015, 87, 4008-4014.	6.5	13
72	Proteomic Analysis of Protein Posttranslational Modifications by Mass Spectrometry. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077743.	0.3	12

#	ARTICLE	IF	CITATIONS
73	The amino acid substitution affects cellular response to mistranslation. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	10
74	Rational Dissection of Binding Surfaces for Mimicking of Discontinuous Antigenic Sites. Chemistry and Biology, 2006, 13, 815-823.	6.0	9
75	Proteome and Phosphoproteome Analysis of Brown Adipocytes Reveals That RICTOR Loss Dampens Global Insulin/AKT Signaling. Molecular and Cellular Proteomics, 2020, 19, 1104-1119.	3.8	9
76	Synthetic Peptides as Functional Mimics of a Viral Discontinuous Antigenic Site. Biologicals, 2001, 29, 265-269.	1.4	8
77	Enrichment of Phosphopeptides via Immobilized Metal Affinity Chromatography. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088005.	0.3	6
78	Enrichment of Modified Peptides via Immunoaffinity Precipitation with Modification-Specific Antibodies. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088013.	0.3	5
79	Analysis of Molecular Networks in the Cerebellum in Chronic Schizophrenia: Modulation by Early Postnatal Life Stressors in Murine Models. International Journal of Molecular Sciences, 2021, 22, 10076.	4.1	5
80	Regulating Expression of Mistranslating tRNAs by Readthrough RNA Polymerase II Transcription. ACS Synthetic Biology, 2021, 10, 3177-3189.	3.8	4
81	A novel mistranslating tRNA model in <i>Drosophila melanogaster</i> has diverse, sexually dimorphic effects. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
82	Drafts of the human proteome. Nature Biotechnology, 2014, 32, 752-753.	17.5	3
83	IsobaricQuant enables crossâ€platform quantification, visualization, and filtering of isobaricallyâ€labeled peptides. Proteomics, 0, , 2100253.	2.2	3
84	University of Washington Nathan Shock Center: innovation to advance aging research. GeroScience, 2021, 43, 2161-2165.	4.6	1
85	A Practical Recipe to Survey Phosphoproteomes. Methods in Molecular Biology, 2014, 1156, 389-405.	0.9	1
86	Genetic background and mistranslation frequency determine the impact of mistranslating tRNASerUGG. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	1