

# Judit Villen

## List of Publications by Year in descending order

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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	A novel mistranslating tRNA model in <i>Drosophila melanogaster</i> has diverse, sexually dimorphic effects. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	4
2	Genetic background and mistranslation frequency determine the impact of mistranslating tRNASerUGG. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	1
3	Identification of phosphosites that alter protein thermal stability. <i>Nature Methods</i> , 2021, 18, 760-762.	19.0	36
4	The amino acid substitution affects cellular response to mistranslation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	10
5	University of Washington Nathan Shock Center: innovation to advance aging research. <i>GeroScience</i> , 2021, 43, 2161-2165.	4.6	1
6	Analysis of Molecular Networks in the Cerebellum in Chronic Schizophrenia: Modulation by Early Postnatal Life Stressors in Murine Models. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10076.	4.1	5
7	Elamipretide (SS-31) treatment attenuates age-associated post-translational modifications of heart proteins. <i>GeroScience</i> , 2021, 43, 2395-2412.	4.6	17
8	Decoding Post-Translational Modification Crosstalk With Proteomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100129.	3.8	92
9	Regulating Expression of Mistranslating tRNAs by Readthrough RNA Polymerase II Transcription. <i>ACS Synthetic Biology</i> , 2021, 10, 3177-3189.	3.8	4
10	PKC downregulation upon rapamycin treatment attenuates mitochondrial disease. <i>Nature Metabolism</i> , 2020, 2, 1472-1481.	11.9	26
11	Calcium-binding proteins are altered in the cerebellum in schizophrenia. <i>PLoS ONE</i> , 2020, 15, e0230400.	2.5	16
12	Proteome and Phosphoproteome Analysis of Brown Adipocytes Reveals That RICTOR Loss Dampens Global Insulin/AKT Signaling. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1104-1119.	3.8	9
13	mTORC2-AKT signaling to ATP-citrate lyase drives brown adipogenesis and de novo lipogenesis. <i>Nature Communications</i> , 2020, 11, 575.	12.8	97
14	Thesaurus: quantifying phosphopeptide positional isomers. <i>Nature Methods</i> , 2019, 16, 703-706.	19.0	44
15	Modulating Mistranslation Potential of tRNASer in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 213, 849-863.	2.9	21
16	R2â€P2 rapidâ€robotic phosphoproteomics enables multidimensional cell signaling studies. <i>Molecular Systems Biology</i> , 2019, 15, e9021.	7.2	102
17	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. <i>Nature Communications</i> , 2018, 9, 5128.	12.8	337
18	TORC1 and TORC2 converge to regulate the SAGA coâ€activator in response to nutrient availability. <i>EMBO Reports</i> , 2017, 18, 2197-2218.	4.5	39

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19	The phosphatidic acid-binding, polybasic domain is responsible for the differences in the phosphoregulation of lipins 1 and 3. <i>Journal of Biological Chemistry</i> , 2017, 292, 20481-20493.	3.4	27
20	Determinants and Regulation of Protein Turnover in Yeast. <i>Cell Systems</i> , 2017, 5, 283-294.e5.	6.2	85
21	An atlas of human kinase regulation. <i>Molecular Systems Biology</i> , 2016, 12, 888.	7.2	98
22	Evolution of protein phosphorylation across 18 fungal species. <i>Science</i> , 2016, 354, 229-232.	12.6	93
23	Altered CSNK1E, FABP4 and NEFH protein levels in the dorsolateral prefrontal cortex in schizophrenia. <i>Schizophrenia Research</i> , 2016, 177, 88-97.	2.0	26
24	Enrichment of Phosphopeptides via Immobilized Metal Affinity Chromatography. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088005.	0.3	6
25	Plug-and-play analysis of the human phosphoproteome by targeted high-resolution mass spectrometry. <i>Nature Methods</i> , 2016, 13, 431-434.	19.0	106
26	Enrichment of Modified Peptides via Immunoaffinity Precipitation with Modification-Specific Antibodies. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088013.	0.3	5
27	Proteomic Analysis of Protein Posttranslational Modifications by Mass Spectrometry. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077743.	0.3	12
28	Phosphorylation of ubiquitin at Ser65 affects its polymerization, targets, and proteome-wide turnover. <i>EMBO Reports</i> , 2015, 16, 1131-1144.	4.5	63
29	Feasibility of Protein Turnover Studies in Prototroph <i>Saccharomyces cerevisiae</i> Strains. <i>Analytical Chemistry</i> , 2015, 87, 4008-4014.	6.5	13
30	E2~Ub conjugates regulate the kinase activity of Shigella effector OspG during pathogenesis. <i>EMBO Journal</i> , 2014, 33, n/a-n/a.	7.8	53
31	Lipin 2 Binds Phosphatidic Acid by the Electrostatic Hydrogen Bond Switch Mechanism Independent of Phosphorylation. <i>Journal of Biological Chemistry</i> , 2014, 289, 18055-18066.	3.4	28
32	Drafts of the human proteome. <i>Nature Biotechnology</i> , 2014, 32, 752-753.	17.5	3
33	mRNA Destabilization Is the Dominant Effect of Mammalian MicroRNAs by the Time Substantial Repression Ensues. <i>Molecular Cell</i> , 2014, 56, 104-115.	9.7	424
34	Genetic inhibition of hepatic acetyl-CoA carboxylase activity increases liver fat and alters global protein acetylation. <i>Molecular Metabolism</i> , 2014, 3, 419-431.	6.5	87
35	A Practical Recipe to Survey Phosphoproteomes. <i>Methods in Molecular Biology</i> , 2014, 1156, 389-405.	0.9	1
36	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. <i>Nature Methods</i> , 2013, 10, 676-682.	19.0	520

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37	The histone H3 Lys 27 demethylase JMJD3 regulates gene expression by impacting transcriptional elongation. <i>Genes and Development</i> , 2012, 26, 1364-1375.	5.9	141
38	Affinity-Based Probes Based on Type II Kinase Inhibitors. <i>Journal of the American Chemical Society</i> , 2012, 134, 19017-19025.	13.7	47
39	Systematic Functional Prioritization of Protein Posttranslational Modifications. <i>Cell</i> , 2012, 150, 413-425.	28.9	375
40	Angiogenin-Induced tRNA Fragments Inhibit Translation Initiation. <i>Molecular Cell</i> , 2011, 43, 613-623.	9.7	776
41	Chemical Genetic Screen for AMPK $\pm$ 2 Substrates Uncovers a Network of Proteins Involved in Mitosis. <i>Molecular Cell</i> , 2011, 44, 878-892.	9.7	232
42	Phosphoproteomic Analysis Identifies Grb10 as an mTORC1 Substrate That Negatively Regulates Insulin Signaling. <i>Science</i> , 2011, 332, 1322-1326.	12.6	772
43	Survey of Activated FLT3 Signaling in Leukemia. <i>PLoS ONE</i> , 2011, 6, e19169.	2.5	53
44	Hypomorphic Notch 3 alleles link Notch signaling to ischemic cerebral small-vessel disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E128-35.	7.1	106
45	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. <i>EMBO Journal</i> , 2011, 30, 2843-2852.	7.8	63
46	Global phosphorylation analysis of $\beta$ -arrestin $\alpha$ -mediated signaling downstream of a seven transmembrane receptor (7TMR). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15299-15304.	7.1	182
47	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	28.9	1,564
48	Akt $\alpha$ -RSK $\alpha$ -S6 Kinase Signaling Networks Activated by Oncogenic Receptor Tyrosine Kinases. <i>Science Signaling</i> , 2010, 3, ra64.	3.6	263
49	A site-specific, multiplexed kinase activity assay using stable-isotope dilution and high-resolution mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11606-11611.	7.1	78
50	Regulation of Neuronal Cell Death by MST1-FOXO1 Signaling. <i>Journal of Biological Chemistry</i> , 2009, 284, 11285-11292.	3.4	153
51	Sensitive multiplexed analysis of kinase activities and activity-based kinase identification. <i>Nature Biotechnology</i> , 2009, 27, 933-940.	17.5	99
52	Global Analysis of Cdk1 Substrate Phosphorylation Sites Provides Insights into Evolution. <i>Science</i> , 2009, 325, 1682-1686.	12.6	821
53	Evaluation of the utility of neutral $\alpha$ -cross $\alpha$ -dependent MS3 strategies in large $\alpha$ -scale phosphorylation analysis. <i>Proteomics</i> , 2008, 8, 4444-4452.	2.2	85
54	The impact of microRNAs on protein output. <i>Nature</i> , 2008, 455, 64-71.	27.8	3,270

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55	Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 873-880.	8.2	97
56	The SCX/IMAC enrichment approach for global phosphorylation analysis by mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 1630-1638.	12.0	566
57	Phosphoproteome Analysis of Fission Yeast. <i>Journal of Proteome Research</i> , 2008, 7, 1088-1097.	3.7	173
58	The Impact of Peptide Abundance and Dynamic Range on Stable-Isotope-Based Quantitative Proteomic Analyses. <i>Journal of Proteome Research</i> , 2008, 7, 4756-4765.	3.7	111
59	Phosphoproteome Analysis of <i>Drosophila melanogaster</i> Embryos. <i>Journal of Proteome Research</i> , 2008, 7, 1675-1682.	3.7	250
60	Signaling networks assembled by oncogenic EGFR and c-Met. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 692-697.	7.1	480
61	A quantitative atlas of mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10762-10767.	7.1	1,435
62	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. <i>Genes and Development</i> , 2008, 22, 3184-3195.	5.9	81
63	The Septins Function in G1 Pathways that Influence the Pattern of Cell Growth in Budding Yeast. <i>PLoS ONE</i> , 2008, 3, e2022.	2.5	41
64	Unphosphorylated SR-Like Protein Npl3 Stimulates RNA Polymerase II Elongation. <i>PLoS ONE</i> , 2008, 3, e3273.	2.5	64
65	Targeting of AMSH to Endosomes Is Required for Epidermal Growth Factor Receptor Degradation. <i>Journal of Biological Chemistry</i> , 2007, 282, 9805-9812.	3.4	75
66	Large-scale phosphorylation analysis of mouse liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1488-1493.	7.1	691
67	Global Survey of Phosphotyrosine Signaling Identifies Oncogenic Kinases in Lung Cancer. <i>Cell</i> , 2007, 131, 1190-1203.	28.9	2,139
68	<i>S. pombe</i> LSD1 Homologs Regulate Heterochromatin Propagation and Euchromatic Gene Transcription. <i>Molecular Cell</i> , 2007, 26, 89-101.	9.7	102
69	Large-Scale Phosphorylation Analysis of $\hat{\pm}$ -Factor-Arrested <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2007, 6, 1190-1197.	3.7	276
70	Two different Argonaute complexes are required for siRNA generation and heterochromatin assembly in fission yeast. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 200-207.	8.2	105
71	An AMPK-FOXO Pathway Mediates Longevity Induced by a Novel Method of Dietary Restriction in <i>C. elegans</i> . <i>Current Biology</i> , 2007, 17, 1646-1656.	3.9	701
72	A Conserved MST-FOXO Signaling Pathway Mediates Oxidative-Stress Responses and Extends Life Span. <i>Cell</i> , 2006, 125, 987-1001.	28.9	758

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73	Proteomic Profiling of ClpXP Substrates after DNA Damage Reveals Extensive Instability within SOS Regulon. <i>Molecular Cell</i> , 2006, 22, 193-204.	9.7	172
74	A probability-based approach for high-throughput protein phosphorylation analysis and site localization. <i>Nature Biotechnology</i> , 2006, 24, 1285-1292.	17.5	1,482
75	Rational Dissection of Binding Surfaces for Mimicking of Discontinuous Antigenic Sites. <i>Chemistry and Biology</i> , 2006, 13, 815-823.	6.0	9
76	Inhibition of homologous recombination by a cohesin-associated clamp complex recruited to the rDNA recombination enhancer. <i>Genes and Development</i> , 2006, 20, 2887-2901.	5.9	144
77	Optimization and Use of Peptide Mass Measurement Accuracy in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1326-1337.	3.8	253
78	Studies on the Mechanism of RNAi-dependent Heterochromatin Assembly. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006, 71, 461-471.	1.1	40
79	A Cullin E3 Ubiquitin Ligase Complex Associates with Rik1 and the Clr4 Histone H3-K9 Methyltransferase and is Required for RNAi-Mediated Heterochromatin Formation. <i>RNA Biology</i> , 2005, 2, 106-111.	3.1	149
80	Phosphoproteomic Analysis of the Developing Mouse Brain. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1093-1101.	3.8	322
81	Large-scale characterization of HeLa cell nuclear phosphoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12130-12135.	7.1	1,434
82	Towards a multi-site synthetic vaccine to foot-and-mouth disease: addition of discontinuous site peptide mimic increases the neutralization response in immunized animals. <i>Vaccine</i> , 2004, 22, 3523-3529.	3.8	15
83	Synthetic Approaches to Multivalent Lipopeptide Dendrimers Containing Cyclic Disulfide Epitopes of Foot-and-Mouth Disease Virus. <i>Bioconjugate Chemistry</i> , 2003, 14, 144-152.	3.6	31
84	Functional Mimicry of a Discontinuous Antigenic Site by a Designed Synthetic Peptide. <i>ChemBioChem</i> , 2002, 3, 175-182.	2.6	20
85	Synthetic Peptides as Functional Mimics of a Viral Discontinuous Antigenic Site. <i>Biologicals</i> , 2001, 29, 265-269.	1.4	8
86	IsobaricQuant enables cross-platform quantification, visualization, and filtering of isobarically labeled peptides. <i>Proteomics</i> , 0, , 2100253.	2.2	3