

Christine Vogel

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

4,318
citations

516710

16
h-index

330143

37
g-index

56
all docs

56
docs citations

56
times ranked

10507
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. <i>Nature Reviews Genetics</i> , 2012, 13, 227-232.	16.8	3,228
2	K63 polyubiquitination is a new modulator of the oxidative stress response. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 116-123.	8.2	162
3	Differential dynamics of the mammalian <scp>mRNA</scp> and protein expression response to misfolding stress. <i>Molecular Systems Biology</i> , 2016, 12, 855.	7.2	154
4	Protein Expression Regulation under Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009217.	3.8	113
5	iOmicsPASS: network-based integration of multiomics data for predictive subnetwork discovery. <i>Npj Systems Biology and Applications</i> , 2019, 5, 22.	3.0	79
6	High-throughput analyses of hnRNP H1 dissects its multi-functional aspect. <i>RNA Biology</i> , 2016, 13, 400-411.	3.1	50
7	BONLAC: A combinatorial proteomic technique to measure stimulus-induced translational profiles in brain slices. <i>Neuropharmacology</i> , 2016, 100, 76-89.	4.1	47
8	New insights into the cellular temporal response to proteostatic stress. <i>ELife</i> , 2018, 7, .	6.0	47
9	Exploiting Interdata Relationships in Next-generation Proteomics Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S5-S14.	3.8	39
10	Stem cell-derived cranial and spinal motor neurons reveal proteostatic differences between ALS resistant and sensitive motor neurons. <i>ELife</i> , 2019, 8, .	6.0	30
11	Quantifying gene expression: the importance of being subtle. <i>Molecular Systems Biology</i> , 2016, 12, 885.	7.2	29
12	Phenazines Regulate Nap-Dependent Denitrification in <i>Pseudomonas aeruginosa</i> Biofilms. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	29
13	Site-Specific K63 Ubiquitinomics Provides Insights into Translation Regulation under Stress. <i>Journal of Proteome Research</i> , 2019, 18, 309-318.	3.7	29
14	Label-Free Protein Quantitation Using Weighted Spectral Counting. <i>Methods in Molecular Biology</i> , 2012, 893, 321-341.	0.9	26
15	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. <i>Biomolecules</i> , 2015, 5, 1441-1466.	4.0	26
16	Condition-Specific Modeling of Biophysical Parameters Advances Inference of Regulatory Networks. <i>Cell Reports</i> , 2018, 23, 376-388.	6.4	23
17	Polyubiquitin Chains Linked by Lysine Residue 48 (K48) Selectively Target Oxidized Proteins<i> In Vivo</i>. <i>Antioxidants and Redox Signaling</i> , 2019, 31, 1133-1149.	5.4	22
18	Structural impact of K63 ubiquitin on yeast translocating ribosomes under oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22157-22166.	7.1	21

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19	Nucleobindins and encoded peptides: From cell signaling to physiology. <i>Advances in Protein Chemistry and Structural Biology</i> , 2019, 116, 91-133.	2.3	19
20	Translation's coming of age. <i>Molecular Systems Biology</i> , 2011, 7, 498.	7.2	17
21	Protein Expression Under Pressure. <i>Science</i> , 2013, 342, 1052-1053.	12.6	16
22	PTMscape: an open source tool to predict generic post-translational modifications and map modification crosstalk in protein domains and biological processes. <i>Molecular Omics</i> , 2018, 14, 197-209.	2.8	12
23	Prevaccination Glycan Markers of Response to an Influenza Vaccine Implicate the Complement Pathway. <i>Journal of Proteome Research</i> , 2022, 21, 1974-1985.	3.7	12
24	Evaluation of determinants of the serological response to the quadrivalent split-inactivated influenza vaccine. <i>Molecular Systems Biology</i> , 2022, 18, e10724.	7.2	11
25	PECAplus: statistical analysis of time-dependent regulatory changes in dynamic single-omics and dual-omics experiments. <i>Npj Systems Biology and Applications</i> , 2018, 4, 3.	3.0	10
26	New Proteomic Signatures to Distinguish Between Zika and Dengue Infections. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100052.	3.8	10
27	New horizons in the stormy sea of multimodal single-cell data integration. <i>Molecular Cell</i> , 2022, 82, 248-259.	9.7	9
28	Mass spectrometry analysis of K63-ubiquitinated targets in response to oxidative stress. <i>Data in Brief</i> , 2015, 4, 130-134.	1.0	8
29	Simple Method to Quantify Protein Abundances from 1000 Cells. <i>ACS Omega</i> , 2020, 5, 15537-15546.	3.5	6
30	Time-course proteomics dataset monitoring HeLa cells subjected to DTT induced endoplasmic reticulum stress. <i>Data in Brief</i> , 2016, 8, 1168-1172.	1.0	5
31	Integration of large-scale multi-omic datasets: A protein-centric view. <i>Current Opinion in Systems Biology</i> , 2018, 11, 74-81.	2.6	5
32	EBprotV2: A Perseus Plugin for Differential Protein Abundance Analysis of Labeling-Based Quantitative Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 748-752.	3.7	5
33	“Structuromics” another step toward a holistic view of the cell. <i>Cell</i> , 2021, 184, 301-303.	28.9	5
34	Quantifying protein (dis)order. <i>Science</i> , 2017, 355, 794-795.	12.6	3
35	Linking Marine Ecosystem Services to the North Sea’s Energy Fields in Transnational Marine Spatial Planning. <i>Environments - MDPI</i> , 2018, 5, 67.	3.3	3
36	A protein-centric approach for exome variant aggregation enables sensitive association analysis with clinical outcomes. <i>Human Mutation</i> , 2020, 41, 934-945.	2.5	3

#	ARTICLE	IF	CITATIONS
37	Systems Approaches to the Eukaryotic Stress Response. PLoS Computational Biology, 2016, 12, e1004757.	3.2	1
38	Integrated multi-omics analysis of RB-loss identifies widespread cellular programming and synthetic weaknesses. Communications Biology, 2021, 4, 977.	4.4	1
39	Deciphering the effect of Endoplasmic Reticulum (ER) stress on near-mitochondrial localized translation. FASEB Journal, 2018, 32, 543.19.	0.5	0