

Danielle L Swaney

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

11,480
citations

94433

37
h-index

133252

59
g-index

78
all docs

78
docs citations

78
times ranked

19800
citing authors

#	ARTICLE	IF	CITATIONS
1	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	27.8	3,542
2	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	28.9	825
3	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. <i>Nature Methods</i> , 2013, 10, 676-682.	19.0	520
4	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	12.6	508
5	Value of Using Multiple Proteases for Large-Scale Mass Spectrometry-Based Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 1323-1329.	3.7	398
6	Systematic Functional Prioritization of Protein Posttranslational Modifications. <i>Cell</i> , 2012, 150, 413-425.	28.9	375
7	Supplemental Activation Method for High-Efficiency Electron-Transfer Dissociation of Doubly Protonated Peptide Precursors. <i>Analytical Chemistry</i> , 2007, 79, 477-485.	6.5	341
8	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. <i>Science</i> , 2020, 370, 1473-1479.	12.6	336
9	Probing the dynamics of O-GlcNAc glycosylation in the brain using quantitative proteomics. <i>Nature Chemical Biology</i> , 2007, 3, 339-348.	8.0	302
10	Decision tree-driven tandem mass spectrometry for shotgun proteomics. <i>Nature Methods</i> , 2008, 5, 959-964.	19.0	289
11	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	17.5	273
12	Proteomic and phosphoproteomic comparison of human ES and iPS cells. <i>Nature Methods</i> , 2011, 8, 821-827.	19.0	254
13	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. <i>Cell</i> , 2018, 175, 1931-1945.e18.	28.9	252
14	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	27.8	237
15	Human embryonic stem cell phosphoproteome revealed by electron transfer dissociation tandem mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 995-1000.	7.1	186
16	Chaperone-mediated autophagy prevents collapse of the neuronal metastable proteome. <i>Cell</i> , 2021, 184, 2696-2714.e25.	28.9	151
17	Phosphoproteomics for the Masses. <i>ACS Chemical Biology</i> , 2010, 5, 105-119.	3.4	150
18	A Proteomics Grade Electron Transfer Dissociation-Enabled Hybrid Linear Ion Trap-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2008, 7, 3127-3136.	3.7	137

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19	Large-Scale Phosphoprotein Analysis in <i>Medicago truncatula</i> Roots Provides Insight into in Vivo Kinase Activity in Legumes. <i>Plant Physiology</i> , 2009, 152, 19-28.	4.8	133
20	Dual-Pressure Linear Ion Trap Mass Spectrometer Improving the Analysis of Complex Protein Mixtures. <i>Analytical Chemistry</i> , 2009, 81, 7757-7765.	6.5	130
21	KRAS ^{G12C} inhibition produces a driver-limited state revealing collateral dependencies. <i>Science Signaling</i> , 2019, 12, .	3.6	123
22	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. <i>Cell</i> , 2022, 185, 712-728.e14.	28.9	114
23	Tandem Phosphorylation of Ser-911 and Thr-912 at the C Terminus of Yeast Plasma Membrane H ⁺ -ATPase Leads to Glucose-dependent Activation. <i>Journal of Biological Chemistry</i> , 2007, 282, 35471-35481.	3.4	110
24	Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. <i>Cell</i> , 2019, 178, 1452-1464.e13.	28.9	105
25	Evolution of protein phosphorylation across 18 fungal species. <i>Science</i> , 2016, 354, 229-232.	12.6	93
26	Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities. <i>Nature Genetics</i> , 2022, 54, 649-659.	21.4	93
27	The AMBRA1 E3 ligase adaptor regulates the stability of cyclin D. <i>Nature</i> , 2021, 592, 794-798.	27.8	76
28	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus Host Protein Network. <i>Cancer Discovery</i> , 2018, 8, 1474-1489.	9.4	67
29	A protein interaction landscape of breast cancer. <i>Science</i> , 2021, 374, eabf3066.	12.6	66
30	Adhesion-mediated mechanosignaling forces mitohormesis. <i>Cell Metabolism</i> , 2021, 33, 1322-1341.e13.	16.2	65
31	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
32	Phosphorylation of ubiquitin at Ser65 affects its polymerization, targets, and proteome-wide turnover. <i>EMBO Reports</i> , 2015, 16, 1131-1144.	4.5	63
33	Systematic Identification of Host Cell Regulators of <i>Legionella pneumophila</i> Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019, 26, 551-563.e6.	11.0	62
34	Neuronal Apolipoprotein E4 Expression Results in Proteome-Wide Alterations and Compromises Bioenergetic Capacity by Disrupting Mitochondrial Function. <i>Journal of Alzheimer's Disease</i> , 2019, 68, 991-1011.	2.6	57
35	Unbiased Proteomic Profiling Uncovers a Targetable GNAS/PKA/PP2A Axis in Small Cell Lung Cancer Stem Cells. <i>Cancer Cell</i> , 2020, 38, 129-143.e7.	16.8	57
36	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

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37	Affinity-Based Probes Based on Type II Kinase Inhibitors. <i>Journal of the American Chemical Society</i> , 2012, 134, 19017-19025.	13.7	47
38	Dynamic post-translational modification profiling of <i>Mycobacterium tuberculosis</i> -infected primary macrophages. <i>ELife</i> , 2020, 9, .	6.0	44
39	A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. <i>Science</i> , 2021, 374, eabf2911.	12.6	37
40	Proteome Imbalance of Mitochondrial Electron Transport Chain in Brown Adipocytes Leads to Metabolic Benefits. <i>Cell Metabolism</i> , 2018, 27, 616-629.e4.	16.2	34
41	A New Probabilistic Database Search Algorithm for ETD Spectra. <i>Journal of Proteome Research</i> , 2009, 8, 3198-3205.	3.7	33
42	Sympathetic inputs regulate adaptive thermogenesis in brown adipose tissue through cAMP-Salt inducible kinase axis. <i>Scientific Reports</i> , 2018, 8, 11001.	3.3	33
43	Interpretation of cancer mutations using a multiscale map of protein systems. <i>Science</i> , 2021, 374, eabf3067.	12.6	29
44	A ciliopathy complex builds distal appendages to initiate ciliogenesis. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	26
45	Restriction factor compendium for influenza A virus reveals a mechanism for evasion of autophagy. <i>Nature Microbiology</i> , 2021, 6, 1319-1333.	13.3	23
46	Toward defining the phosphoproteome of <i>Xenopus laevis</i> embryos. <i>Developmental Dynamics</i> , 2009, 238, 1433-1443.	1.8	21
47	Therapeutic implications of activating noncanonical PIK3CA mutations in head and neck squamous cell carcinoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	20
48	A Quantitative Genetic Interaction Map of HIV Infection. <i>Molecular Cell</i> , 2020, 78, 197-209.e7.	9.7	17
49	Brown adipocyte ATF4 activation improves thermoregulation and systemic metabolism. <i>Cell Reports</i> , 2021, 36, 109742.	6.4	15
50	Systems-level effects of allosteric perturbations to a model molecular switch. <i>Nature</i> , 2021, 599, 152-157.	27.8	13
51	Toward Comprehensive Plasma Proteomics by Orthogonal Protease Digestion. <i>Journal of Proteome Research</i> , 2021, 20, 4031-4040.	3.7	11
52	Caveolin-1 and Sox-2 are predictive biomarkers of cetuximab response in head and neck cancer. <i>JCI Insight</i> , 2021, 6, .	5.0	10
53	CIDer: A Statistical Framework for Interpreting Differences in CID and HCD Fragmentation. <i>Journal of Proteome Research</i> , 2021, 20, 1951-1965.	3.7	9
54	Data-Independent Acquisition Protease-Multiplexing Enables Increased Proteome Sequence Coverage Across Multiple Fragmentation Modes. <i>Journal of Proteome Research</i> , 2022, 21, 1124-1136.	3.7	8

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55	The E3 ligase TRIM1 ubiquitinates LRRK2 and controls its localization, degradation, and toxicity. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	8
56	Enrichment of Phosphopeptides via Immobilized Metal Affinity Chromatography. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088005.	0.3	6
57	The kinase Isr1 negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2020, 16, e1008840.	3.5	3
58	TCO, a Putative Transcriptional Regulator in Arabidopsis, Is a Target of the Protein Kinase CK2. <i>International Journal of Molecular Sciences</i> , 2019, 20, 99.	4.1	0
59	The kinase Isr1 negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
60	The kinase Isr1 negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
61	The kinase Isr1 negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
62	The kinase Isr1 negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0