

# 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	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. <i>Cell</i> , 2022, 185, 712-728.e14.	28.9	114
2	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
3	The E3 ligase TRIM1 ubiquitinates LRRK2 and controls its localization, degradation, and toxicity. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	8
4	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	27.8	237
5	Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities. <i>Nature Genetics</i> , 2022, 54, 649-659.	21.4	93
6	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
7	The AMBRA1 E3 ligase adaptor regulates the stability of cyclin D. <i>Nature</i> , 2021, 592, 794-798.	27.8	76
8	Chaperone-mediated autophagy prevents collapse of the neuronal metastable proteome. <i>Cell</i> , 2021, 184, 2696-2714.e25.	28.9	151
9	Toward Comprehensive Plasma Proteomics by Orthogonal Protease Digestion. <i>Journal of Proteome Research</i> , 2021, 20, 4031-4040.	3.7	11
10	Adhesion-mediated mechanosignaling forces mitohormesis. <i>Cell Metabolism</i> , 2021, 33, 1322-1341.e13.	16.2	65
11	A ciliopathy complex builds distal appendages to initiate ciliogenesis. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	26
12	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
13	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
14	Brown adipocyte ATF4 activation improves thermoregulation and systemic metabolism. <i>Cell Reports</i> , 2021, 36, 109742.	6.4	15
15	A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. <i>Science</i> , 2021, 374, eabf2911.	12.6	37
16	A protein interaction landscape of breast cancer. <i>Science</i> , 2021, 374, eabf3066.	12.6	66
17	Interpretation of cancer mutations using a multiscale map of protein systems. <i>Science</i> , 2021, 374, eabf3067.	12.6	29
18	Systems-level effects of allosteric perturbations to a model molecular switch. <i>Nature</i> , 2021, 599, 152-157.	27.8	13

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19	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
20	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	17.5	273
21	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	12.6	508
22	An ultrapotent synthetic nanobody neutralizes SARS-CoV-2 by stabilizing inactive Spike. <i>Science</i> , 2020, 370, 1473-1479.	12.6	336
23	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
24	The Global Phosphorylation Landscape of SARS-CoV-2 Infection. <i>Cell</i> , 2020, 182, 685-712.e19.	28.9	825
25	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	27.8	3,542
26	The kinase <i>Isr1</i> negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2020, 16, e1008840.	3.5	3
27	A Quantitative Genetic Interaction Map of HIV Infection. <i>Molecular Cell</i> , 2020, 78, 197-209.e7.	9.7	17
28	Dynamic post-translational modification profiling of <i>Mycobacterium tuberculosis</i> -infected primary macrophages. <i>ELife</i> , 2020, 9, .	6.0	44
29	The kinase <i>Isr1</i> negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
30	The kinase <i>Isr1</i> negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
31	The kinase <i>Isr1</i> negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
32	The kinase <i>Isr1</i> negatively regulates hexosamine biosynthesis in <i>S. cerevisiae</i> . , 2020, 16, e1008840.		0
33	Anti-CRISPR-Associated Proteins Are Crucial Repressors of Anti-CRISPR Transcription. <i>Cell</i> , 2019, 178, 1452-1464.e13.	28.9	105
34	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
35	KRAS <sup>G12C</sup> inhibition produces a driver-limited state revealing collateral dependencies. <i>Science Signaling</i> , 2019, 12, .	3.6	123
36	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

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37	TCO, a Putative Transcriptional Regulator in Arabidopsis, Is a Target of the Protein Kinase CK2. International Journal of Molecular Sciences, 2019, 20, 99.	4.1	0
38	Proteome Imbalance of Mitochondrial Electron Transport Chain in Brown Adipocytes Leads to Metabolic Benefits. Cell Metabolism, 2018, 27, 616-629.e4.	16.2	34
39	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. Cell, 2018, 175, 1931-1945.e18.	28.9	252
40	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus-Host Protein Network. Cancer Discovery, 2018, 8, 1474-1489.	9.4	67
41	Sympathetic inputs regulate adaptive thermogenesis in brown adipose tissue through cAMP-Salt inducible kinase axis. Scientific Reports, 2018, 8, 11001.	3.3	33
42	Evolution of protein phosphorylation across 18 fungal species. Science, 2016, 354, 229-232.	12.6	93
43	Enrichment of Phosphopeptides via Immobilized Metal Affinity Chromatography. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088005.	0.3	6
44	Phosphorylation of ubiquitin at Ser65 affects its polymerization, targets, and proteome-wide turnover. EMBO Reports, 2015, 16, 1131-1144.	4.5	63
45	E2-Ub conjugates regulate the kinase activity of Shigella effector OspG during pathogenesis. EMBO Journal, 2014, 33, n/a-n/a.	7.8	53
46	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nature Methods, 2013, 10, 676-682.	19.0	520
47	Affinity-Based Probes Based on Type II Kinase Inhibitors. Journal of the American Chemical Society, 2012, 134, 19017-19025.	13.7	47
48	Systematic Functional Prioritization of Protein Posttranslational Modifications. Cell, 2012, 150, 413-425.	28.9	375
49	Proteomic and phosphoproteomic comparison of human ES and iPS cells. Nature Methods, 2011, 8, 821-827.	19.0	254
50	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. EMBO Journal, 2011, 30, 2843-2852.	7.8	63
51	Value of Using Multiple Proteases for Large-Scale Mass Spectrometry-Based Proteomics. Journal of Proteome Research, 2010, 9, 1323-1329.	3.7	398
52	Phosphoproteomics for the Masses. ACS Chemical Biology, 2010, 5, 105-119.	3.4	150
53	Toward defining the phosphoproteome of <i>Xenopus laevis</i> embryos. Developmental Dynamics, 2009, 238, 1433-1443.	1.8	21
54	A New Probabilistic Database Search Algorithm for ETD Spectra. Journal of Proteome Research, 2009, 8, 3198-3205.	3.7	33

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55	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
56	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
57	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
58	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
59	Decision tree-driven tandem mass spectrometry for shotgun proteomics. <i>Nature Methods</i> , 2008, 5, 959-964.	19.0	289
60	Tandem Phosphorylation of Ser-911 and Thr-912 at the C Terminus of Yeast Plasma Membrane H <sup>+</sup> -ATPase Leads to Glucose-dependent Activation. <i>Journal of Biological Chemistry</i> , 2007, 282, 35471-35481.	3.4	110
61	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
62	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