

Scott A Gerber

List of Publications by Year in descending order

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72
papers

16,278
citations

81900

39
h-index

88630

70
g-index

82
all docs

82
docs citations

82
times ranked

18314
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellular Calcium Levels Influenced by NCA-2 Impact Circadian Period Determination in <i>Neurospora</i> . <i>MBio</i> , 2021, 12, e0149321.	4.1	6
2	Let-7b-5p in vesicles secreted by human airway cells reduces biofilm formation and increases antibiotic sensitivity of <i>P. aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	24
3	Affinity-based profiling of endogenous phosphoprotein phosphatases by mass spectrometry. <i>Nature Protocols</i> , 2021, 16, 4919-4943.	12.0	6
4	Direct regulation of Chk1 protein stability by E3 ubiquitin ligase HUWE1. <i>FEBS Journal</i> , 2020, 287, 1985-1999.	4.7	35
5	Limiting Self-Renewal of the Basal Compartment by PKA Activation Induces Differentiation and Alters the Evolution of Mammary Tumors. <i>Developmental Cell</i> , 2020, 55, 544-557.e6.	7.0	20
6	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23626-23635.	7.1	18
7	WBP11 is required for splicing the TUBGCP6 pre-mRNA to promote centriole duplication. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	11
8	Phosphoregulation provides specificity to biomolecular condensates in the cell cycle and cell polarity. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	18
9	Tobramycin reduces key virulence determinants in the proteome of <i>Pseudomonas aeruginosa</i> outer membrane vesicles. <i>PLoS ONE</i> , 2019, 14, e0211290.	2.5	24
10	CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. <i>Nature Communications</i> , 2019, 10, 1757.	12.8	159
11	The iron deficiency response in <i>Arabidopsis thaliana</i> requires the phosphorylated transcription factor URI. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24933-24942.	7.1	120
12	Global assessment of its network dynamics reveals that the kinase Plk1 inhibits the phosphatase PP6 to promote Aurora A activity. <i>Science Signaling</i> , 2018, 11, .	3.6	25
13	A HAD family phosphatase CSP-6 regulates the circadian output pathway in <i>Neurospora crassa</i> . <i>PLoS Genetics</i> , 2018, 14, e1007192.	3.5	22
14	A bifurcated signaling cascade of NIMA-related kinases controls distinct kinesins in anaphase. <i>Journal of Cell Biology</i> , 2017, 216, 2339-2354.	5.2	27
15	Offline pentafluorophenyl (PFP)-RP prefractionation as an alternative to high-pH RP for comprehensive LC-MS/MS proteomics and phosphoproteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 4615-4625.	3.7	41
16	Biophysical and Functional Characterization of Rhesus Macaque IgG Subclasses. <i>Frontiers in Immunology</i> , 2016, 7, 589.	4.8	32
17	Phosphorylation Regulates Id2 Degradation and Mediates the Proliferation of Neural Precursor Cells. <i>Stem Cells</i> , 2016, 34, 1321-1331.	3.2	18
18	Tempest: Accelerated MS/MS Database Search Software for Heterogeneous Computing Platforms. <i>Current Protocols in Bioinformatics</i> , 2016, 55, 13.29.1-13.29.23.	25.8	1

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19	Stress granules and RNA processing bodies are novel autoantibody targets in systemic sclerosis. <i>Arthritis Research and Therapy</i> , 2016, 18, 27.	3.5	16
20	Visualizing the Mechanism of Epoxide Hydrolysis by the Bacterial Virulence Enzyme Cif. <i>Biochemistry</i> , 2016, 55, 788-797.	2.5	10
21	LRRK2 Facilitates tau Phosphorylation through Strong Interaction with tau and cdk5. <i>Biochemistry</i> , 2015, 54, 5198-5208.	2.5	28
22	Quantitative Phosphoproteomics Reveals Pathways for Coordination of Cell Growth and Division by the Conserved Fission Yeast Kinase Pom1*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1275-1287.	3.8	80
23	SPECHT " Single-stage phosphopeptide enrichment and stable-isotope chemical tagging: Quantitative phosphoproteomics of insulin action in muscle. <i>Journal of Proteomics</i> , 2015, 114, 48-60.	2.4	11
24	Neurospora WC-1 Recruits SWI/SNF to Remodel frequency and Initiate a Circadian Cycle. <i>PLoS Genetics</i> , 2014, 10, e1004599.	3.5	61
25	Dueling Kinases Regulate Cell Size at Division through the SAD Kinase Cdr2. <i>Current Biology</i> , 2014, 24, 428-433.	3.9	37
26	Quantitative phosphoproteomic profiling of human non-small cell lung cancer tumors. <i>Journal of Proteomics</i> , 2013, 91, 286-296.	2.4	92
27	Structures of Down Syndrome Kinases, DYRKs, Reveal Mechanisms of Kinase Activation and Substrate Recognition. <i>Structure</i> , 2013, 21, 986-996.	3.3	127
28	SILAC Surrogates: Rescue of Quantitative Information for Orphan Analytes in Spike-In SILAC Experiments. <i>Analytical Chemistry</i> , 2013, 85, 10812-10819.	6.5	9
29	Plk1 regulates the kinesin-13 protein Kif2b to promote faithful chromosome segregation. <i>Molecular Biology of the Cell</i> , 2012, 23, 2264-2274.	2.1	56
30	MMFPh: a maximal motif finder for phosphoproteomics datasets. <i>Bioinformatics</i> , 2012, 28, 1562-1570.	4.1	30
31	The Tlo Proteins Are Stoichiometric Components of <i>Candida albicans</i> Mediator Anchored via the Med3 Subunit. <i>Eukaryotic Cell</i> , 2012, 11, 874-884.	3.4	47
32	Thioredoxin reductase is inhibited by the carbamoylating activity of the anticancer sulfonylhydrazine drug laromustine. <i>Molecular and Cellular Biochemistry</i> , 2012, 370, 199-207.	3.1	7
33	Tempest: GPU-CPU Computing for High-Throughput Database Spectral Matching. <i>Journal of Proteome Research</i> , 2012, 11, 3581-3591.	3.7	19
34	Rapid Determination of Multiple Linear Kinase Substrate Motifs by Mass Spectrometry. <i>Chemistry and Biology</i> , 2012, 19, 608-618.	6.0	73
35	Increasing phosphoproteomic coverage through sequential digestion by complementary proteases. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 711-720.	3.7	34
36	Rapid and Reproducible Single-Stage Phosphopeptide Enrichment of Complex Peptide Mixtures: Application to General and Phosphotyrosine-Specific Phosphoproteomics Experiments. <i>Analytical Chemistry</i> , 2011, 83, 7635-7644.	6.5	151

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37	Kinetic, Mechanistic, and Structural Modeling Studies of Truncated Wild-Type Leucine-Rich Repeat Kinase 2 and the G2019S Mutant. <i>Biochemistry</i> , 2011, 50, 9399-9408.	2.5	42
38	Proteomic Analysis Shows Synthetic Oleanane Triterpenoid Binds to mTOR. <i>PLoS ONE</i> , 2011, 6, e22862.	2.5	88
39	Absolute quantification of protein and post-translational modification abundance with stable isotope- ¹⁵ N labeled synthetic peptides. <i>Nature Protocols</i> , 2011, 6, 175-186.	12.0	141
40	Quantitative Phosphoproteomics Identifies Substrates and Functional Modules of Aurora and Polo-Like Kinase Activities in Mitotic Cells. <i>Science Signaling</i> , 2011, 4, rs5.	3.6	447
41	Insulin-stimulated GLUT4 Protein Translocation in Adipocytes Requires the Rab10 Guanine Nucleotide Exchange Factor Dennd4C. <i>Journal of Biological Chemistry</i> , 2011, 286, 16541-16545.	3.4	67
42	Myc protein is stabilized by suppression of a novel E3 ligase complex in cancer cells. <i>Genes and Development</i> , 2010, 24, 1236-1241.	5.9	93
43	MacroSEQUEST: Efficient Candidate-Centric Searching and High-Resolution Correlation Analysis for Large-Scale Proteomics Data Sets. <i>Analytical Chemistry</i> , 2010, 82, 6821-6829.	6.5	23
44	Multisite Phosphorylation of the Guanine Nucleotide Exchange Factor Cdc24 during Yeast Cell Polarization. <i>PLoS ONE</i> , 2009, 4, e6563.	2.5	33
45	INF2 is an endoplasmic reticulum-associated formin protein. <i>Journal of Cell Science</i> , 2009, 122, 1430-1440.	2.0	118
46	Insulin stimulates the phosphorylation of the exocyst protein Sec8 in adipocytes. <i>Bioscience Reports</i> , 2009, 29, 229-235.	2.4	15
47	Quantitative Proteomics Reveals a Dynamic Interactome and Phase-Specific Phosphorylation in the <i>Neurospora</i> Circadian Clock. <i>Molecular Cell</i> , 2009, 34, 354-363.	9.7	186
48	Identification of RIP1 kinase as a specific cellular target of necrostatins. <i>Nature Chemical Biology</i> , 2008, 4, 313-321.	8.0	1,708
49	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
50	Yeast Chfr homologs retard cell cycle at G1 and G2/M via Ubc4 and Ubc13/Mms2-dependent ubiquitination. <i>Cell Cycle</i> , 2008, 7, 96-105.	2.6	29
51	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
52	Transcriptional interference among the murine β -like globin genes. <i>Blood</i> , 2007, 109, 2210-2216.	1.4	29
53	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
54	The Absolute Quantification Strategy. <i>Methods in Molecular Biology</i> , 2007, 359, 71-86.	0.9	40

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55	Enhanced Analysis of Metastatic Prostate Cancer Using Stable Isotopes and High Mass Accuracy Instrumentation. <i>Journal of Proteome Research</i> , 2006, 5, 1224-1231.	3.7	71
56	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
57	Optimization and Use of Peptide Mass Measurement Accuracy in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1326-1337.	3.8	253
58	A Proteomic Strategy for Gaining Insights into Protein Sumoylation in Yeast. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 246-254.	3.8	227
59	Characterization of Mouse Spleen Cells by Subtractive Proteomics. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1459-1470.	3.8	44
60	Quantitative phosphorylation profiling of the ERK/p90 ribosomal S6 kinase-signaling cassette and its targets, the tuberous sclerosis tumor suppressors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 667-672.	7.1	201
61	The absolute quantification strategy: a general procedure for the quantification of proteins and post-translational modifications. <i>Methods</i> , 2005, 35, 265-273.	3.8	518
62	The Majority of the <i>Saccharomyces cerevisiae</i> Septin Complexes Do Not Exchange Guanine Nucleotides. <i>Journal of Biological Chemistry</i> , 2004, 279, 3111-3118.	3.4	70
63	Budding Yeast Silencing Complexes and Regulation of Sir2 Activity by Protein-Protein Interactions. <i>Molecular and Cellular Biology</i> , 2004, 24, 6931-6946.	2.3	73
64	Two RNAi Complexes, RITS and RDRC, Physically Interact and Localize to Noncoding Centromeric RNAs. <i>Cell</i> , 2004, 119, 789-802.	28.9	506
65	Absolute quantification of proteins and phosphoproteins from cell lysates by tandem MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6940-6945.	7.1	1,701
66	Steps in Assembly of Silent Chromatin in Yeast: Sir3-Independent Binding of a Sir2/Sir4 Complex to Silencers and Role for Sir2-Dependent Deacetylation. <i>Molecular and Cellular Biology</i> , 2002, 22, 4167-4180.	2.3	275
67	Dual Inhibition of Sister Chromatid Separation at Metaphase. <i>Cell</i> , 2001, 107, 715-726.	28.9	417
68	Design and Synthesis of Substrate and Internal Standard Conjugates for Profiling Enzyme Activity in the Sanfilippo Syndrome by Affinity Chromatography/Electrospray Ionization Mass Spectrometry. <i>Bioconjugate Chemistry</i> , 2001, 12, 603-615.	3.6	25
69	Direct Profiling of Multiple Enzyme Activities in Human Cell Lysates by Affinity Chromatography/Electrospray Ionization Mass Spectrometry: A Application to Clinical Enzymology. <i>Analytical Chemistry</i> , 2001, 73, 1651-1657.	6.5	53
70	Quantitative analysis of complex protein mixtures using isotope-coded affinity tags. <i>Nature Biotechnology</i> , 1999, 17, 994-999.	17.5	4,673
71	Analysis of Rates of Multiple Enzymes in Cell Lysates by Electrospray Ionization Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999, 121, 1102-1103.	13.7	45
72	The Absolute Quantification Strategy: Application to Phosphorylation Profiling of Human Serine 1126. , 0, , 71-86.		0