

Daniel Schwartz

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

5,602
citations

430874

18
h-index

677142

22
g-index

29
all docs

29
docs citations

29
times ranked

7614
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomics approach to understanding protein ubiquitination. <i>Nature Biotechnology</i> , 2003, 21, 921-926.	17.5	1,465
2	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
3	An iterative statistical approach to the identification of protein phosphorylation motifs from large-scale data sets. <i>Nature Biotechnology</i> , 2005, 23, 1391-1398.	17.5	837
4	pLogo: a probabilistic approach to visualizing sequence motifs. <i>Nature Methods</i> , 2013, 10, 1211-1212.	19.0	384
5	Biological Sequence Motif Discovery Using <i>motif-x</i> . <i>Current Protocols in Bioinformatics</i> , 2011, 35, Unit 13.15-24.	25.8	330
6	Phosphoproteomic Analysis of the Developing Mouse Brain. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1093-1101.	3.8	322
7	Extensive phosphorylation with overlapping specificity by <i>Mycobacterium tuberculosis</i> serine/threonine protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7521-7526.	7.1	245
8	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
9	Predicting Protein Post-translational Modifications Using Meta-analysis of Proteome Scale Data Sets. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 365-379.	3.8	96
10	Imaging outcome measures of neuroprotection and repair in MS. <i>Neurology</i> , 2019, 92, 519-533.	1.1	53
11	Identification of 14-3-3 μ Substrates from Embryonic Murine Brain. <i>Journal of Proteome Research</i> , 2006, 5, 2372-2379.	3.7	41
12	Ultraconserved Elements: Analyses of Dosage Sensitivity, Motifs and Boundaries. <i>Genetics</i> , 2008, 180, 2277-2293.	2.9	37
13	An autophosphorylation site database for leucine-rich repeat receptor-like kinases in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2015, 82, 1042-1060.	5.7	34
14	Protein kinases PknA and PknB independently and coordinately regulate essential <i>Mycobacterium tuberculosis</i> physiologies and antimicrobial susceptibility. <i>PLoS Pathogens</i> , 2020, 16, e1008452.	4.7	33
15	Collection and Motif-Based Prediction of Phosphorylation Sites in Human Viruses. <i>Science Signaling</i> , 2010, 3, rs2.	3.6	30
16	Using Bacteria to Determine Protein Kinase Specificity and Predict Target Substrates. <i>PLoS ONE</i> , 2012, 7, e52747.	2.5	26
17	Prediction of lysine post-translational modifications using bioinformatic tools. <i>Essays in Biochemistry</i> , 2012, 52, 165-177.	4.7	23
18	Transphosphorylation of <i>E. coli</i> Proteins during Production of Recombinant Protein Kinases Provides a Robust System to Characterize Kinase Specificity. <i>Frontiers in Plant Science</i> , 2012, 3, 262.	3.6	20

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19	Cushing's syndrome mutant ^L^{205R} exhibits altered substrate specificity. FEBS Letters, 2017, 591, 459-467.	2.8	20
20	Using the scanProtein Web Site to Predict Protein Posttranslational Modifications. Current Protocols in Bioinformatics, 2011, 36, Unit 13.16..	25.8	12
21	Characterizing Protein Kinase Substrate Specificity Using the Proteomic Peptide Library (ProPeL) Approach. Current Protocols in Chemical Biology, 2018, 10, e38.	1.7	11
22	The Okur-Chung Neurodevelopmental Syndrome Mutation CK2K198R Leads to a Rewiring of Kinase Specificity. Frontiers in Molecular Biosciences, 2022, 9, 850661.	3.5	8
23	Invited: "Going viral" with biological sequence analysis. , 2011, , .		0
24	ProPeL: A method to discover specific kinase motifs and predict target substrates. FASEB Journal, 2013, 27, 597.4.	0.5	0
25	An interactive and probabilistic strategy for visualizing linear biological sequence motifs. FASEB Journal, 2013, 27, 810.8.	0.5	0
26	Using ProPeL to discover the binding specificity of human DYRK1a. FASEB Journal, 2013, 27, 1045.3.	0.5	0