Daniel Schwartz

List of Publications by Year
in descending order

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	The Okur-Chung Neurodevelopmental Syndrome Mutation CK2K198R Leads to a Rewiring of Kinase Specificity. Frontiers in Molecular Biosciences, 2022, 9, 850661.	3.5	8
2	Protein kinases PknA and PknB independently and coordinately regulate essential Mycobacterium tuberculosis physiologies and antimicrobial susceptibility. PLoS Pathogens, 2020, 16, e1008452.	4.7	33
3	Imaging outcome measures of neuroprotection and repair in MS. Neurology, 2019, 92, 519-533.	1.1	53
4	Characterizing Protein Kinase Substrate Specificity Using the Proteomic Peptide Library (ProPeL) Approach. Current Protocols in Chemical Biology, 2018, 10, e38.	1.7	11
5	Cushing's syndrome mutant PKA^{L205R} exhibits altered substrate specificity. FEBS Letters, 2017, 591, 459-467.	2.8	20
6	An autophosphorylation site database for leucine-rich repeat receptor-like kinases in *Arabidopsis thaliana*. Plant Journal, 2015, 82, 1042-1060.	5.7	34
7	pLogo: a probabilistic approach to visualizing sequence motifs. Nature Methods, 2013, 10, 1211-1212.	19.0	384
8	ProPeL: A method to discover specific kinase motifs and predict target substrates. FASEB Journal, 2013, 27, 597.4.	0.5	0
9	An interactive and probabilistic strategy for visualizing linear biological sequence motifs. FASEB Journal, 2013, 27, 810.8.	0.5	0
10	Using ProPeL to discover the binding specificity of human DYRK1a. FASEB Journal, 2013, 27, 1045.3.	0.5	0
11	Transphosphorylation of E. coli Proteins during Production of Recombinant Protein Kinases Provides a Robust System to Characterize Kinase Specificity. Frontiers in Plant Science, 2012, 3, 262.	3.6	20
12	Prediction of lysine post-translational modifications using bioinformatic tools. Essays in Biochemistry, 2012, 52, 165-177.	4.7	23
13	Using Bacteria to Determine Protein Kinase Specificity and Predict Target Substrates. PLoS ONE, 2012, 7, e52747.	2.5	26
14	Invited: “Going viral” with biological sequence analysis. , 2011, , .		0
15	Using the scan-x Web Site to Predict Protein Post-Translational Modifications. Current Protocols in Bioinformatics, 2011, 36, Unit 13.16..	25.8	12
16	Biological Sequence Motif Discovery Using *motif-x*. Current Protocols in Bioinformatics, 2011, 35, Unit 13.15-24.	25.8	330
17	Collection and Motif-Based Prediction of Phosphorylation Sites in Human Viruses. Science Signaling, 2010, 3, rs2.	3.6	30
18	Extensive phosphorylation with overlapping specificity by *Mycobacterium tuberculosis* serine/threonine protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7521-7526.	7.1	245

#	Article	IF	Citations
19	Predicting Protein Post-translational Modifications Using Meta-analysis of Proteome Scale Data Sets. Molecular and Cellular Proteomics, 2009, 8, 365-379.	3.8	96
20	Large-Scale Phosphoprotein Analysis in<i>Medicago truncatula</i>Roots Provides Insight into in Vivo Kinase Activity in Legumes Â. Plant Physiology, 2009, 152, 19-28.	4.8	133
21	Ultraconserved Elements: Analyses of Dosage Sensitivity, Motifs and Boundaries. Genetics, 2008, 180, 2277-2293.	2.9	37
22	Identification of 14-3-3Îµ Substrates from Embryonic Murine Brain. Journal of Proteome Research, 2006, 5, 2372-2379.	3.7	41
23	An iterative statistical approach to the identification of protein phosphorylation motifs from large-scale data sets. Nature Biotechnology, 2005, 23, 1391-1398.	17.5	837
24	Phosphoproteomic Analysis of the Developing Mouse Brain. Molecular and Cellular Proteomics, 2004, 3, 1093-1101.	3.8	322
25	Large-scale characterization of HeLa cell nuclear phosphoproteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12130-12135.	7.1	1,434
26	A proteomics approach to understanding protein ubiquitination. Nature Biotechnology, 2003, 21, 921-926.	17.5	1,465