

# Alejandro Wolf-Yadlin

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

2,405  
citations

361413

20  
h-index

580821

25  
g-index

28  
all docs

28  
docs citations

28  
times ranked

3576  
citing authors

#	ARTICLE	IF	CITATIONS
1	Time-resolved Mass Spectrometry of Tyrosine Phosphorylation Sites in the Epidermal Growth Factor Receptor Signaling Network Reveals Dynamic Modules. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1240-1250.	3.8	494
2	Multiple reaction monitoring for robust quantitative proteomic analysis of cellular signaling networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5860-5865.	7.1	472
3	Effects of HER2 overexpression on cell signaling networks governing proliferation and migration. <i>Molecular Systems Biology</i> , 2006, 2, 54.	7.2	217
4	Technical advances in proteomics: new developments in data-independent acquisition. <i>F1000Research</i> , 2016, 5, 419.	1.6	172
5	A disease-associated PTPN22 variant promotes systemic autoimmunity in murine models. <i>Journal of Clinical Investigation</i> , 2013, 123, 2024-2036.	8.2	162
6	A General Molecular Affinity Strategy for Global Detection and Proteomic Analysis of Lysine Methylation. <i>Molecular Cell</i> , 2013, 50, 444-456.	9.7	143
7	Modeling HER2 Effects on Cell Behavior from Mass Spectrometry Phosphotyrosine Data. <i>PLoS Computational Biology</i> , 2007, 3, e4.	3.2	92
8	Dissecting protein function and signaling using protein microarrays. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 398-405.	6.1	85
9	The surface exposed amino acid residues of monomeric proteins determine the partitioning in aqueous two-phase systems. <i>BBA - Proteins and Proteomics</i> , 2002, 1596, 253-268.	2.1	76
10	Receptor Tyrosine Kinases Fall into Distinct Classes Based on Their Inferred Signaling Networks. <i>Science Signaling</i> , 2013, 6, ra58.	3.6	55
11	Integrated systems biology analysis of KSHV latent infection reveals viral induction and reliance on peroxisome mediated lipid metabolism. <i>PLoS Pathogens</i> , 2017, 13, e1006256.	4.7	53
12	Linear combinations of docking affinities explain quantitative differences in RTK signaling. <i>Molecular Systems Biology</i> , 2009, 5, 235.	7.2	52
13	Quantitative proteomic analysis of HIV-1 infected CD4+ T cells reveals an early host response in important biological pathways: Protein synthesis, cell proliferation, and T-cell activation. <i>Virology</i> , 2012, 429, 37-46.	2.4	43
14	Lysate Microarrays Enable High-throughput, Quantitative Investigations of Cellular Signaling. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005363.	3.8	38
15	Maximum Entropy Reconstructions of Dynamic Signaling Networks from Quantitative Proteomics Data. <i>PLoS ONE</i> , 2009, 4, e6522.	2.5	31
16	The Tec Kinase Regulated Phosphoproteome Reveals a Mechanism for the Regulation of Inhibitory Signals in Murine Macrophages. <i>Journal of Immunology</i> , 2015, 195, 246-256.	0.8	31
17	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. <i>Cell Reports</i> , 2018, 24, 3607-3618.	6.4	30
18	Protein Kinase PKN1 Represses Wnt/ $\beta$ -Catenin Signaling in Human Melanoma Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 34658-34670.	3.4	29

#	ARTICLE	IF	CITATIONS
19	Methods for the Analysis of Protein Phosphorylationâ€“Mediated Cellular Signaling Networks. Annual Review of Analytical Chemistry, 2016, 9, 295-315.	5.4	27
20	Quantitative Proteomic Analysis of Phosphotyrosine-Mediated Cellular Signaling Networks. Methods in Molecular Biology, 2007, 359, 203-212.	0.9	25
21	Endogenous N-terminal Domain Cleavage Modulates Î±1D-Adrenergic Receptor Pharmacodynamics. Journal of Biological Chemistry, 2016, 291, 18210-18221.	3.4	23
22	A computationally engineered RAS rheostat reveals RASâ€™ERK signaling dynamics. Nature Chemical Biology, 2017, 13, 119-126.	8.0	21
23	Individual protomers of a G protein-coupled receptor dimer integrate distinct functional modules. Cell Discovery, 2015, 1, .	6.7	17
24	Dynamic mass redistribution reveals diverging importance of PDZ-ligands for G protein-coupled receptor pharmacodynamics. Pharmacological Research, 2016, 105, 13-21.	7.1	7
25	Machine Learning Prediction of Adenovirus D8 Conjunctivitis Complications from Viral Whole-Genome Sequence. Ophthalmology Science, 2022, 2, 100166.	2.5	5
26	Development of Selected Reaction Monitoring Methods to Systematically Quantify Kinase Abundance and Phosphorylation Stoichiometry in Human Samples. Methods in Molecular Biology, 2017, 1636, 353-369.	0.9	2