Alejandro Wolf-Yadlin

List of Publications by Year
in descending order

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	Machine Learning Prediction of Adenovirus D8 Conjunctivitis Complications from Viral Whole-Genome Sequence. Ophthalmology Science, 2022, 2, 100166.	2.5	5
2	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. Cell Reports, 2018, 24, 3607-3618.	6.4	30
3	A computationally engineered RAS rheostat reveals RAS–ERK signaling dynamics. Nature Chemical Biology, 2017, 13, 119-126.	8.0	21
4	Integrated systems biology analysis of KSHV latent infection reveals viral induction and reliance on peroxisome mediated lipid metabolism. PLoS Pathogens, 2017, 13, e1006256.	4.7	53
5	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
6	Technical advances in proteomics: new developments in data-independent acquisition. F1000Research, 2016, 5, 419.	1.6	172
7	Endogenous N-terminal Domain Cleavage Modulates α1D-Adrenergic Receptor Pharmacodynamics. Journal of Biological Chemistry, 2016, 291, 18210-18221.	3.4	23
8	Methods for the Analysis of Protein Phosphorylation–Mediated Cellular Signaling Networks. Annual Review of Analytical Chemistry, 2016, 9, 295-315.	5.4	27
9	Dynamic mass redistribution reveals diverging importance of PDZ-ligands for G protein-coupled receptor pharmacodynamics. Pharmacological Research, 2016, 105, 13-21.	7.1	7
10	Individual protomers of a G protein-coupled receptor dimer integrate distinct functional modules. Cell Discovery, 2015, 1, .	6.7	17
11	The Tec Kinase–Regulated Phosphoproteome Reveals a Mechanism for the Regulation of Inhibitory Signals in Murine Macrophages. Journal of Immunology, 2015, 195, 246-256.	0.8	31
12	A General Molecular Affinity Strategy for Global Detection and Proteomic Analysis of Lysine Methylation. Molecular Cell, 2013, 50, 444-456.	9.7	143
13	Receptor Tyrosine Kinases Fall into Distinct Classes Based on Their Inferred Signaling Networks. Science Signaling, 2013, 6, ra58.	3.6	55
14	Protein Kinase PKN1 Represses Wnt/β-Catenin Signaling in Human Melanoma Cells. Journal of Biological Chemistry, 2013, 288, 34658-34670.	3.4	29
15	A disease-associated PTPN22 variant promotes systemic autoimmunity in murine models. Journal of Clinical Investigation, 2013, 123, 2024-2036.	8.2	162
16	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. Virology, 2012, 429, 37-46.	2.4	43
17	Lysate Microarrays Enable High-throughput, Quantitative Investigations of Cellular Signaling. Molecular and Cellular Proteomics, 2011, 10, M110.005363.	3.8	38
18	Maximum Entropy Reconstructions of Dynamic Signaling Networks from Quantitative Proteomics Data. PLoS ONE, 2009, 4, e6522.	2.5	31

#	Article	IF	Citations
19	Linear combinations of docking affinities explain quantitative differences in RTK signaling. Molecular Systems Biology, 2009, 5, 235.	7.2	52
20	Dissecting protein function and signaling using protein microarrays. Current Opinion in Chemical Biology, 2009, 13, 398-405.	6.1	85
21	Modeling HER2 Effects on Cell Behavior from Mass Spectrometry Phosphotyrosine Data. PLoS Computational Biology, 2007, 3, e4.	3.2	92
22	Multiple reaction monitoring for robust quantitative proteomic analysis of cellular signaling networks. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5860-5865.	7.1	472
23	Quantitative Proteomic Analysis of Phosphotyrosine-Mediated Cellular Signaling Networks. Methods in Molecular Biology, 2007, 359, 203-212.	0.9	25
24	Effects of HER2 overexpression on cell signaling networks governing proliferation and migration. Molecular Systems Biology, 2006, 2, 54.	7.2	217
25	Time-resolved Mass Spectrometry of Tyrosine Phosphorylation Sites in the Epidermal Growth Factor Receptor Signaling Network Reveals Dynamic Modules. Molecular and Cellular Proteomics, 2005, 4, 1240-1250.	3.8	494
26	The surface exposed amino acid residues of monomeric proteins determine the partitioning in aqueous two-phase systems. BBA - Proteins and Proteomics, 2002, 1596, 253-268.	2.1	76