Dorothea Rutishauser

List of Publications by Year in descending order

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44 papers 2,407 citations

236925 25 h-index 243625 44 g-index

45 all docs

45 docs citations

45 times ranked

4950 citing authors

#	Article	IF	CITATIONS
1	PARP1 ADP-ribosylates lysine residues of the core histone tails. Nucleic Acids Research, 2010, 38, 6350-6362.	14.5	226
2	Qualitative and Quantitative Analyses of Protein Phosphorylation in Naive and Stimulated Mouse Synaptosomal Preparations. Molecular and Cellular Proteomics, 2007, 6, 283-293.	3.8	211
3	Systemsâ€based analysis of Arabidopsis leaf growth reveals adaptation to water deficit. Molecular Systems Biology, 2012, 8, 606.	7.2	191
4	Comparative phosphoproteome profiling reveals a function of the STN8 kinase in fine-tuning of cyclic electron flow (CEF). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12955-12960.	7.1	148
5	Implementation and evaluation of relative and absolute quantification in shotgun proteomics with label-free methods. Journal of Proteomics, 2010, 73, 1740-1746.	2.4	139
6	Proteomic analysis of synaptosomes using isotope-coded affinity tags and mass spectrometry. Proteomics, 2005, 5, 2531-2541.	2.2	117
7	Shared immunological targets in the lungs and joints of patients with rheumatoid arthritis: identification and validation. Annals of the Rheumatic Diseases, 2015, 74, 1772-1777.	0.9	112
8	Molecular profiling of prostate cancer derived exosomes may reveal a predictive signature for response to docetaxel. Oncotarget, 2015, 6, 21740-21754.	1.8	109
9	Highâ€throughput proteomic analysis of <scp>FFPE</scp> tissue samples facilitates tumor stratification. Molecular Oncology, 2019, 13, 2305-2328.	4.6	100
10	A crosstalk between \hat{l}^21 and \hat{l}^23 integrins controls glycine receptor and gephyrin trafficking at synapses. Nature Neuroscience, 2010, 13, 1388-1395.	14.8	86
11	In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models. Molecular and Cellular Proteomics, 2013, 12, 2324-2331.	3.8	81
12	Urinary Prognostic Biomarkers and Classification of IgA Nephropathy by High Resolution Mass Spectrometry Coupled with Liquid Chromatography. PLoS ONE, 2013, 8, e80830.	2.5	73
13	The Comprehensive Native Interactome of a Fully Functional Tagged Prion Protein. PLoS ONE, 2009, 4, e4446.	2.5	69
14	Blood Plasma IgG Fc Glycans are Significantly Altered in Alzheimer's Disease and Progressive Mild Cognitive Impairment. Journal of Alzheimer's Disease, 2013, 38, 567-579.	2.6	66
15	Periostin is identified as a putative metastatic marker in breast cancer-derived exosomes. Oncotarget, 2016, 7, 74966-74978.	1.8	61
16	Identification of proteins from human permanent erupted enamel. European Journal of Oral Sciences, 2015, 123, 390-395.	1.5	57
17	Binding of Pro-Gly-Pro at the active site of leukotriene A ₄ hydrolase/aminopeptidase and development of an epoxide hydrolase selective inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4227-4232.	7.1	50
18	Approach for Identifying Human Leukocyte Antigen (HLA)-DR Bound Peptides from Scarce Clinical Samples. Molecular and Cellular Proteomics, 2016, 15, 3017-3029.	3.8	46

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19	Prognostic Polypeptide Blood Plasma Biomarkers of Alzheimer's Disease Progression. Journal of Alzheimer's Disease, 2014, 40, 659-666.	2.6	44
20	Identification of a large protein network involved in epigenetic transmission in replicating DNA of embryonic stem cells. Nucleic Acids Research, 2014, 42, 6972-6986.	14.5	42
21	Chemosensory proteins, major salivary factors in caterpillar mandibular glands. Insect Biochemistry and Molecular Biology, 2012, 42, 796-805.	2.7	38
22	Extracellular Hemoglobin Polarizes the Macrophage Proteome toward Hb-Clearance, Enhanced Antioxidant Capacity and Suppressed HLA Class 2 Expression. Journal of Proteome Research, 2011, 10, 2397-2408.	3.7	36
23	lgG Fc galactosylation predicts response to methotrexate in early rheumatoid arthritis. Arthritis Research and Therapy, 2017, 19, 182.	3.5	35
24	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. Nature Communications, 2019, 10, 2524.	12.8	35
25	Predictive urinary biomarkers for steroid-resistant and steroid-sensitive focal segmental glomerulosclerosis using high resolution mass spectrometry and multivariate statistical analysis. BMC Nephrology, 2014, 15, 141.	1.8	30
26	SpotLight Proteomics: uncovering the hidden blood proteome improves diagnostic power of proteomics. Scientific Reports, 2017, 7, 41929.	3.3	27
27	Urinary Prognostic Biomarkers in Patients With Focal Segmental Glomerulosclerosis. Nephro-Urology Monthly, 2014, 6, e16806.	0.1	24
28	Wobble decoding by the Escherichia coli selenocysteine insertion machinery. Nucleic Acids Research, 2013, 41, 9800-9811.	14.5	20
29	Expression proteomics study to determine metallodrug targets and optimal drug combinations. Scientific Reports, 2017, 7, 1590.	3.3	19
30	Convergent network effects along the axis of gene expression during prostate cancer progression. Genome Biology, 2020, 21, 302.	8.8	17
31	Liquid Biopsies in Renal Cell Carcinoma—Recent Advances and Promising New Technologies for the Early Detection of Metastatic Disease. Frontiers in Oncology, 2020, 10, 582843.	2.8	16
32	The Mass Distance Fingerprint: A statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 854, 173-182.	2.3	13
33	Phosphorylated serine and threonine residues promote siteâ€specific fragmentation of singly charged, arginineâ€containing peptide ions. Rapid Communications in Mass Spectrometry, 2009, 23, 1435-1445.	1.5	10
34	Effect of host plant and immune challenge on the levels of chemosensory and odorant-binding proteins in caterpillar salivary glands. Insect Biochemistry and Molecular Biology, 2015, 61, 34-45.	2.7	10
35	The Nucleus-Localized Epidermal Growth Factor Receptor Is SUMOylated. Biochemistry, 2015, 54, 5157-5166.	2.5	10
36	Database independent detection of isotopically labeled MS/MS spectrum peptide pairs. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 817, 225-230.	2.3	8

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37	Identification of shared citrullinated immunological targets in the lungs and joints of patients with rheumatoid arthritis. Annals of the Rheumatic Diseases, 2012, 71, A19.1-A19.	0.9	6
38	Post-translational Regulation of DNA Polymerase \hat{l} , a Connection to Damage-Induced Cohesion in Saccharomyces cerevisiae. Genetics, 2020, 216, 1009-1022.	2.9	5
39	ILâ€16 processing in sentinel node regulatory T cells is a factor in bladder cancer immunity. Scandinavian Journal of Immunology, 2020, 92, e12926.	2.7	5
40	Inferring clonal composition from multiple tumor biopsies. Npj Systems Biology and Applications, 2020, 6, 27.	3.0	5
41	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. BMC Bioinformatics, 2012, 13, 34.	2.6	4
42	Employment of Complementary Dissociation Techniques for Body Fluid Characterization and Biomarker Discovery. Methods in Molecular Biology, 2013, 1002, 223-232.	0.9	2
43	FRET-Based Sorting of Live Cells Reveals Shifted Balance between PLK1 and CDK1 Activities During Checkpoint Recovery. Cells, 2020, 9, 2126.	4.1	2
44	Changes in the plasma microvesicle proteome during the ovarian hyperstimulation phase of assisted reproductive technology. Scientific Reports, 2020, 10, 13645.	3.3	1