

# Dorothea Rutishauser

## List of Publications by Year in descending order

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44  
papers

2,407  
citations

270111

25  
h-index

274796

44  
g-index

45  
all docs

45  
docs citations

45  
times ranked

5439  
citing authors

#	ARTICLE	IF	CITATIONS
1	Post-translational Regulation of DNA Polymerase $\delta$ , a Connection to Damage-Induced Cohesion in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2020, 216, 1009-1022.	1.2	5
2	Liquid Biopsies in Renal Cell Carcinoma—Recent Advances and Promising New Technologies for the Early Detection of Metastatic Disease. <i>Frontiers in Oncology</i> , 2020, 10, 582843.	1.3	16
3	IL-16 processing in sentinel node regulatory T cells is a factor in bladder cancer immunity. <i>Scandinavian Journal of Immunology</i> , 2020, 92, e12926.	1.3	5
4	FRET-Based Sorting of Live Cells Reveals Shifted Balance between PLK1 and CDK1 Activities During Checkpoint Recovery. <i>Cells</i> , 2020, 9, 2126.	1.8	2
5	Inferring clonal composition from multiple tumor biopsies. <i>Npj Systems Biology and Applications</i> , 2020, 6, 27.	1.4	5
6	Changes in the plasma microvesicle proteome during the ovarian hyperstimulation phase of assisted reproductive technology. <i>Scientific Reports</i> , 2020, 10, 13645.	1.6	1
7	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020, 21, 302.	3.8	17
8	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019, 13, 2305-2328.	2.1	100
9	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	5.8	35
10	SpotLight Proteomics: uncovering the hidden blood proteome improves diagnostic power of proteomics. <i>Scientific Reports</i> , 2017, 7, 41929.	1.6	27
11	Expression proteomics study to determine metalloprotein targets and optimal drug combinations. <i>Scientific Reports</i> , 2017, 7, 1590.	1.6	19
12	IgG Fc galactosylation predicts response to methotrexate in early rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2017, 19, 182.	1.6	35
13	Approach for Identifying Human Leukocyte Antigen (HLA)-DR Bound Peptides from Scarce Clinical Samples. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3017-3029.	2.5	46
14	Periostin is identified as a putative metastatic marker in breast cancer-derived exosomes. <i>Oncotarget</i> , 2016, 7, 74966-74978.	0.8	61
15	Identification of proteins from human permanent erupted enamel. <i>European Journal of Oral Sciences</i> , 2015, 123, 390-395.	0.7	57
16	Molecular profiling of prostate cancer derived exosomes may reveal a predictive signature for response to docetaxel. <i>Oncotarget</i> , 2015, 6, 21740-21754.	0.8	109
17	Effect of host plant and immune challenge on the levels of chemosensory and odorant-binding proteins in caterpillar salivary glands. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 61, 34-45.	1.2	10
18	The Nucleus-Localized Epidermal Growth Factor Receptor Is SUMOylated. <i>Biochemistry</i> , 2015, 54, 5157-5166.	1.2	10

#	ARTICLE	IF	CITATIONS
19	Shared immunological targets in the lungs and joints of patients with rheumatoid arthritis: identification and validation. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1772-1777.	0.5	112
20	Binding of Pro-Gly-Pro at the active site of leukotriene A <sub>4</sub> hydrolase/aminopeptidase and development of an epoxide hydrolase selective inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4227-4232.	3.3	50
21	Urinary Prognostic Biomarkers in Patients With Focal Segmental Glomerulosclerosis. <i>Nephro-Urology Monthly</i> , 2014, 6, e16806.	0.0	24
22	Predictive urinary biomarkers for steroid-resistant and steroid-sensitive focal segmental glomerulosclerosis using high resolution mass spectrometry and multivariate statistical analysis. <i>BMC Nephrology</i> , 2014, 15, 141.	0.8	30
23	Identification of a large protein network involved in epigenetic transmission in replicating DNA of embryonic stem cells. <i>Nucleic Acids Research</i> , 2014, 42, 6972-6986.	6.5	42
24	Prognostic Polypeptide Blood Plasma Biomarkers of Alzheimer's Disease Progression. <i>Journal of Alzheimer's Disease</i> , 2014, 40, 659-666.	1.2	44
25	Employment of Complementary Dissociation Techniques for Body Fluid Characterization and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2013, 1002, 223-232.	0.4	2
26	In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2324-2331.	2.5	81
27	Wobble decoding by the Escherichia coli selenocysteine insertion machinery. <i>Nucleic Acids Research</i> , 2013, 41, 9800-9811.	6.5	20
28	Blood Plasma IgG Fc Glycans are Significantly Altered in Alzheimer's Disease and Progressive Mild Cognitive Impairment. <i>Journal of Alzheimer's Disease</i> , 2013, 38, 567-579.	1.2	66
29	Urinary Prognostic Biomarkers and Classification of IgA Nephropathy by High Resolution Mass Spectrometry Coupled with Liquid Chromatography. <i>PLoS ONE</i> , 2013, 8, e80830.	1.1	73
30	Identification of shared citrullinated immunological targets in the lungs and joints of patients with rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, A19.1-A19.	0.5	6
31	Systems-based analysis of Arabidopsis leaf growth reveals adaptation to water deficit. <i>Molecular Systems Biology</i> , 2012, 8, 606.	3.2	191
32	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. <i>BMC Bioinformatics</i> , 2012, 13, 34.	1.2	4
33	Chemosensory proteins, major salivary factors in caterpillar mandibular glands. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 796-805.	1.2	38
34	Extracellular Hemoglobin Polarizes the Macrophage Proteome toward Hb-Clearance, Enhanced Antioxidant Capacity and Suppressed HLA Class 2 Expression. <i>Journal of Proteome Research</i> , 2011, 10, 2397-2408.	1.8	36
35	Comparative phosphoproteome profiling reveals a function of the STN8 kinase in fine-tuning of cyclic electron flow (CEF). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12955-12960.	3.3	148
36	Implementation and evaluation of relative and absolute quantification in shotgun proteomics with label-free methods. <i>Journal of Proteomics</i> , 2010, 73, 1740-1746.	1.2	139

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37	A crosstalk between $\beta^1$ and $\beta^3$ integrins controls glycine receptor and gephyrin trafficking at synapses. <i>Nature Neuroscience</i> , 2010, 13, 1388-1395.	7.1	86
38	PARP1 ADP-ribosylates lysine residues of the core histone tails. <i>Nucleic Acids Research</i> , 2010, 38, 6350-6362.	6.5	226
39	The Comprehensive Native Interactome of a Fully Functional Tagged Prion Protein. <i>PLoS ONE</i> , 2009, 4, e4446.	1.1	69
40	Phosphorylated serine and threonine residues promote site-specific fragmentation of singly charged, arginine-containing peptide ions. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1435-1445.	0.7	10
41	Qualitative and Quantitative Analyses of Protein Phosphorylation in Naive and Stimulated Mouse Synaptosomal Preparations. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 283-293.	2.5	211
42	The Mass Distance Fingerprint: A statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 854, 173-182.	1.2	13
43	Database independent detection of isotopically labeled MS/MS spectrum peptide pairs. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 817, 225-230.	1.2	8
44	Proteomic analysis of synaptosomes using isotope-coded affinity tags and mass spectrometry. <i>Proteomics</i> , 2005, 5, 2531-2541.	1.3	117