

Ralph Schlapbach

List of Publications by Year in descending order

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87
papers

6,235
citations

109321

35
h-index

71685

76
g-index

90
all docs

90
docs citations

90
times ranked

11248
citing authors

#	ARTICLE	IF	CITATIONS
1	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16428-16433.	7.1	774
2	Oxidants in mitochondria: from physiology to diseases. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 1995, 1271, 67-74.	3.8	459
3	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. Nature Communications, 2017, 8, 291.	12.8	423
4	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. Science Signaling, 2010, 3, rs4.	3.6	277
5	A high-quality catalog of the Drosophila melanogaster proteome. Nature Biotechnology, 2007, 25, 576-583.	17.5	247
6	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
7	Gain and Loss of Multiple Genes During the Evolution of Helicobacter pylori. PLoS Genetics, 2005, 1, e43.	3.5	198
8	PhosphoPep—a database of protein phosphorylation sites in model organisms. Nature Biotechnology, 2008, 26, 1339-1340.	17.5	192
9	PhosphoPep—a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. Molecular Systems Biology, 2007, 3, 139.	7.2	168
10	Genome-wide analysis of transcriptional hierarchy and feedback regulation in the flagellar system of Helicobacter pylori. Molecular Microbiology, 2004, 52, 947-961.	2.5	165
11	Myc-mediated repression of microRNA-34a promotes high-grade transformation of B-cell lymphoma by dysregulation of FoxP1. Blood, 2011, 117, 6227-6236.	1.4	165
12	TNF- α and IFN- γ render microglia sensitive to Fas ligand-induced apoptosis by induction of Fas expression and down-regulation of Bcl-2 and Bcl-xL. European Journal of Immunology, 1998, 28, 4398-4408.	2.9	142
13	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
14	Characterization of the Interactome of the Human MutL Homologues MLH1, PMS1, and PMS2. Journal of Biological Chemistry, 2007, 282, 2976-2986.	3.4	129
15	The SystemMHC Atlas project. Nucleic Acids Research, 2018, 46, D1237-D1247.	14.5	119
16	B-Type Natriuretic Peptide Concentrations Predict the Progression of Nondiabetic Chronic Kidney Disease: The Mild-to-Moderate Kidney Disease Study. Clinical Chemistry, 2007, 53, 1264-1272.	3.2	111
17	Pushing the limits of de novo genome assembly for complex prokaryotic genomes harboring very long, near identical repeats. Nucleic Acids Research, 2018, 46, 8953-8965.	14.5	104
18	Identification of a SIRT1 Mutation in a Family with Type 1 Diabetes. Cell Metabolism, 2013, 17, 448-455.	16.2	103

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19	New insights into the performance of human whole-exome capture platforms. <i>Nucleic Acids Research</i> , 2015, 43, e76-e76.	14.5	103
20	TGF β 2 directs gene expression of activated microglia to an anti-inflammatory phenotype strongly focusing on chemokine genes and cell migratory genes. <i>Glia</i> , 2003, 44, 219-231.	4.9	100
21	Nitric-Oxide Kills Hepatocytes by Mobilizing Mitochondrial Calcium. <i>Biochemical and Biophysical Research Communications</i> , 1994, 205, 1143-1150.	2.1	99
22	The draft genome of <i>Primula veris</i> yields insights into the molecular basis of heterostyly. <i>Genome Biology</i> , 2015, 16, 12.	8.8	96
23	SUSHI: an exquisite recipe for fully documented, reproducible and reusable NGS data analysis. <i>BMC Bioinformatics</i> , 2016, 17, 228.	2.6	90
24	Multiple hybrid de novo genome assembly of finger millet, an orphan allotetraploid crop. <i>DNA Research</i> , 2018, 25, 39-47.	3.4	85
25	Identification and relative quantification of membrane proteins by surface biotinylation and two-dimensional peptide mapping. <i>Proteomics</i> , 2005, 5, 2718-2728.	2.2	79
26	Targeted Proteomics Guided by Label-free Quantitative Proteome Analysis in Saliva Reveal Transition Signatures from Health to Periodontal Disease. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1392-1409.	3.8	74
27	iTRAQ-Based and Label-Free Proteomics Approaches for Studies of Human Adenovirus Infections. <i>International Journal of Proteomics</i> , 2013, 2013, 1-16.	2.0	73
28	<i>Shigella</i> reroutes host cell central metabolism to obtain high-flux nutrient supply for vigorous intracellular growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9929-9934.	7.1	71
29	TGF- β 2 induces the expression of the FLICE-inhibitory protein and inhibits Fas-mediated apoptosis of microglia. <i>European Journal of Immunology</i> , 2000, 30, 3680-3688.	2.9	68
30	Long fragments achieve lower base quality in Illumina paired-end sequencing. <i>Scientific Reports</i> , 2019, 9, 2856.	3.3	66
31	Environmental marine pathogen isolation using mesocosm culture of sharpnose seabream: striking genomic and morphological features of novel <i>Endozoicomonas</i> sp.. <i>Scientific Reports</i> , 2015, 5, 17609.	3.3	60
32	B-Fabric. , 2010, , .		52
33	Institutional core facilities: prerequisite for breakthroughs in the life sciences. <i>EMBO Reports</i> , 2016, 17, 1088-1093.	4.5	44
34	Differential antiproliferative mechanisms of novel derivative of benzimidazo[1,2- <i>b</i>]quinoline in colon cancer cells depending on their p53 status. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 2121-2132.	4.1	40
35	Blind spots of quantitative RNA-seq: the limits for assessing abundance, differential expression, and isoform switching. <i>BMC Bioinformatics</i> , 2013, 14, 370.	2.6	38
36	Targeted proteomics coming of age – SRM, PRM and DIA performance evaluated from a core facility perspective. <i>Proteomics</i> , 2016, 16, 2183-2192.	2.2	38

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37	Pain-Associated Transcriptome Changes in Synovium of Knee Osteoarthritis Patients. <i>Genes</i> , 2018, 9, 338.	2.4	37
38	A preliminary investigation demonstrating the effect of quercetin on the expression of genes related to cell-cycle arrest, apoptosis and xenobiotic metabolism in human CO115 colon-adenocarcinoma cells using DNA microarray. <i>Biotechnology and Applied Biochemistry</i> , 2006, 45, 29.	3.1	36
39	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular $\hat{1}^2$ -proteobacteria. <i>ISME Journal</i> , 2016, 10, 1791-1803.	9.8	34
40	Mining co-regulated gene profiles for the detection of functional associations in gene expression data. <i>Bioinformatics</i> , 2007, 23, 1927-1935.	4.1	31
41	An international multicenter study on HIV-1 drug resistance testing by 454 ultra-deep pyrosequencing. <i>Journal of Virological Methods</i> , 2014, 204, 31-37.	2.1	31
42	Differential activity of bcl-2 and ICE enzyme family protease inhibitors on Fas and puromycin-induced apoptosis of glioma cells. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 1997, 1359, 174-180.	4.1	29
43	RNA-Seq Data Analysis: From Raw Data Quality Control to Differential Expression Analysis. <i>Methods in Molecular Biology</i> , 2017, 1669, 295-307.	0.9	29
44	rawDiag: An R Package Supporting Rational LC-MS Method Optimization for Bottom-up Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2908-2914.	3.7	29
45	The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. <i>GigaScience</i> , 2022, 11, .	6.4	29
46	Prognostic value of cross-omics screening for kidney clear cell renal cancer survival. <i>Biology Direct</i> , 2016, 11, 68.	4.6	28
47	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017, 18, 3219-3226.	6.4	28
48	Network integration and modelling of dynamic drug responses at multi-omics levels. <i>Communications Biology</i> , 2020, 3, 573.	4.4	28
49	An integrated proteomics approach for studying the molecular pathogenesis of Dupuytren's disease. <i>Journal of Pathology</i> , 2009, 217, 524-533.	4.5	27
50	Cell Cycle Constraints and Environmental Control of Local DNA Hypomethylation in $\hat{1}^{\pm}$ -Proteobacteria. <i>PLoS Genetics</i> , 2016, 12, e1006499.	3.5	25
51	Casting light on molecular events underlying anti-cancer drug treatment: What can be seen from the proteomics point of view?. <i>Cancer Treatment Reviews</i> , 2006, 32, 619-629.	7.7	23
52	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1670-1680.	3.8	23
53	A model-based assay design to reproduce in vivo patterns of acute drug-induced toxicity. <i>Archives of Toxicology</i> , 2018, 92, 553-555.	4.2	23
54	Gas-Phase Fragmentation of ADP-Ribosylated Peptides: Arginine-Specific Side-Chain Losses and Their Implication in Database Searches. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 157-168.	2.8	23

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55	Involvement of the N-methyl-D-aspartate receptor in neuronal cell death induced by cytotoxic T cell-derived secretory granules. <i>European Journal of Immunology</i> , 1999, 29, 3053-3062.	2.9	16
56	PhyloDetect: a likelihood-based strategy for detecting microorganisms with diagnostic microarrays. <i>Bioinformatics</i> , 2008, 24, i83-i89.	4.1	16
57	Development and experimental validation of a <i>nifH</i> oligonucleotide microarray to study diazotrophic communities in a glacier forefield. <i>Environmental Microbiology</i> , 2009, 11, 2179-2189.	3.8	16
58	Highly sensitive, non-invasive detection of colorectal cancer mutations using single molecule, third generation sequencing. <i>Applied & Translational Genomics</i> , 2015, 7, 32-39.	2.1	16
59	Single-molecule DNA hybridisation studied by using a modified DNA sequencer: a comparison with surface plasmon resonance data. <i>Methods and Applications in Fluorescence</i> , 2016, 4, 015002.	2.3	16
60	MnSOD marks cord blood late outgrowth endothelial cells and accompanies robust resistance to oxidative stress. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 364-369.	2.1	15
61	MAGMA: analysis of two-channel microarrays made easy. <i>Nucleic Acids Research</i> , 2007, 35, W86-W90.	14.5	15
62	PTM MarkerFinder, a software tool to detect and validate spectra from peptides carrying post-translational modifications. <i>Proteomics</i> , 2013, 13, 2251-2255.	2.2	15
63	A Follow-Up of the Multicenter Collaborative Study on HIV-1 Drug Resistance and Tropism Testing Using 454 Ultra Deep Pyrosequencing. <i>PLoS ONE</i> , 2016, 11, e0146687.	2.5	15
64	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.	2.3	13
65	Host-Associated Genomic Features of the Novel Uncultured Intracellular Pathogen <i>Ca. Ichthyocystis</i> Revealed by Direct Sequencing of Epitheliocysts. <i>Genome Biology and Evolution</i> , 2016, 8, 1672-1689.	2.5	12
66	One step ahead. <i>EMBO Reports</i> , 2019, 20, .	4.5	12
67	Translational Proteomics Analysis of Anthracycline-Induced Cardiotoxicity From Cardiac Microtissues to Human Heart Biopsies. <i>Frontiers in Genetics</i> , 2021, 12, 695625.	2.3	12
68	specLab™ an R/Bioconductor package to prepare peptide spectrum matches for use in targeted proteomics. <i>Bioinformatics</i> , 2015, 31, 2228-2231.	4.1	11
69	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.	1.5	10
70	Precise breakpoint localization of large genomic deletions using PacBio and Illumina next-generation sequencers. <i>BioTechniques</i> , 2013, 54, 98-100.	1.8	10
71	<i>Ca. Endozoicomonas cretensis</i> : A Novel Fish Pathogen Characterized by Genome Plasticity. <i>Genome Biology and Evolution</i> , 2018, 10, 1363-1374.	2.5	10
72	TNF- α and IFN- β render microglia sensitive to Fas ligand-induced apoptosis by induction of Fas expression and down-regulation of Bcl-2 and Bcl-xL. <i>European Journal of Immunology</i> , 1998, 28, 4398-4408.	2.9	9

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73	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.	2.3	8
74	An improved draft genome assembly of <i>Meloidogyne graminicola</i> IARI strain using long-read sequencing. <i>Gene</i> , 2021, 793, 145748.	2.2	8
75	B-Fabric: A Data and Application Integration Framework for Life Sciences Research. , 2007, , 37-47.		8
76	The SwissBioGrid Project: Objectivse, Preliminary Results and Lessons Learned. , 2006, , .		7
77	Dependence of Fluorescence Quenching of CY3 Oligonucleotide Conjugates on the Oxidation Potential of the Stacking Base Pair. <i>Molecules</i> , 2020, 25, 5369.	3.8	6
78	B-Fabric: An Open Source Life Sciences Data Management System. <i>Lecture Notes in Computer Science</i> , 2009, , 185-190.	1.3	5
79	Preferred analysis methods for single genomic regions in RNA sequencing revealed by processing the shape of coverage. <i>Nucleic Acids Research</i> , 2012, 40, e63-e63.	14.5	4
80	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. <i>BMC Bioinformatics</i> , 2012, 13, 34.	2.6	4
81	Single-molecule chemistry. Part I: monitoring oxidation of G in oligonucleotides using CY3 fluorescence. <i>Methods and Applications in Fluorescence</i> , 2020, 8, 035010.	2.3	4
82	Mapping Spatial Genetic Landscapes in Tissue Sections through Microscale Integration of Sampling Methodology into Genomic Workflows. <i>Small</i> , 2021, 17, 2007901.	10.0	3
83	Rapid Profiling of Human Pathogenic Bacteria and Antibiotic Resistance Employing Specific Tryptic Peptides as Biomarkers. , 2016, , 275-303.		3
84	When Time-to-Result Matters: Identification of Microbes Based on MALDI-TOF Protein and Peptide Profiling. <i>Chimia</i> , 2014, 68, 453.	0.6	2
85	Minimizing DNA microarrays to a single molecule per spot: using zero-mode waveguide technology to obtain kinetic data for a large number of short oligonucleotide hybridization reactions. , 2016, , .		2
86	Single molecule interactions studied by using a modified DNA sequencer: a comparison with surface plasmon resonance. <i>Proceedings of SPIE</i> , 2013, , .	0.8	1
87	Mass Spectrometric Proteome Analysis of Small Three-Dimensional Microtissues Allows for the Quantitative Description of Toxic Effects of Drugs. <i>Chimia</i> , 2015, 69, 494.	0.6	0