

Frank Schmidt

List of Publications by Year in descending order

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94
papers

3,907
citations

136885

32
h-index

138417

58
g-index

96
all docs

96
docs citations

96
times ranked

7749
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic profiling of metformin effects in 3T3-L1 adipocytes by SILAC-based quantification. <i>Proteomics</i> , 2022, , 2100196.	1.3	1
2	Specific domain V reduction of beta-2-glycoprotein I induces protein flexibility and alters pathogenic antibody binding. <i>Scientific Reports</i> , 2021, 11, 4542.	1.6	3
3	A Comprehensive View on the Human Antibody Repertoire Against <i>Staphylococcus aureus</i> Antigens in the General Population. <i>Frontiers in Immunology</i> , 2021, 12, 651619.	2.2	24
4	Sputum Proteome Signatures of Mechanically Ventilated Intensive Care Unit Patients Distinguish Samples with or without Anti-pneumococcal Activity. <i>MSystems</i> , 2021, 6, .	1.7	4
5	Technical report: xMAPr – High-dynamic-range (HDR) quantification of antigen-specific antibody binding. <i>Journal of Proteomics</i> , 2020, 212, 103577.	1.2	7
6	Hfq modulates global protein pattern and stress response in <i>Bordetella pertussis</i> . <i>Journal of Proteomics</i> , 2020, 211, 103559.	1.2	5
7	Comparative Proteomic Profiling of 3T3-L1 Adipocyte Differentiation Using SILAC Quantification. <i>Journal of Proteome Research</i> , 2020, 19, 4884-4900.	1.8	5
8	Exploring metal availability in the natural niche of <i>Streptococcus pneumoniae</i> to discover potential vaccine antigens. <i>Virulence</i> , 2020, 11, 1310-1328.	1.8	8
9	Chromosome-free bacterial cells are safe and programmable platforms for synthetic biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6752-6761.	3.3	32
10	Early-Stage <i>Staphylococcus aureus</i> Bloodstream Infection Causes Changes in the Concentrations of Lipoproteins and Acute-Phase Proteins and Is Associated with Low Antibody Titers against Bacterial Virulence Factors. <i>MSystems</i> , 2020, 5, .	1.7	7
11	Defensive Function of Transposable Elements in Bacteria. <i>ACS Synthetic Biology</i> , 2019, 8, 2141-2151.	1.9	27
12	In vivo proteomics identifies the competence regulon and AliB oligopeptide transporter as pathogenic factors in pneumococcal meningitis. <i>PLoS Pathogens</i> , 2019, 15, e1007987.	2.1	25
13	Single-Cell and Time-Resolved Profiling of Intracellular <i>Salmonella</i> Metabolism in Primary Human Cells. <i>Analytical Chemistry</i> , 2019, 91, 7729-7737.	3.2	20
14	Proteome profiling of secreted and membrane vesicle associated proteins of an invasive and a commensal <i>Staphylococcus haemolyticus</i> isolate. <i>Data in Brief</i> , 2019, 22, 914-919.	0.5	2
15	Translation initiation factor IF2 contributes to ribosome assembly and maturation during cold adaptation. <i>Nucleic Acids Research</i> , 2019, 47, 4652-4662.	6.5	17
16	Comparative exoproteome profiling of an invasive and a commensal <i>Staphylococcus haemolyticus</i> isolate. <i>Journal of Proteomics</i> , 2019, 197, 106-114.	1.2	16
17	Secreted Immunomodulatory Proteins of <i>Staphylococcus aureus</i> Activate Platelets and Induce Platelet Aggregation. <i>Thrombosis and Haemostasis</i> , 2018, 47, 745-757.	1.8	27
18	Intranasal Vaccination With Lipoproteins Confers Protection Against Pneumococcal Colonisation. <i>Frontiers in Immunology</i> , 2018, 9, 2405.	2.2	33

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19	Sulfur-34S and 36S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34/36) of Proteome Analyses. <i>Methods in Molecular Biology</i> , 2018, 1841, 163-174.	0.4	0
20	In vivo Proteomics Approaches for the Analysis of Bacterial Adaptation Reactions in Host-Pathogen Settings. <i>Methods in Molecular Biology</i> , 2018, 1841, 207-228.	0.4	0
21	Analysis of Staphylococcus aureus proteins secreted inside infected human epithelial cells. <i>International Journal of Medical Microbiology</i> , 2018, 308, 664-674.	1.5	4
22	Staphylococcal serine protease-like proteins are pacemakers of allergic airway reactions to Staphylococcus aureus. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 492-500.e8.	1.5	118
23	Characterization of human and Staphylococcus aureus proteins in respiratory mucosa by in vivo- and immunoproteomics. <i>Journal of Proteomics</i> , 2017, 155, 31-39.	1.2	36
24	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	3.0	39
25	A global Staphylococcus aureus proteome resource applied to the in vivo characterization of host-pathogen interactions. <i>Scientific Reports</i> , 2017, 7, 9718.	1.6	42
26	Laboratory Mice Are Frequently Colonized with Staphylococcus aureus and Mount a Systemic Immune Response—Note of Caution for In vivo Infection Experiments. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 152.	1.8	30
27	Omics Approaches for the Study of Adaptive Immunity to Staphylococcus aureus and the Selection of Vaccine Candidates. <i>Proteomes</i> , 2016, 4, 11.	1.7	15
28	Staphylococcus aureus Transcriptome Architecture: From Laboratory to Infection-Mimicking Conditions. <i>PLoS Genetics</i> , 2016, 12, e1005962.	1.5	170
29	Adaptive immune response to lipoproteins of Staphylococcus aureus in healthy subjects. <i>Proteomics</i> , 2016, 16, 2667-2677.	1.3	13
30	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	2.6	60
31	Proteome data from a host-pathogen interaction study with Staphylococcus aureus and human lung epithelial cells. <i>Data in Brief</i> , 2016, 7, 1031-1037.	0.5	1
32	Alternative fluorescent labeling strategies for characterizing gram-positive pathogenic bacteria: Flow cytometry supported counting, sorting, and proteome analysis of <i>Staphylococcus aureus</i> retrieved from infected host cells. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 932-940.	1.1	20
33	Proteome analysis of Bordetella pertussis isolated from human macrophages. <i>Journal of Proteomics</i> , 2016, 136, 55-67.	1.2	19
34	A peptide resource for the analysis of Staphylococcus aureus in host-pathogen interaction studies. <i>Proteomics</i> , 2015, 15, 3648-3661.	1.3	24
35	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015, 70, 758-762.	0.2	0
36	The Proteome of the Isolated Chlamydia trachomatis Containing Vacuole Reveals a Complex Trafficking Platform Enriched for Retromer Components. <i>PLoS Pathogens</i> , 2015, 11, e1004883.	2.1	74

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37	A proteomic perspective of the interplay of <i>Staphylococcus aureus</i> and human alveolar epithelial cells during infection. <i>Journal of Proteomics</i> , 2015, 128, 203-217.	1.2	24
38	Shotgun proteome analysis of <i>Bordetella pertussis</i> reveals a distinct influence of iron availability on the bacterial metabolism, virulence, and defense response. <i>Proteomics</i> , 2015, 15, 2258-2266.	1.3	12
39	reSpect: Software for Identification of High and Low Abundance Ion Species in Chimeric Tandem Mass Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1837-1847.	1.2	17
40	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
41	Specific serum IgG at diagnosis of <i>Staphylococcus aureus</i> bloodstream invasion is correlated with disease progression. <i>Journal of Proteomics</i> , 2015, 128, 1-7.	1.2	49
42	Comparative proteome analysis reveals conserved and specific adaptation patterns of <i>Staphylococcus aureus</i> after internalization by different types of human non-professional phagocytic host cells. <i>Frontiers in Microbiology</i> , 2014, 5, 392.	1.5	32
43	Labeling of the pathogenic bacterium <i>Staphylococcus aureus</i> with gold or ferric oxide core nanoparticles highlights new capabilities for investigation of host-pathogen interactions. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 140-150.	1.1	13
44	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. <i>Nature Genetics</i> , 2014, 46, 629-634.	9.4	113
45	Quantitative proteomics in the field of microbiology. <i>Proteomics</i> , 2014, 14, 547-565.	1.3	66
46	Altered immune proteome of <i>Staphylococcus aureus</i> under iron-restricted growth conditions. <i>Proteomics</i> , 2014, 14, 1857-1867.	1.3	13
47	Bone marrow-derived macrophages from BALB/c and C57BL/6 mice fundamentally differ in their respiratory chain complex proteins, lysosomal enzymes and components of antioxidant stress systems. <i>Journal of Proteomics</i> , 2014, 103, 72-86.	1.2	26
48	Activation of the alternative sigma factor SigB of <i>Staphylococcus aureus</i> following internalization by epithelial cells – An in vivo proteomics perspective. <i>International Journal of Medical Microbiology</i> , 2014, 304, 177-187.	1.5	29
49	A proteomics workflow for quantitative and time-resolved analysis of adaptation reactions of internalized bacteria. <i>Methods</i> , 2013, 61, 244-250.	1.9	25
50	Data visualization in environmental proteomics. <i>Proteomics</i> , 2013, 13, 2805-2821.	1.3	21
51	Proteomics approaches for the analysis of enriched microbial subpopulations and visualization of complex functional information. <i>Current Opinion in Biotechnology</i> , 2013, 24, 112-119.	3.3	30
52	Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. <i>ISME Journal</i> , 2013, 7, 1877-1885.	4.4	107
53	Sulfur-34S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34) of Proteomic Changes in <i>Pseudomonas fluorescens</i> during Naphthalene Degradation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2060-2069.	2.5	17
54	Identification of Lactobacilli from Deep Carious Lesions by Means of Species-Specific PCR and MALDI-TOF Mass Spectrometry. <i>Clinical Laboratory</i> , 2013, 59, 1373-9.	0.2	23

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55	Sulfur- ³⁶ S stable isotope labeling of amino acids for quantification (SULAQ). <i>Proteomics</i> , 2012, 12, 37-42.	1.3	20
56	Protein-based stable isotope probing (protein-SIP) in functional metaproteomics. <i>Mass Spectrometry Reviews</i> , 2012, 31, 683-697.	2.8	61
57	Functional genomics of the initial phase of cold adaptation of <i>Pseudomonas putida</i> KT2440. <i>FEMS Microbiology Letters</i> , 2011, 318, 47-54.	0.7	26
58	Quantitative proteome analysis of the 20S proteasome of apoptotic Jurkat T cells. <i>Amino Acids</i> , 2011, 41, 351-361.	1.2	16
59	Time resolved protein-based stable isotope probing (Protein-SIP) analysis allows quantification of induced proteins in substrate shift experiments. <i>Proteomics</i> , 2011, 11, 2265-2274.	1.3	40
60	Proteome analysis of host-pathogen interactions: Investigation of pathogen responses to the host cell environment. <i>Proteomics</i> , 2011, 11, 3203-3211.	1.3	68
61	Impairment of Immunoproteasome Function by ¹²⁵ I/LMP7 Subunit Deficiency Results in Severe Enterovirus Myocarditis. <i>PLoS Pathogens</i> , 2011, 7, e1002233.	2.1	78
62	Advanced tool for characterization of microbial cultures by combining cytomics and proteomics. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 575-584.	1.7	44
63	Calculation of partial isotope incorporation into peptides measured by mass spectrometry. <i>BMC Research Notes</i> , 2010, 3, 178.	0.6	7
64	Proteomic characterization of a <i>pilR</i> regulatory mutant of <i>Azoarcus</i> sp. strain BH72 with the aid of gel-based and gel-free approaches. <i>Proteomics</i> , 2010, 10, 458-469.	1.3	10
65	Time-resolved quantitative proteome profiling of host-pathogen interactions: The response of <i>Staphylococcus aureus</i> RN1HG to internalisation by human airway epithelial cells. <i>Proteomics</i> , 2010, 10, 2801-2811.	1.3	45
66	Protein-based stable isotope probing. <i>Nature Protocols</i> , 2010, 5, 1957-1966.	5.5	97
67	Decimal Place Slope, A Fast and Precise Method for Quantifying ¹³ C Incorporation Levels for Detecting the Metabolic Activity of Microbial Species. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1221-1227.	2.5	19
68	Combined Genomic and Proteomic Approaches Identify Gene Clusters Involved in Anaerobic 2-Methylnaphthalene Degradation in the Sulfate-Reducing Enrichment Culture N47. <i>Journal of Bacteriology</i> , 2010, 192, 295-306.	1.0	101
69	Declining Capacity of Starving <i>Delftia acidovorans</i> MC1 to Degrade Phenoxypropionate Herbicides Correlates with Oxidative Modification of the Initial Enzyme. <i>Environmental Science & Technology</i> , 2010, 44, 3793-3799.	4.6	14
70	Prediction of flocculation ability of brewing yeast inoculates by flow cytometry, proteome analysis, and mRNA profiling. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009, 75A, 140-147.	1.1	23
71	Shotgun mass mapping of <i>Lactobacillus</i> species and subspecies from caries related isolates by MALDI-MS. <i>Proteomics</i> , 2009, 9, 1994-2003.	1.3	35
72	Comparison of methods for simultaneous identification of bacterial species and determination of metabolic activity by protein-based stable isotope probing (Protein-SIP) experiments. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1871-1878.	0.7	28

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73	Identification of harmless and pathogenic algae of the genus <i>Prototheca</i> by MALDI-MS. <i>Proteomics - Clinical Applications</i> , 2009, 3, 774-784.	0.8	44
74	Assembling proteomics data as a prerequisite for the analysis of large scale experiments. <i>Chemistry Central Journal</i> , 2009, 3, 2.	2.6	5
75	A plasmid RK2-based broad-host-range cloning vector useful for transfer of metagenomic libraries to a variety of bacterial species. <i>FEMS Microbiology Letters</i> , 2009, 296, 149-158.	0.7	94
76	Incorporation of carbon and nitrogen atoms into proteins measured by protein-based stable isotope probing (Protein-SIP). <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 2889-2897.	0.7	77
77	Protein-based stable isotope probing (Protein-SIP) reveals active species within anoxic mixed cultures. <i>ISME Journal</i> , 2008, 2, 1122-1133.	4.4	126
78	Quantitative proteome analysis of cisplatin-induced apoptotic Jurkat T cells by stable isotope labeling with amino acids in cell culture, SDS-PAGE, and LC-MALDI-TOF/TOF MS. <i>Electrophoresis</i> , 2007, 28, 4359-4368.	1.3	24
79	Rapid determination of amino acid incorporation by stable isotope labeling with amino acids in cell culture (SILAC). <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 3919-3926.	0.7	28
80	An improved strategy for selective and efficient enrichment of integral plasma membrane proteins of mycobacteria. <i>Proteomics</i> , 2007, 7, 1687-1701.	1.3	33
81	Distinctive mass losses of tryptic peptides generated by matrix-assisted laser desorption/ionization time-of-flight/time-of-flight. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 933-936.	0.7	12
82	Proteins unique to intraphagosomally grown <i>Mycobacterium tuberculosis</i> . <i>Proteomics</i> , 2006, 6, 2485-2494.	1.3	75
83	Comprehensive quantitative proteome analysis of 20S proteasome subtypes from rat liver by isotope coded affinity tag and 2-D gel-based approaches. <i>Proteomics</i> , 2006, 6, 4622-4632.	1.3	50
84	Peptide mass fingerprinting. <i>Methods</i> , 2005, 35, 237-247.	1.9	202
85	Complementary Analysis of the <i>Mycobacterium tuberculosis</i> Proteome by Two-dimensional Electrophoresis and Isotope-coded Affinity Tag Technology. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 24-42.	2.5	160
86	Web-accessible proteome databases for microbial research. <i>Proteomics</i> , 2004, 4, 1305-1313.	1.3	41
87	Protein identification and tracking in two-dimensional electrophoretic gels by minimal protein identifiers. <i>Proteomics</i> , 2004, 4, 2927-2941.	1.3	29
88	Comparative proteome analysis of culture supernatant proteins from virulent <i>Mycobacterium tuberculosis</i> H37Rv and attenuated <i>M. bovis</i> BCG Copenhagen. <i>Electrophoresis</i> , 2003, 24, 3405-3420.	1.3	156
89	Iterative data analysis is the key for exhaustive analysis of peptide mass fingerprints from proteins separated by two-dimensional electrophoresis. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 943-956.	1.2	73
90	Analysis of Automatically Generated Peptide Mass Fingerprints of Cellular Proteins and Antigens from <i>Helicobacter pylori</i> 26695 Separated by Two-dimensional Electrophoresis. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1271-1283.	2.5	25

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91	Generation of minimal protein identifiers of proteins from two-dimensional gels and recombinant proteins. <i>Electrophoresis</i> , 2002, 23, 621-625.	1.3	18
92	Protein identification and tracking in two-dimensional electrophoretic gels by minimal protein identifiers. , 0, , 97-120.		1
93	Web-accessible proteome databases for microbial research. , 0, , 63-74.		0
94	Protein Stable Isotope Probing. , 0, , 73-95.		0