

# Birgit Schilling

## List of Publications by Year in descending order

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129  
papers

12,476  
citations

28274

55  
h-index

28297

105  
g-index

159  
all docs

159  
docs citations

159  
times ranked

16452  
citing authors

#	ARTICLE	IF	CITATIONS
1	Advanced mass spectrometry-based methods for protein molecular-structural biologists. , 2022, , 311-326.		8
2	MicroRNA sequence codes for small extracellular vesicle release and cellular retention. Nature, 2022, 601, 446-451.	27.8	300
3	Dietary restriction and the transcription factor clock delay eye aging to extend lifespan in Drosophila Melanogaster. Nature Communications, 2022, 13, .	12.8	12
4	Comprehensive proteomic quantification of bladder stone progression in a cystinuric mouse model using data-independent acquisitions. PLoS ONE, 2022, 17, e0250137.	2.5	3
5	Quantification and Identification of Post-Translational Modifications Using Modern Proteomics Approaches. Methods in Molecular Biology, 2021, 2228, 225-235.	0.9	11
6	Quantitative Proteomic Analysis of the Senescence-Associated Secretory Phenotype by Data-Independent Acquisition. Current Protocols, 2021, 1, e32.	2.9	25
7	Improved SILAC Quantification with Data-Independent Acquisition to Investigate Bortezomib-Induced Protein Degradation. Journal of Proteome Research, 2021, 20, 1918-1927.	3.7	36
8	Proteomics in aging research: A roadmap to clinical, translational research. Aging Cell, 2021, 20, e13325.	6.7	59
9	Algorithmic assessment of cellular senescence in experimental and clinical specimens. Nature Protocols, 2021, 16, 2471-2498.	12.0	92
10	Proximity labeling and other novel mass spectrometric approaches for spatiotemporal protein dynamics. Expert Review of Proteomics, 2021, 18, 757-765.	3.0	6
11	Accumulation of "Old Proteins" and the Critical Need for MS-based Protein Turnover Measurements in Aging and Longevity. Proteomics, 2020, 20, e1800403.	2.2	24
12	SUCLA2 mutations cause global protein succinylation contributing to the pathomechanism of a hereditary mitochondrial disease. Nature Communications, 2020, 11, 5927.	12.8	35
13	Cytotrophoblast extracellular vesicles enhance decidual cell secretion of immune modulators via TNF-alpha. Development (Cambridge), 2020, 147, .	2.5	12
14	Lysine and Arginine Protein Post-translational Modifications by Enhanced DIA Libraries: Quantification in Murine Liver Disease. Journal of Proteome Research, 2020, 19, 4163-4178.	3.7	18
15	Senescent cells promote tissue NAD+ decline during ageing via the activation of CD38+ macrophages. Nature Metabolism, 2020, 2, 1265-1283.	11.9	206
16	The power of proteomics to monitor senescence-associated secretory phenotypes and beyond: toward clinical applications. Expert Review of Proteomics, 2020, 17, 297-308.	3.0	40
17	Simultaneous Affinity Enrichment of Two Post-Translational Modifications for Quantification and Site Localization. Journal of Visualized Experiments, 2020, , .	0.3	7
18	Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveal coordinate control of lipid metabolism. Molecular Biology of the Cell, 2020, 31, 1069-1084.	2.1	30

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19	A proteomic atlas of senescence-associated secretomes for aging biomarker development. <i>PLoS Biology</i> , 2020, 18, e3000599.	5.6	694
20	Skyline for Small Molecules: A Unifying Software Package for Quantitative Metabolomics. <i>Journal of Proteome Research</i> , 2020, 19, 1447-1458.	3.7	253
21	Activating transcription factor 4 (ATF4) promotes skeletal muscle atrophy by forming a heterodimer with the transcriptional regulator C/EBP $\beta$ . <i>Journal of Biological Chemistry</i> , 2020, 295, 2787-2803.	3.4	45
22	Emerging mass spectrometry-based proteomics methodologies for novel biomedical applications. <i>Biochemical Society Transactions</i> , 2020, 48, 1953-1966.	3.4	22
23	Translational control of one-carbon metabolism underpins ribosomal protein phenotypes in cell division and longevity. <i>ELife</i> , 2020, 9, .	6.0	24
24	Plasma proteomic biomarker signature of age predicts health and life span. <i>ELife</i> , 2020, 9, .	6.0	78
25	Quantification of Insoluble Protein Aggregation in <i>Caenorhabditis elegans</i> during Aging with a Novel Data-Independent Acquisition Workflow. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	3
26	Post-translational Protein Acetylation: An Elegant Mechanism for Bacteria to Dynamically Regulate Metabolic Functions. <i>Frontiers in Microbiology</i> , 2019, 10, 1604.	3.5	122
27	Proteome and Secretome Dynamics of Human Retinal Pigment Epithelium in Response to Reactive Oxygen Species. <i>Scientific Reports</i> , 2019, 9, 15440.	3.3	22
28	Sirtuin 5 Regulates Proximal Tubule Fatty Acid Oxidation to Protect against AKI. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2384-2398.	6.1	85
29	Dietary Sugars Alter Hepatic Fatty Acid Oxidation via Transcriptional and Post-translational Modifications of Mitochondrial Proteins. <i>Cell Metabolism</i> , 2019, 30, 735-753.e4.	16.2	136
30	SILAC Analysis Reveals Increased Secretion of Hemostasis-Related Factors by Senescent Cells. <i>Cell Reports</i> , 2019, 28, 3329-3337.e5.	6.4	94
31	High-Resolution Mass Spectrometry to Identify and Quantify Acetylation Protein Targets. <i>Methods in Molecular Biology</i> , 2019, 1983, 3-16.	0.9	15
32	Regulation of UCP1 and Mitochondrial Metabolism in Brown Adipose Tissue by Reversible Succinylation. <i>Molecular Cell</i> , 2019, 74, 844-857.e7.	9.7	123
33	Mechanisms, Detection, and Relevance of Protein Acetylation in Prokaryotes. <i>MBio</i> , 2019, 10, .	4.1	94
34	JNK modifies neuronal metabolism to promote proteostasis and longevity. <i>Aging Cell</i> , 2019, 18, e12849.	6.7	18
35	Global Lysine Acetylation in <i>Escherichia coli</i> Results from Growth Conditions That Favor Acetate Fermentation. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	34
36	Quantification of Site-specific Protein Lysine Acetylation and Succinylation Stoichiometry Using Data-independent Acquisition Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	9

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37	Protein Turnover in Aging and Longevity. <i>Proteomics</i> , 2018, 18, e1700108.	2.2	78
38	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1239-1244.	3.8	177
39	An acetylatabe lysine controls CRP function in <i>E. coli</i> . <i>Molecular Microbiology</i> , 2018, 107, 116-131.	2.5	51
40	Temporal dynamics of liver mitochondrial protein acetylation and succinylation and metabolites due to high fat diet and/or excess glucose or fructose. <i>PLoS ONE</i> , 2018, 13, e0208973.	2.5	38
41	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	4.1	86
42	Simultaneous Quantification of the Acetylome and Succinylome by $\epsilon$ -OnePot <sup>™</sup> Affinity Enrichment. <i>Proteomics</i> , 2018, 18, e1800123.	2.2	31
43	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018, 28, 866-880.e15.	16.2	154
44	Identifying ubiquitinated proteins and aggregates. <i>Aging</i> , 2018, 10, 2549-2550.	3.1	6
45	Generation of High-Quality SWATH <sup>®</sup> Acquisition Data for Label-free Quantitative Proteomics Studies Using TripleTOF <sup>®</sup> Mass Spectrometers. <i>Methods in Molecular Biology</i> , 2017, 1550, 223-233.	0.9	75
46	Clinical applications of quantitative proteomics using targeted and untargeted data-independent acquisition techniques. <i>Expert Review of Proteomics</i> , 2017, 14, 419-429.	3.0	114
47	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1335-1347.	3.8	21
48	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	12.8	423
49	Ancient Regulatory Role of Lysine Acetylation in Central Metabolism. <i>MBio</i> , 2017, 8, .	4.1	105
50	PIQED: automated identification and quantification of protein modifications from DIA-MS data. <i>Nature Methods</i> , 2017, 14, 646-647.	19.0	52
51	INVESTIGATING PROTEIN HOMEOSTASIS IN <i>C.ÆLEGANS</i> AND <i>C.ÆBRIGGSÆ</i> STRAINS USING MASS SPECTROMETRY. <i>Innovation in Aging</i> , 2017, 1, 1210-1211.	0.1	1
52	Identification and characterization of AckA-dependent protein acetylation in <i>Neisseria gonorrhoeae</i> . <i>PLoS ONE</i> , 2017, 12, e0179621.	2.5	17
53	Gadd45a Protein Promotes Skeletal Muscle Atrophy by Forming a Complex with the Protein Kinase MEK4. <i>Journal of Biological Chemistry</i> , 2016, 291, 17496-17509.	3.4	37
54	Acetylated Tau Obstructs KIBRA-Mediated Signaling in Synaptic Plasticity and Promotes Tauopathy-Related Memory Loss. <i>Neuron</i> , 2016, 90, 245-260.	8.1	195

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55	Stable nuclear expression of <i>ATP8</i> and <i>ATP6</i> genes rescues a mtDNA Complex V null mutant. <i>Nucleic Acids Research</i> , 2016, 44, gkrw756.	14.5	35
56	Quantification of Lysine Acetylation and Succinylation Stoichiometry in Proteins Using Mass Spectrometric Data-Independent Acquisitions (SWATH). <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1758-1771.	2.8	73
57	Vitamin D Promotes Protein Homeostasis and Longevity via the Stress Response Pathway Genes <i>skn-1</i> , <i>ire-1</i> , and <i>xbp-1</i> . <i>Cell Reports</i> , 2016, 17, 1227-1237.	6.4	65
58	Chapter 9. Informatics Solutions for Selected Reaction Monitoring. <i>New Developments in Mass Spectrometry</i> , 2016, , 178-199.	0.2	0
59	The <i>E. coli</i> sirtuin CobB shows no preference for enzymatic and nonenzymatic lysine acetylation substrate sites. <i>MicrobiologyOpen</i> , 2015, 4, 66-83.	3.0	87
60	Protein acetylation dynamics in response to carbon overflow in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2015, 98, 847-863.	2.5	164
61	Wavelet-Based Peak Detection and a New Charge Inference Procedure for MS/MS Implemented in ProteoWizard's msConvert. <i>Journal of Proteome Research</i> , 2015, 14, 1299-1307.	3.7	38
62	MS1 Peptide Ion Intensity Chromatograms in MS2 (SWATH) Data Independent Acquisitions. Improving Post Acquisition Analysis of Proteomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2405-2419.	3.8	57
63	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2357-2374.	3.8	153
64	SIRT1 deacetylates ROR $\alpha$ and enhances Th17 cell generation. <i>Journal of Experimental Medicine</i> , 2015, 212, 607-617.	8.5	126
65	Multiplexed, Scheduled, High-Resolution Parallel Reaction Monitoring on a Full Scan QqTOF Instrument with Integrated Data-Dependent and Targeted Mass Spectrometric Workflows. <i>Analytical Chemistry</i> , 2015, 87, 10222-10229.	6.5	88
66	Critical role of acetylation in tau-mediated neurodegeneration and cognitive deficits. <i>Nature Medicine</i> , 2015, 21, 1154-1162.	30.7	398
67	Integration-independent Transgenic Huntington Disease Fragment Mouse Models Reveal Distinct Phenotypes and Life Span in Vivo. <i>Journal of Biological Chemistry</i> , 2015, 290, 19287-19306.	3.4	20
68	Structural, Kinetic and Proteomic Characterization of Acetyl Phosphate-Dependent Bacterial Protein Acetylation. <i>PLoS ONE</i> , 2014, 9, e94816.	2.5	249
69	Iron promotes protein insolubility and aging in <i>C. elegans</i> . <i>Aging</i> , 2014, 6, 975-988.	3.1	57
70	Ubiquitin-specific peptidase 9, X-linked (USP9X) modulates activity of mammalian target of rapamycin (mTOR).. <i>Journal of Biological Chemistry</i> , 2014, 289, 14965.	3.4	2
71	Phosphoprotein Secretome of Tumor Cells as a Source of Candidates for Breast Cancer Biomarkers in Plasma. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1034-1049.	3.8	41
72	A framework for installable external tools in Skyline. <i>Bioinformatics</i> , 2014, 30, 2521-2523.	4.1	36

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73	Site-specific acylation changes in the lipid A of <i>Escherichia coli</i> $\Delta$ pxL mutants grown at high temperatures. <i>Innate Immunity</i> , 2014, 20, 269-282.	2.4	11
74	Variation and quantification among a target set of phosphopeptides in human plasma by multiple reaction monitoring and SWATH-MS2 data-independent acquisition. <i>Electrophoresis</i> , 2014, 35, 3487-3497.	2.4	22
75	Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210.	3.7	205
76	RPL24: a potential therapeutic target whose depletion or acetylation inhibits polysome assembly and cancer cell growth. <i>Oncotarget</i> , 2014, 5, 5165-5176.	1.8	34
77	Design, Implementation and Multisite Evaluation of a System Suitability Protocol for the Quantitative Assessment of Instrument Performance in Liquid Chromatography-Multiple Reaction Monitoring-MS (LC-MRM-MS). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2623-2639.	3.8	100
78	Label-free quantitative proteomics of the lysine acetylome in mitochondria identifies substrates of SIRT3 in metabolic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6601-6606.	7.1	414
79	Platform-independent and Label-free Quantitation of Proteomic Data Using MS1 Extracted Ion Chromatograms in Skyline. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 202-214.	3.8	428
80	Ligand Binding Promotes CDK-Dependent Phosphorylation of ER-Alpha on Hinge Serine 294 but Inhibits Ligand-Independent Phosphorylation of Serine 305. <i>Molecular Cancer Research</i> , 2012, 10, 1120-1132.	3.4	27
81	Ubiquitin-specific Peptidase 9, X-linked (USP9X) Modulates Activity of Mammalian Target of Rapamycin (mTOR). <i>Journal of Biological Chemistry</i> , 2012, 287, 21164-21175.	3.4	47
82	QuaMeter: Multivendor Performance Metrics for LC-MS/MS Proteomics Instrumentation. <i>Analytical Chemistry</i> , 2012, 84, 5845-5850.	6.5	50
83	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. <i>Journal of Proteome Research</i> , 2012, 11, 2508-2520.	3.7	49
84	Proteomic Analysis of <i>Neisseria gonorrhoeae</i> Biofilms Shows Shift to Anaerobic Respiration and Changes in Nutrient Transport and Outer membrane Proteins. <i>PLoS ONE</i> , 2012, 7, e38303.	2.5	64
85	ScanRanker: Quality Assessment of Tandem Mass Spectra via Sequence Tagging. <i>Journal of Proteome Research</i> , 2011, 10, 2896-2904.	3.7	30
86	A lectin affinity workflow targeting glycosite-specific, cancer-related carbohydrate structures in trypsin-digested human plasma. <i>Analytical Biochemistry</i> , 2011, 408, 71-85.	2.4	59
87	Identification of new modulators and protein alterations in non-apoptotic programmed cell death. <i>Journal of Cellular Biochemistry</i> , 2010, 111, 1401-1412.	2.6	59
88	Interlaboratory Study Characterizing a Yeast Performance Standard for Benchmarking LC-MS Platform Performance. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 242-254.	3.8	148
89	Targeted Quantitation of Site-Specific Cysteine Oxidation in Endogenous Proteins Using a Differential Alkylation and Multiple Reaction Monitoring Mass Spectrometry Approach. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1400-1410.	3.8	120
90	The <i>Mycobacterium bovis</i> Bacille Calmette-Guérin Phagosome Proteome. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 32-53.	3.8	58

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91	Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 761-776.	3.7	505
92	Performance Metrics for Liquid Chromatography-Tandem Mass Spectrometry Systems in Proteomics Analyses. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 225-241.	3.8	167
93	Systematic Mapping of Posttranslational Modifications in Human Estrogen Receptor- $\alpha$ with Emphasis on Novel Phosphorylation Sites. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 467-480.	3.8	64
94	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009, 27, 633-641.	17.5	958
95	IDPicker 2.0: Improved Protein Assembly with High Discrimination Peptide Identification Filtering. <i>Journal of Proteome Research</i> , 2009, 8, 3872-3881.	3.7	320
96	Preferentially Increased Nitration of $\alpha$ -Synuclein at Tyrosine-39 in a Cellular Oxidative Model of Parkinson's Disease. <i>Analytical Chemistry</i> , 2009, 81, 7823-7828.	6.5	103
97	Partial Acetylation of Lysine Residues Improves Intraprotein Cross-Linking. <i>Analytical Chemistry</i> , 2008, 80, 951-960.	6.5	34
98	Identification of LpxL, a Late Acyltransferase of <i>Francisella tularensis</i> . <i>Infection and Immunity</i> , 2007, 75, 5518-5531.	2.2	22
99	Characterization of Lipid A Acylation Patterns in <i>Francisella tularensis</i> , <i>Francisella novicida</i> , and <i>Francisella philomiragia</i> Using Multiple-Stage Mass Spectrometry and Matrix-Assisted Laser Desorption/Ionization on an Intermediate Vacuum Source Linear Ion Trap. <i>Analytical Chemistry</i> , 2007, 79, 1034-1042.	6.5	51
100	Mitochondrial Oxidative Stress Causes Hyperphosphorylation of Tau. <i>PLoS ONE</i> , 2007, 2, e536.	2.5	291
101	Small-scale immunopurification of cytochrome c oxidase for a high-throughput multiplexing analysis of enzyme activity and amount. <i>Biotechnology and Applied Biochemistry</i> , 2007, 48, 167.	3.1	13
102	Novel Pathways Associated with Quinone-Induced Stress in Breast Cancer Cells. <i>Drug Metabolism Reviews</i> , 2006, 38, 601-613.	3.6	19
103	Huntingtin Phosphorylation Sites Mapped by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2006, 281, 23686-23697.	3.4	131
104	A pilot proteomic study of amyloid precursor interactors in Alzheimer's disease. <i>Annals of Neurology</i> , 2005, 58, 277-289.	5.3	62
105	Rapid Purification and Mass Spectrometric Characterization of Mitochondrial NADH Dehydrogenase (Complex I) from Rodent Brain and a Dopaminergic Neuronal Cell Line. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 84-96.	3.8	47
106	Mass spectrometric identification of a novel phosphorylation site in subunit NDUF10 of bovine mitochondrial complex I. <i>FEBS Letters</i> , 2005, 579, 2485-2490.	2.8	60
107	Proteomic and immunochemical characterization of a role for stathmin in adult neurogenesis. <i>FASEB Journal</i> , 2004, 18, 287-299.	0.5	84
108	A Novel Lectin, DltA, Is Required for Expression of a Full Serum Resistance Phenotype in <i>Haemophilus ducreyi</i> . <i>Infection and Immunity</i> , 2004, 72, 3418-3428.	2.2	25

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109	Molecular Components of a Cell Death Pathway Activated by Endoplasmic Reticulum Stress. <i>Journal of Biological Chemistry</i> , 2004, 279, 177-187.	3.4	130
110	Determining cysteine oxidation status using differential alkylation. <i>International Journal of Mass Spectrometry</i> , 2004, 236, 117-127.	1.5	33
111	Novel Modification of Lipid A of <i>Francisella tularensis</i> . <i>Infection and Immunity</i> , 2004, 72, 5340-5348.	2.2	135
112	Isotopically labeled crosslinking reagents: resolution of mass degeneracy in the identification of crosslinked peptides. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2003, 13, 4023-4026.	2.2	48
113	MS2Assign, automated assignment and nomenclature of tandem mass spectra of chemically crosslinked peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 834-850.	2.8	250
114	Phosphospecific proteolysis for mapping sites of protein phosphorylation. <i>Nature Biotechnology</i> , 2003, 21, 1047-1054.	17.5	237
115	Metabolic incorporation of unnatural sialic acids into <i>Haemophilus ducreyi</i> lipooligosaccharides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3089-3094.	7.1	53
116	Cathepsin L in secretory vesicles functions as a prohormone-processing enzyme for production of the enkephalin peptide neurotransmitter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9590-9595.	7.1	199
117	Characterization of lipooligosaccharides from <i>Haemophilus ducreyi</i> containing poly lactosamine repeats. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 724-734.	2.8	11
118	Biosynthesis of Sialylated Lipooligosaccharides in <i>Haemophilus ducreyi</i> Dependent on Exogenous Sialic Acid and Not Mannosamine. Incorporation Studies Using N-Acylmannosamine Analogues, N-Glycolylneuraminic Acid, and <sup>13</sup> C-Labeled N-Acetylneuraminic Acid. <i>Biochemistry</i> , 2001, 40, 12666-12677.	2.5	37
119	14-3-3 Interacts with Regulator of G Protein Signaling Proteins and Modulates Their Activity. <i>Journal of Biological Chemistry</i> , 2000, 275, 28167-28172.	3.4	104
120	Construction and Characterization of <i>Haemophilus ducreyi</i> Lipooligosaccharide (LOS) Mutants Defective in Expression of Heptosyltransferase III and <sup>1,4</sup> -Glucosyltransferase: Identification of LOS Glycoforms Containing Lactosamine Repeats. <i>Infection and Immunity</i> , 2000, 68, 3352-3361.	2.2	36
121	Cloning and Characterization of the Lipooligosaccharide Galactosyltransferase II Gene of <i>Haemophilus ducreyi</i> . <i>Journal of Bacteriology</i> , 2000, 182, 2292-2298.	2.2	24
122	Fragmentation and sequencing of cyclic peptides by matrix-assisted laser desorption/ionization post-source decay mass spectrometry. <i>Journal of Mass Spectrometry</i> , 1999, 34, 2174-2179.		24
123	Suzuki Coupling of Chiral 1,1'-Binaphthyl Systems - New Synthetic Routes to Functionalize the 2- and 2'-Positions. <i>European Journal of Organic Chemistry</i> , 1998, 1998, 701-709.	2.4	25
124	Synthesis and Structure of 2,2'-Boryl-, Germyl-, and Stannyl-Substituted 1,1'-Binaphthyl Systems. <i>Chemische Berichte</i> , 1997, 130, 923-932.	0.2	51
125	Crystal structure of 2,2'-bis(trimethylgermyl)-1,1'-binaphthyl, (C <sub>10</sub> H <sub>6</sub> Ge(CH <sub>3</sub> ) <sub>3</sub> ) <sub>2</sub> . <i>Zeitschrift Fur Kristallographie - New Crystal Structures</i> , 1997, 212, 146-148.	0.3	0
126	Crystal structure of 2,2',7,7'-tetramethyldinaphtho[2,1-c;1',2',-e]-1,2,7-oxa-disilolepin, (C <sub>10</sub> H <sub>6</sub> Si(CH <sub>3</sub> ) <sub>2</sub> ) <sub>2</sub> O. <i>Zeitschrift Fur Kristallographie - New Crystal Structures</i> , 1997, 212, 149-150.	0.3	0



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127	Crystal structure of 2,2'-bis(trimethylsilyl)-1,1'-binaphthyl, (C <sub>10</sub> H <sub>6</sub> Si(CH <sub>3</sub> ) <sub>3</sub> ) <sub>2</sub> . Zeitschrift Fur Kristallographie - New Crystal Structures, 1997, 212, 143-145.	0.3	0
128	A Proteomic Atlas of Senescence-Associated Secretomes for Aging Biomarker Development. SSRN Electronic Journal, 0, , .	0.4	5
129	Extracellular Nicotinamide Phosphoribosyltransferase Is a Component of the Senescence-Associated Secretory Phenotype. Frontiers in Endocrinology, 0, 13, .	3.5	5