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	Multi-site assessment of the precision and reproducibility of multiple reaction monitoringâ€“based measurements of proteins in plasma. Nature Biotechnology, 2009, 27, 633-641.	17.5	958
2	A proteomic atlas of senescence-associated secretomes for aging biomarker development. PLoS Biology, 2020, 18, e3000599.	5.6	694
3	Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatographyâˆ’Tandem Mass Spectrometry. Journal of Proteome Research, 2010, 9, 761-776.	3.7	505
4	Platform-independent and Label-free Quantitation of Proteomic Data Using MS1 Extracted Ion Chromatograms in Skyline. Molecular and Cellular Proteomics, 2012, 11, 202-214.	3.8	428
5	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. Nature Communications, 2017, 8, 291.	12.8	423
6	Label-free quantitative proteomics of the lysine acetylome in mitochondria identifies substrates of SIRT3 in metabolic pathways. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6601-6606.	7.1	414
7	Critical role of acetylation in tau-mediated neurodegeneration and cognitive deficits. Nature Medicine, 2015, 21, 1154-1162.	30.7	398
8	IDPicker 2.0: Improved Protein Assembly with High Discrimination Peptide Identification Filtering. Journal of Proteome Research, 2009, 8, 3872-3881.	3.7	320
9	MicroRNA sequence codes for small extracellular vesicle release and cellular retention. Nature, 2022, 601, 446-451.	27.8	300
10	Mitochondrial Oxidative Stress Causes Hyperphosphorylation of Tau. PLoS ONE, 2007, 2, e536.	2.5	291
11	Skyline for Small Molecules: A Unifying Software Package for Quantitative Metabolomics. Journal of Proteome Research, 2020, 19, 1447-1458.	3.7	253
12	MS2Assign, automated assignment and nomenclature of tandem mass spectra of chemically crosslinked peptides. Journal of the American Society for Mass Spectrometry, 2003, 14, 834-850.	2.8	250
13	Structural, Kinetic and Proteomic Characterization of Acetyl Phosphate-Dependent Bacterial Protein Acetylation. PLoS ONE, 2014, 9, e94816.	2.5	249
14	Phosphospecific proteolysis for mapping sites of protein phosphorylation. Nature Biotechnology, 2003, 21, 1047-1054.	17.5	237
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	Panorama: A Targeted Proteomics Knowledge Base. Journal of Proteome Research, 2014, 13, 4205-4210.	3.7	205
17	Cathepsin L in secretory vesicles functions as a prohormone-processing enzyme for production of the enkephalin peptide neurotransmitter. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9590-9595.	7.1	199
18	Acetylated Tau Obstructs KIBRA-Mediated Signaling in Synaptic Plasticity and Promotes Tauopathy-Related Memory Loss. Neuron, 2016, 90, 245-260.	8.1	195

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19	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. Molecular and Cellular Proteomics, 2018, 17, 1239-1244.	3.8	177
20	Performance Metrics for Liquid Chromatography-Tandem Mass Spectrometry Systems in Proteomics Analyses. Molecular and Cellular Proteomics, 2010, 9, 225-241.	3.8	167
21	Protein acetylation dynamics in response to carbon overflow in <scp><i>E</i></scp><i>scherichia coli</i>. Molecular Microbiology, 2015, 98, 847-863.	2.5	164
22	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. Cell Metabolism, 2018, 28, 866-880.e15.	16.2	154
23	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. Molecular and Cellular Proteomics, 2015, 14, 2357-2374.	3.8	153
24	Interlaboratory Study Characterizing a Yeast Performance Standard for Benchmarking LC-MS Platform Performance. Molecular and Cellular Proteomics, 2010, 9, 242-254.	3.8	148
25	Dietary Sugars Alter Hepatic Fatty Acid Oxidation via Transcriptional and Post-translational Modifications of Mitochondrial Proteins. Cell Metabolism, 2019, 30, 735-753.e4.	16.2	136
26	Novel Modification of Lipid A of Francisella tularensis. Infection and Immunity, 2004, 72, 5340-5348.	2.2	135
27	Huntingtin Phosphorylation Sites Mapped by Mass Spectrometry. Journal of Biological Chemistry, 2006, 281, 23686-23697.	3.4	131
28	Molecular Components of a Cell Death Pathway Activated by Endoplasmic Reticulum Stress. Journal of Biological Chemistry, 2004, 279, 177-187.	3.4	130
29	SIRT1 deacetylates RORÎ³t and enhances Th17 cell generation. Journal of Experimental Medicine, 2015, 212, 607-617.	8.5	126
30	Regulation of UCP1 and Mitochondrial Metabolism in Brown Adipose Tissue by Reversible Succinylation. Molecular Cell, 2019, 74, 844-857.e7.	9.7	123
31	Post-translational Protein Acetylation: An Elegant Mechanism for Bacteria to Dynamically Regulate Metabolic Functions. Frontiers in Microbiology, 2019, 10, 1604.	3.5	122
32	Targeted Quantitation of Site-Specific Cysteine Oxidation in Endogenous Proteins Using a Differential Alkylation and Multiple Reaction Monitoring Mass Spectrometry Approach. Molecular and Cellular Proteomics, 2010, 9, 1400-1410.	3.8	120
33	Clinical applications of quantitative proteomics using targeted and untargeted data-independent acquisition techniques. Expert Review of Proteomics, 2017, 14, 419-429.	3.0	114
34	Ancient Regulatory Role of Lysine Acetylation in Central Metabolism. MBio, 2017, 8, .	4.1	105
35	14-3-3 Interacts with Regulator of G Protein Signaling Proteins and Modulates Their Activity. Journal of Biological Chemistry, 2000, 275, 28167-28172.	3.4	104
36	Preferentially Increased Nitration of Î±-Synuclein at Tyrosine-39 in a Cellular Oxidative Model of Parkinsonâ€™s Disease. Analytical Chemistry, 2009, 81, 7823-7828.	6.5	103

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37	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). Molecular and Cellular Proteomics, 2013, 12, 2623-2639.	3.8	100
38	SILAC Analysis Reveals Increased Secretion of Hemostasis-Related Factors by Senescent Cells. Cell Reports, 2019, 28, 3329-3337.e5.	6.4	94
39	Mechanisms, Detection, and Relevance of Protein Acetylation in Prokaryotes. MBio, 2019, 10, .	4.1	94
40	Algorithmic assessment of cellular senescence in experimental and clinical specimens. Nature Protocols, 2021, 16, 2471-2498.	12.0	92
41	Multiplexed, Scheduled, High-Resolution Parallel Reaction Monitoring on a Full Scan QqTOF Instrument with Integrated Data-Dependent and Targeted Mass Spectrometric Workflows. Analytical Chemistry, 2015, 87, 10222-10229.	6.5	88
42	The <i>E. coli</i> sirtuin CobB shows no preference for enzymatic and nonenzymatic lysine acetylation substrate sites. MicrobiologyOpen, 2015, 4, 66-83.	3.0	87
43	Identification of Novel Protein Lysine Acetyltransferases in Escherichia coli. MBio, 2018, 9, .	4.1	86
44	Sirtuin 5 Regulates Proximal Tubule Fatty Acid Oxidation to Protect against AKI. Journal of the American Society of Nephrology: JASN, 2019, 30, 2384-2398.	6.1	85
45	Proteomic and immunochemical characterization of a role for stathmin in adult neurogenesis. FASEB Journal, 2004, 18, 287-299.	0.5	84
46	Protein Turnover in Aging and Longevity. Proteomics, 2018, 18, e1700108.	2.2	78
47	Plasma proteomic biomarker signature of age predicts health and life span. ELife, 2020, 9, .	6.0	78
48	Generation of High-Quality SWATHÂ® Acquisition Data for Label-free Quantitative Proteomics Studies Using TripleTOFÂ® Mass Spectrometers. Methods in Molecular Biology, 2017, 1550, 223-233.	0.9	75
49	Quantification of Lysine Acetylation and Succinylation Stoichiometry in Proteins Using Mass Spectrometric Data-Independent Acquisitions (SWATH). Journal of the American Society for Mass Spectrometry, 2016, 27, 1758-1771.	2.8	73
50	Vitamin D Promotes Protein Homeostasis and Longevity via the Stress Response Pathway Genes skn-1, ire-1, and xbp-1. Cell Reports, 2016, 17, 1227-1237.	6.4	65
51	Systematic Mapping of Posttranslational Modifications in Human Estrogen Receptor-Î± with Emphasis on Novel Phosphorylation Sites. Molecular and Cellular Proteomics, 2009, 8, 467-480.	3.8	64
52	Proteomic Analysis of Neisseria gonorrhoeae Biofilms Shows Shift to Anaerobic Respiration and Changes in Nutrient Transport and Outermembrane Proteins. PLoS ONE, 2012, 7, e38303.	2.5	64
53	A pilot proteomic study of amyloid precursor interactors in Alzheimer's disease. Annals of Neurology, 2005, 58, 277-289.	5.3	62
54	Mass spectrometric identification of a novel phosphorylation site in subunit NDUFA10 of bovine mitochondrial complex I. FEBS Letters, 2005, 579, 2485-2490.	2.8	60

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55	Identification of new modulators and protein alterations in nonâ€apoptotic programmed cell death. Journal of Cellular Biochemistry, 2010, 111, 1401-1412.	2.6	59
56	A lectin affinity workflow targeting glycosite-specific, cancer-related carbohydrate structures in trypsin-digested human plasma. Analytical Biochemistry, 2011, 408, 71-85.	2.4	59
57	Proteomics in aging research: A roadmap to clinical, translational research. Aging Cell, 2021, 20, e13325.	6.7	59
58	The Mycobacterium bovis Bacille Calmette-GuÃ©rin Phagosome Proteome. Molecular and Cellular Proteomics, 2010, 9, 32-53.	3.8	58
59	Iron promotes protein insolubility and aging in C. elegans. Aging, 2014, 6, 975-988.	3.1	57
60	MS1 Peptide Ion Intensity Chromatograms in MS2 (SWATH) Data Independent Acquisitions. Improving Post Acquisition Analysis of Proteomic Experiments. Molecular and Cellular Proteomics, 2015, 14, 2405-2419.	3.8	57
61	Metabolic incorporation of unnatural sialic acids into Haemophilus ducreyi lipooligosaccharides. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3089-3094.	7.1	53
62	PIQED: automated identification and quantification of protein modifications from DIA-MS data. Nature Methods, 2017, 14, 646-647.	19.0	52
63	Synthesis and Structure of 2,2â€² â€Borylâ€, Germylâ€Silylâ€, and Stannylâ€Substituted 1,1â€² â€Binaphthyl Systems. Chemische Berichte, 1997, 130, 923-932.	0.2	51
64	Characterization of Lipid A Acylation Patterns inFrancisella tularensis,Francisellanovicida, andFrancisellaphilomiragiaUsing Multiple-Stage Mass Spectrometry and Matrix-Assisted Laser Desorption/Ionization on an Intermediate Vacuum Source Linear Ion Trap. Analytical Chemistry, 2007, 79, 1034-1042.	6.5	51
65	An acetylatable lysine controls CRP function in <i>E. coli</i>. Molecular Microbiology, 2018, 107, 116-131.	2.5	51
66	QuaMeter: Multivendor Performance Metrics for LCâ€"MS/MS Proteomics Instrumentation. Analytical Chemistry, 2012, 84, 5845-5850.	6.5	50
67	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. Journal of Proteome Research, 2012, 11, 2508-2520.	3.7	49
68	Isotopically labeled crosslinking reagents: resolution of mass degeneracy in the identification of crosslinked peptides. Bioorganic and Medicinal Chemistry Letters, 2003, 13, 4023-4026.	2.2	48
69	Rapid Purification and Mass Spectrometric Characterization of Mitochondrial NADH Dehydrogenase (Complex I) from Rodent Brain and a Dopaminergic Neuronal Cell Line. Molecular and Cellular Proteomics, 2005, 4, 84-96.	3.8	47
70	Ubiquitin-specific Peptidase 9, X-linked (USP9X) Modulates Activity of Mammalian Target of Rapamycin (mTOR). Journal of Biological Chemistry, 2012, 287, 21164-21175.	3.4	47
71	Activating transcription factor 4 (ATF4) promotes skeletal muscle atrophy by forming a heterodimer with the transcriptional regulator C/EBPÎ². Journal of Biological Chemistry, 2020, 295, 2787-2803.	3.4	45
72	Phosphoprotein Secretome of Tumor Cells as a Source of Candidates for Breast Cancer Biomarkers in Plasma. Molecular and Cellular Proteomics, 2014, 13, 1034-1049.	3.8	41

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73	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
74	Wavelet-Based Peak Detection and a New Charge Inference Procedure for MS/MS Implemented in ProteoWizardâ€™s msConvert. Journal of Proteome Research, 2015, 14, 1299-1307.	3.7	38
75	Temporal dynamics of liver mitochondrial protein acetylation and succinylation and metabolites due to high fat diet and/or excess glucose or fructose. PLoS ONE, 2018, 13, e0208973.	2.5	38
76	Biosynthesis of Sialylated Lipooligosaccharides inHaemophilus ducreyiIs Dependent on Exogenous Sialic Acid and Not Mannosamine. Incorporation Studies UsingN-Acylmannosamine Analogues,N-Glycolylneuraminic Acid, and13C-LabeledN-Acetylneuraminic Acidâ€. Biochemistry, 2001, 40, 12666-12677.	2.5	37
77	Gadd45a Protein Promotes Skeletal Muscle Atrophy by Forming a Complex with the Protein Kinase MEKK4. Journal of Biological Chemistry, 2016, 291, 17496-17509.	3.4	37
78	Construction and Characterization of Haemophilus ducreyi Lipooligosaccharide (LOS) Mutants Defective in Expression of Heptosyltransferase III and Î²1,4-Glucosyltransferase: Identification of LOS Glycoforms Containing Lactosamine Repeats. Infection and Immunity, 2000, 68, 3352-3361.	2.2	36
79	A framework for installable external tools in Skyline. Bioinformatics, 2014, 30, 2521-2523.	4.1	36
80	Improved SILAC Quantification with Data-Independent Acquisition to Investigate Bortezomib-Induced Protein Degradation. Journal of Proteome Research, 2021, 20, 1918-1927.	3.7	36
81	Stable nuclear expression of<i>ATP8</i>and<i>ATP6</i>genes rescues a mtDNA Complex V<i>null</i>mutant. Nucleic Acids Research, 2016, 44, gkw756.	14.5	35
82	SUCLA2 mutations cause global protein succinylation contributing to the pathomechanism of a hereditary mitochondrial disease. Nature Communications, 2020, 11, 5927.	12.8	35
83	Partial Acetylation of Lysine Residues Improves Intraprotein Cross-Linking. Analytical Chemistry, 2008, 80, 951-960.	6.5	34
84	Global Lysine Acetylation in <i>Escherichia coli</i> Results from Growth Conditions That Favor Acetate Fermentation. Journal of Bacteriology, 2019, 201, .	2.2	34
85	RPL24: a potential therapeutic target whose depletion or acetylation inhibits polysome assembly and cancer cell growth. Oncotarget, 2014, 5, 5165-5176.	1.8	34
86	Determining cysteine oxidation status using differential alkylation. International Journal of Mass Spectrometry, 2004, 236, 117-127.	1.5	33
87	Simultaneous Quantification of the Acetylome and Succinylome by â€˜Oneâ€Potâ€™ Affinity Enrichment. Proteomics, 2018, 18, e1800123.	2.2	31
88	ScanRanker: Quality Assessment of Tandem Mass Spectra via Sequence Tagging. Journal of Proteome Research, 2011, 10, 2896-2904.	3.7	30
89	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
90	Ligand Binding Promotes CDK-Dependent Phosphorylation of ER-Alpha on Hinge Serine 294 but Inhibits Ligand-Independent Phosphorylation of Serine 305. Molecular Cancer Research, 2012, 10, 1120-1132.	3.4	27

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91	Suzuki Coupling of Chiral 1,1â€²-Binaphthyl Systems âˆ’ New Synthetic Routes to Functionalize the 2- and 2,2â€²-Positions. European Journal of Organic Chemistry, 1998, 1998, 701-709.	2.4	25
92	A Novel Lectin, DltA, Is Required for Expression of a Full Serum Resistance Phenotype in Haemophilus ducreyi. Infection and Immunity, 2004, 72, 3418-3428.	2.2	25
93	Quantitative Proteomic Analysis of the Senescenceâ€•Associated Secretory Phenotype by Dataâ€•Independent Acquisition. Current Protocols, 2021, 1, e32.	2.9	25
94	Fragmentation and sequencing of cyclic peptides by matrix-assisted laser desorption/ionization post-source decay mass spectrometry. , 1999, 13, 2174-2179.		24
95	Cloning and Characterization of the Lipooligosaccharide Galactosyltransferase II Gene of Haemophilus ducreyi. Journal of Bacteriology, 2000, 182, 2292-2298.	2.2	24
96	Accumulation of â€œOld Proteinsâ€•and the Critical Need for MSâ€•based Protein Turnover Measurements in Aging and Longevity. Proteomics, 2020, 20, e1800403.	2.2	24
97	Translational control of one-carbon metabolism underpins ribosomal protein phenotypes in cell division and longevity. ELife, 2020, 9, .	6.0	24
98	Identification of LpxL, a Late Acyltransferase of Francisella tularensis. Infection and Immunity, 2007, 75, 5518-5531.	2.2	22
99	Variation and quantification among a target set of phosphopeptides in human plasma by multiple reaction monitoring and SWATHâ€•MS2 dataâ€•independent acquisition. Electrophoresis, 2014, 35, 3487-3497.	2.4	22
100	Proteome and Secretome Dynamics of Human Retinal Pigment Epithelium in Response to Reactive Oxygen Species. Scientific Reports, 2019, 9, 15440.	3.3	22
101	Emerging mass spectrometry-based proteomics methodologies for novel biomedical applications. Biochemical Society Transactions, 2020, 48, 1953-1966.	3.4	22
102	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. Molecular and Cellular Proteomics, 2017, 16, 1335-1347.	3.8	21
103	Integration-independent Transgenic Huntington Disease Fragment Mouse Models Reveal Distinct Phenotypes and Life Span in Vivo. Journal of Biological Chemistry, 2015, 290, 19287-19306.	3.4	20
104	Novel Pathways Associated with Quinone-Induced Stress in Breast Cancer Cells. Drug Metabolism Reviews, 2006, 38, 601-613.	3.6	19
105	JNK modifies neuronal metabolism to promote proteostasis and longevity. Aging Cell, 2019, 18, e12849.	6.7	18
106	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
107	Identification and characterization of AckA-dependent protein acetylation in Neisseria gonorrhoeae. PLoS ONE, 2017, 12, e0179621.	2.5	17
108	High-Resolution Mass Spectrometry to Identify and Quantify Acetylation Protein Targets. Methods in Molecular Biology, 2019, 1983, 3-16.	0.9	15

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109	Small-scale immunopurification of cytochrome c oxidase for a high-throughput multiplexing analysis of enzyme activity and amount. Biotechnology and Applied Biochemistry, 2007, 48, 167.	3.1	13
110	Cytotrophoblast extracellular vesicles enhance decidual cell secretion of immune modulators via TNF-alpha. Development (Cambridge), 2020, 147, .	2.5	12
111	Dietary restriction and the transcription factor clock delay eye aging to extend lifespan in Drosophila Melanogaster. Nature Communications, 2022, 13, .	12.8	12
112	Characterization of lipooligosaccharides from Haemophilus ducreyi containing polylactosamine repeats. Journal of the American Society for Mass Spectrometry, 2002, 13, 724-734.	2.8	11
113	Site-specific acylation changes in the lipid A of <i>Escherichia coli lpxL</i> mutants grown at high temperatures. Innate Immunity, 2014, 20, 269-282.	2.4	11
114	Quantification and Identification of Post-Translational Modifications Using Modern Proteomics Approaches. Methods in Molecular Biology, 2021, 2228, 225-235.	0.9	11
115	Quantification of Site-specific Protein Lysine Acetylation and Succinylation Stoichiometry Using Data-independent Acquisition Mass Spectrometry. Journal of Visualized Experiments, 2018, , .	0.3	9
116	Advanced mass spectrometry-based methods for protein molecular-structural biologists. , 2022, , 311-326.		8
117	Simultaneous Affinity Enrichment of Two Post-Translational Modifications for Quantification and Site Localization. Journal of Visualized Experiments, 2020, , .	0.3	7
118	Proximity labeling and other novel mass spectrometric approaches for spatiotemporal protein dynamics. Expert Review of Proteomics, 2021, 18, 757-765.	3.0	6
119	Identifying ubiquitinated proteins and aggregates. Aging, 2018, 10, 2549-2550.	3.1	6
120	A Proteomic Atlas of Senescence-Associated Secretomes for Aging Biomarker Development. SSRN Electronic Journal, 0, , .	0.4	5
121	Extracellular Nicotinamide Phosphoribosyltransferase Is a Component of the Senescence-Associated Secretory Phenotype. Frontiers in Endocrinology, 0, 13, .	3.5	5
122	Quantification of Insoluble Protein Aggregation in Caenorhabditis elegans during Aging with a Novel Data-Independent Acquisition Workflow. Journal of Visualized Experiments, 2020, , .	0.3	3
123	Comprehensive proteomic quantification of bladder stone progression in a cystinuric mouse model using data-independent acquisitions. PLoS ONE, 2022, 17, e0250137.	2.5	3
124	Ubiquitin-specific peptidase 9, X-linked (USP9X) modulates activity of mammalian target of rapamycin (mTOR).. Journal of Biological Chemistry, 2014, 289, 14965.	3.4	2
125	INVESTIGATING PROTEIN HOMEOSTASIS IN C.ÂELEGANS AND C.ÂBRIGGSAE STRAINS USING MASS SPECTROMETRY. Innovation in Aging, 2017, 1, 1210-1211.	0.1	1
126	Crystal structure of 2,2'-bis(trimethylgermyl)-1,1'-binaphthyl, (C10H6Ge(CH3)3)2. Zeitschrift Fur Kristallographie - New Crystal Structures, 1997, 212, 146-148.	0.3	0

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127	Crystal structure of 2,2,7,7-tetramethyldinaphtho[2,1-c;1',2',-e]-1,2,7-oxa-disilepin,(C10H6Si(CH3)2)2O. Zeitschrift Fur Kristallographie - New Crystal Structures, 1997, 212, 149-150.	0.3	0
128	Crystal structure of 2,2'-bis(trimethylsilyl)-1,1'-binaphthyl, (C10H6Si(CH3)3)2. Zeitschrift Fur Kristallographie - New Crystal Structures, 1997, 212, 143-145.	0.3	0
129	Chapter 9. Informatics Solutions for Selected Reaction Monitoring. New Developments in Mass Spectrometry, 2016, , 178-199.	0.2	0