

# Hanno Steen

## List of Publications by Year in descending order

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124  
papers

8,346  
citations

61945

43  
h-index

49868

87  
g-index

138  
all docs

138  
docs citations

138  
times ranked

11513  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomics based markers of clinical pain severity in juvenile idiopathic arthritis. <i>Pediatric Rheumatology</i> , 2022, 20, 3.	0.9	3
2	multiFLEX-LF: A Computational Approach to Quantify the Modification Stoichiometries in Label-Free Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2022, 21, 899-909.	1.8	1
3	Urine Proteomics for Noninvasive Monitoring of Biomarkers in Bronchopulmonary Dysplasia. <i>Neonatology</i> , 2022, 119, 193-203.	0.9	12
4	Plasma Proteomic Analysis Distinguishes Severity Outcomes of Human Ebola Virus Disease. <i>MBio</i> , 2022, 13, e0056722.	1.8	5
5	Determinants of B-Cell Compartment Hyperactivation in European Adolescents Living With Perinatally Acquired HIV-1 After Over 10 Years of Suppressive Therapy. <i>Frontiers in Immunology</i> , 2022, 13, 860418.	2.2	6
6	Bacille Calmette-Guérin vaccine reprograms human neonatal lipid metabolism in vivo and in vitro. <i>Cell Reports</i> , 2022, 39, 110772.	2.9	13
7	Antioxidant functions of DHHC3 suppress anti-cancer drug activities. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2341-2353.	2.4	12
8	Delayed Processing of Secretin-Induced Pancreas Fluid Influences the Quality and Integrity of Proteins and Nucleic Acids. <i>Pancreas</i> , 2021, 50, 17-28.	0.5	4
9	Sample Preparation for High-Throughput Urine Proteomics Using 96-Well Polyvinylidene Fluoride (PVDF) Membranes. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1306, 1-12.	0.8	2
10	Biomarkers of Chronic Pancreatitis: A systematic literature review. <i>Pancreatology</i> , 2021, 21, 323-333.	0.5	16
11	Immunophenotyping assessment in a COVID-19 cohort (IMPACC): A prospective longitudinal study. <i>Science Immunology</i> , 2021, 6, .	5.6	20
12	Multi-omic regulatory networks capture downstream effects of kinase inhibition in <i>Mycobacterium tuberculosis</i> . <i>Npj Systems Biology and Applications</i> , 2021, 7, 8.	1.4	3
13	Tau PTM Profiles Identify Patient Heterogeneity and Stages of Alzheimer's Disease. <i>Cell</i> , 2020, 183, 1699-1713.e13.	13.5	354
14	Preparing for Life: Plasma Proteome Changes and Immune System Development During the First Week of Human Life. <i>Frontiers in Immunology</i> , 2020, 11, 578505.	2.2	23
15	Clinical Protocol for a Longitudinal Cohort Study Employing Systems Biology to Identify Markers of Vaccine Immunogenicity in Newborn Infants in The Gambia and Papua New Guinea. <i>Frontiers in Pediatrics</i> , 2020, 8, 197.	0.9	12
16	BCG vaccination-induced emergency granulopoiesis provides rapid protection from neonatal sepsis. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	76
17	Influence of <i>Plasmodium falciparum</i> Calcium-Dependent Protein Kinase 5 (PfCDPK5) on the Late Schizont Stage Phosphoproteome. <i>MSphere</i> , 2020, 5, .	1.3	16
18	Protein kinases PknA and PknB independently and coordinately regulate essential <i>Mycobacterium tuberculosis</i> physiologies and antimicrobial susceptibility. <i>PLoS Pathogens</i> , 2020, 16, e1008452.	2.1	33

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19	FLEXIQuant-LF to quantify protein modification extent in label-free proteomics data. <i>ELife</i> , 2020, 9, .	2.8	4
20	Increased phosphorylation of ACTN4 leads to podocyte vulnerability and proteinuric kidney disease and is stimulated by high glucose and TGF $\beta$ . <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	0
21	Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. <i>Nature Communications</i> , 2019, 10, 1092.	5.8	151
22	Precision Medicine in Pancreatic Disease—Knowledge Gaps and Research Opportunities. <i>Pancreas</i> , 2019, 48, 1250-1258.	0.5	9
23	Prohibitin is a prognostic marker and therapeutic target to block chemotherapy resistance in Wilms's tumor. <i>JCI Insight</i> , 2019, 4, .	2.3	21
24	Multisystem Analysis of <i>Mycobacterium tuberculosis</i> Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. <i>MBio</i> , 2018, 9, .	1.8	57
25	A Cost-Effective High-Throughput Plasma and Serum Proteomics Workflow Enables Mapping of the Molecular Impact of Total Pancreatectomy with Islet Autotransplantation. <i>Journal of Proteome Research</i> , 2018, 17, 1983-1992.	1.8	39
26	Fetal regional brain protein signature in FASD rat model. <i>Reproductive Toxicology</i> , 2018, 76, 84-92.	1.3	17
27	Standard Operating Procedures for Biospecimen Collection, Processing, and Storage. <i>Pancreas</i> , 2018, 47, 1213-1221.	0.5	22
28	PGBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	9.4	69
29	Placental Proteomics Reveal Insights into Fetal Alcohol Spectrum Disorders. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 1551-1558.	1.4	17
30	[O4 <sup>+</sup> 02 <sup>-</sup> 03]: MAPPING THE TAUOPATHY-SPECIFIC MODIFICATION LANDSCAPE ON TAU. <i>Alzheimer's and Dementia</i> , 2017, 13, P1229.	0.4	1
31	High-Throughput Parallel Proteomic Sample Preparation Using 96-Well Polyvinylidene Fluoride (PVDF) Membranes and C18 Purification Plates. <i>Methods in Molecular Biology</i> , 2017, 1619, 395-402.	0.4	16
32	Endoscopic Pancreas Fluid Collection: Methods and Relevance for Clinical Care and Translational Science. <i>American Journal of Gastroenterology</i> , 2016, 111, 1258-1266.	0.2	30
33	Urinary Proteomics Yield Pathological Insights for Ureteropelvic Junction Obstruction. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2607-2615.	2.5	16
34	f-divergence cutoff index to simultaneously identify differential expression in the integrated transcriptome and proteome. <i>Nucleic Acids Research</i> , 2016, 44, e97-e97.	6.5	7
35	Adjuvant-induced Human Monocyte Secretome Profiles Reveal Adjuvant- and Age-specific Protein Signatures. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1877-1894.	2.5	23
36	FLEXITau: Quantifying Post-translational Modifications of Tau Protein <i>in Vitro</i> and in Human Disease. <i>Analytical Chemistry</i> , 2016, 88, 3704-3714.	3.2	103

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37	Progressive Differentiation and Instructive Capacities of Amniotic Fluid and Cerebrospinal Fluid Proteomes following Neural Tube Closure. <i>Developmental Cell</i> , 2015, 35, 789-802.	3.1	77
38	A Specific LSD1/KDM1A Isoform Regulates Neuronal Differentiation through H3K9 Demethylation. <i>Molecular Cell</i> , 2015, 57, 957-970.	4.5	221
39	Abundance-based Classifier for the Prediction of Mass Spectrometric Peptide Detectability Upon Enrichment (PPA). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 430-440.	2.5	23
40	A High-Efficiency Cellular Extraction System for Biological Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 3403-3408.	1.8	26
41	Characterization of the porcine synovial fluid proteome and a comparison to the plasma proteome. <i>Data in Brief</i> , 2015, 5, 241-247.	0.5	4
42	Pancreatic Juice Prostaglandin E2 Concentrations Are Elevated in Chronic Pancreatitis and Improve Detection of Early Disease. <i>Clinical and Translational Gastroenterology</i> , 2015, 6, e72.	1.3	16
43	Advancing Urinary Protein Biomarker Discovery by Data-Independent Acquisition on a Quadrupole-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2015, 14, 4752-4762.	1.8	109
44	MStern Blotting—High Throughput Polyvinylidene Fluoride (PVDF) Membrane-Based Proteomic Sample Preparation for 96-Well Plates. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2814-2823.	2.5	68
45	Optimization of Cell Lysis and Protein Digestion Protocols for Protein Analysis by LC-MS/MS. <i>Methods in Molecular Biology</i> , 2015, 1295, 259-273.	0.4	5
46	An in-depth comparison of the male pediatric and adult urinary proteomes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1044-1050.	1.1	25
47	Quantitative profiling of peptides from RNAs classified as noncoding. <i>Nature Communications</i> , 2014, 5, 5429.	5.8	55
48	A Normative Study of the Synovial Fluid Proteome from Healthy Porcine Knee Joints. <i>Journal of Proteome Research</i> , 2014, 13, 4377-4387.	1.8	68
49	Co-regulation proteomics reveals substrates and mechanisms of APC/C-dependent degradation. <i>EMBO Journal</i> , 2014, 33, 385-399.	3.5	72
50	Abstract IA8: A new class of drugs active in T-ALL is revealed in a zebrafish screen. , 2014, , .		0
51	Nonparametric Bayesian Evaluation of Differential Protein Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 4556-4565.	1.8	22
52	Post-translational modifications of pancreatic fluid proteins collected via the endoscopic pancreatic function test (ePFT). <i>Journal of Proteomics</i> , 2013, 92, 216-227.	1.2	8
53	A Non-parametric Cutout Index for Robust Evaluation of Identified Proteins. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 807-812.	2.5	11
54	Urine proteomics for discovery of improved diagnostic markers of Kawasaki disease. <i>EMBO Molecular Medicine</i> , 2013, 5, 210-220.	3.3	80

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55	Cross-species analysis of nicotine-induced proteomic alterations in pancreatic cells. <i>Proteomics</i> , 2013, 13, 1499-1512.	1.3	20
56	Short Gel, Long Gradient Liquid Chromatography Tandem Mass Spectrometry to Investigate the Urine Proteome of Chronic Pancreatitis. <i>The Open Proteomics Journal</i> , 2013, 6, 1-13.	0.4	8
57	Analysis of endoscopic pancreatic function test (ePFT)-collected pancreatic fluid proteins precipitated via ultracentrifugation. <i>JOP: Journal of the Pancreas</i> , 2013, 14, 176-86.	1.5	4
58	mz5: Space- and Time-efficient Storage of Mass Spectrometry Data Sets. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.011379.	2.5	56
59	Brainstem Deficiency of the 14-3-3 Regulator of Serotonin Synthesis: A Proteomics Analysis in the Sudden Infant Death Syndrome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.009530.	2.5	42
60	Overcoming Species Boundaries in Peptide Identification with Bayesian Information Criterion-driven Error-tolerant Peptide Search (BICEPS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014167-1-M111.014167-12.	2.5	24
61	Proteomic Analysis of Formalin-Fixed Paraffin-Embedded Pancreatic Tissue Using Liquid Chromatography Tandem Mass Spectrometry. <i>Pancreas</i> , 2012, 41, 175-185.	0.5	30
62	Mass Spectrometry-Based (GeLC-MS/MS) Comparative Proteomic Analysis of Endoscopically (ePFT) Collected Pancreatic and Gastroduodenal Fluids. <i>Clinical and Translational Gastroenterology</i> , 2012, 3, e14.	1.3	15
63	FLEXIQinase, a mass spectrometry-based assay, to unveil multikinase mechanisms. <i>Nature Methods</i> , 2012, 9, 504-508.	9.0	26
64	Tiki1 Is Required for Head Formation via Wnt Cleavage-Oxidation and Inactivation. <i>Cell</i> , 2012, 149, 1565-1577.	13.5	125
65	Post-translational modification: nature's escape from genetic imprisonment and the basis for dynamic information encoding. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 565-583.	6.6	288
66	A Practical Guide to the FLEXIQquant Method. <i>Methods in Molecular Biology</i> , 2012, 893, 295-319.	0.4	19
67	Proteomic Analysis (GeLC-MS/MS) of ePFT-Collected Pancreatic Fluid in Chronic Pancreatitis. <i>Journal of Proteome Research</i> , 2012, 11, 1897-1912.	1.8	25
68	Detection and Diagnostic Value of Urine Leucine-Rich Î±2-Glycoprotein in Children With Suspected Acute Appendicitis. <i>Annals of Emergency Medicine</i> , 2012, 60, 78-83.e1.	0.3	50
69	Etiology of limb girdle muscular dystrophy 1D/1E determined by laser capture microdissection proteomics. <i>Annals of Neurology</i> , 2012, 71, 141-145.	2.8	49
70	Phenothiazines Induce Apoptosis in T-Cell Acute Lymphoblastic Leukemia by Activating the Phosphatase Activity of the PP2A Tumor Suppressor. <i>Blood</i> , 2012, 120, 3558-3558.	0.6	2
71	Mass spectrometry-based proteomics for translational research: a technical overview. <i>Yale Journal of Biology and Medicine</i> , 2012, 85, 59-73.	0.2	22
72	Proteomic Analysis of an Immortalized Mouse Pancreatic Stellate Cell Line Identifies Differentially-Expressed Proteins in Activated vs Nonproliferating Cell States. <i>Journal of Proteome Research</i> , 2011, 10, 4835-4844.	1.8	36

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73	Proteomic analysis of a rat pancreatic stellate cell line using liquid chromatography tandem mass spectrometry (LC-MS/MS). <i>Journal of Proteomics</i> , 2011, 75, 708-717.	1.2	31
74	Comparative analysis of Erk phosphorylation suggests a mixed strategy for measuring phosphoform distributions. <i>Molecular Systems Biology</i> , 2011, 7, 482.	3.2	38
75	Cytokine profiling of pancreatic fluid using the ePFT collection method in tandem with a multiplexed microarray assay. <i>Journal of Immunological Methods</i> , 2011, 369, 98-107.	0.6	18
76	Mass spectrometry-based proteomics of endoscopically collected pancreatic fluid in chronic pancreatitis research. <i>Proteomics - Clinical Applications</i> , 2011, 5, 109-120.	0.8	19
77	Optimization of cell lysis and protein digestion protocols for the analysis of HeLa S3 cells by LC-MS/MS. <i>Proteomics</i> , 2011, 11, 4726-4730.	1.3	41
78	Difference gel electrophoresis identifies differentially expressed proteins in endoscopically collected pancreatic fluid. <i>Electrophoresis</i> , 2011, 32, 1939-1951.	1.3	10
79	Life Cycle Stage-resolved Proteomic Analysis of the Excretome/Secretome from <i>Strongyloides ratti</i> —Identification of Stage-specific Proteases. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010157.	2.5	78
80	Quantitative Proteomics Identifies a $\beta$ -Catenin Network as an Element of the Signaling Response to Frizzled-8 Protein-Related Antiproliferative Factor. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.007492.	2.5	31
81	Sample Handling of Body Fluids for Proteomics. , 2011, , 327-360.		6
82	Identification of Pancreas-Specific Proteins in Endoscopically (Endoscopic Pancreatic Function Test) Collected Pancreatic Fluid with Liquid Chromatography- Tandem Mass Spectrometry. <i>Pancreas</i> , 2010, 39, 889-896.	0.5	27
83	Optimized sample preparation of endoscopic collected pancreatic fluid for SDS-PAGE analysis. <i>Electrophoresis</i> , 2010, 31, 2377-2387.	1.3	31
84	Discovery and Validation of Urine Markers of Acute Pediatric Appendicitis Using High-Accuracy Mass Spectrometry. <i>Annals of Emergency Medicine</i> , 2010, 55, 62-70.e4.	0.3	74
85	Proteomic analysis of endoscopically (endoscopic pancreatic function test) collected gastroduodenal fluid using in-gel tryptic digestion followed by LC-MS/MS. <i>Proteomics - Clinical Applications</i> , 2010, 4, 715-725.	0.8	22
86	Phosphoproteomics. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 255-276.	6.6	41
87	Binding Partner Switching on Microtubules and Aurora-B in the Mitosis to Cytokinesis Transition. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 336-350.	2.5	76
88	Proteome Scale Characterization of Human S-Acylated Proteins in Lipid Raft-enriched and Non-raft Membranes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 54-70.	2.5	252
89	Estimating the Confidence of Peptide Identifications without Decoy Databases. <i>Analytical Chemistry</i> , 2010, 82, 4314-4318.	3.2	23
90	Effect of High-Accuracy Precursor Masses on Phosphopeptide Identification from MS <sup>3</sup> Spectra. <i>Analytical Chemistry</i> , 2010, 82, 3977-3980.	3.2	6

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91	One-Step Sample Concentration, Purification, and Albumin Depletion Method for Urinary Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 6082-6089.	1.8	29
92	Quantitative Proteomics Analysis Reveals Molecular Networks Regulated by Epidermal Growth Factor Receptor Level in Head and Neck Cancer. <i>Journal of Proteome Research</i> , 2010, 9, 3073-3082.	1.8	26
93	Proteomic Analysis of Palmitoylated Platelet Proteins. <i>Blood</i> , 2010, 116, 2017-2017.	0.6	1
94	Tyrosine Phosphorylation of Runx1 In Megakaryocytes by Src Family Kinases. <i>Blood</i> , 2010, 116, 742-742.	0.6	2
95	When less can yield more – Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	1.3	73
96	Urine proteomics for profiling of human disease using high accuracy mass spectrometry. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1052-1061.	0.8	117
97	A simple and effective method for detecting phosphopeptides for phosphoproteomic analysis. <i>Journal of Proteomics</i> , 2009, 72, 831-835.	1.2	8
98	FLEXIQuant: A Novel Tool for the Absolute Quantification of Proteins, and the Simultaneous Identification and Quantification of Potentially Modified Peptides. <i>Journal of Proteome Research</i> , 2009, 8, 2201-2210.	1.8	109
99	Proteomics and Opportunities for Clinical Translation in Urological Disease. <i>Journal of Urology</i> , 2009, 182, 835-843.	0.2	17
100	Temporal variations of the postnatal rat urinary proteome as a reflection of systemic maturation. <i>Proteomics</i> , 2008, 8, 1097-1112.	1.3	26
101	NITPICK: peak identification for mass spectrometry data. <i>BMC Bioinformatics</i> , 2008, 9, 355.	1.2	66
102	Robust Prediction of the MASCOT Score for an Improved Quality Assessment in Mass Spectrometric Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 3708-3717.	1.8	182
103	Different phosphorylation states of the anaphase promoting complex in response to antimetabolic drugs: A quantitative proteomic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6069-6074.	3.3	77
104	Optimizing Sample Handling for Urinary Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 4022-4030.	1.8	68
105	Phosphorylation Analysis by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 172-181.	2.5	313
106	Stable isotope-free relative and absolute quantitation of protein phosphorylation stoichiometry by MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3948-3953.	3.3	202
107	The abc's (and xyz's) of peptide sequencing. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 699-711.	16.1	948
108	Phosphotyrosine Mapping in Bcr/Abl Oncoprotein Using Phosphotyrosine-specific Immonium Ion Scanning. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 138-145.	2.5	46

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109	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. <i>Science Signaling</i> , 2002, 2002, pl16-pl16.	1.6	38
110	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. <i>Journal of Biological Chemistry</i> , 2002, 277, 1031-1039.	1.6	175
111	Analysis of Bromotryptophan and Hydroxyproline Modifications by High-Resolution, High-Accuracy Precursor Ion Scanning Utilizing Fragment Ions with Mass-Deficient Mass Tags. <i>Analytical Chemistry</i> , 2002, 74, 6230-6236.	3.2	41
112	Multi-Protein Complexes Studied by Mass Spectrometry. <i>Scientific World Journal, The</i> , 2002, 2, 91-92.	0.8	1
113	Proteomics goes quantitative: measuring protein abundance. <i>Trends in Biotechnology</i> , 2002, 20, 361-364.	4.9	64
114	Directed Proteomic Analysis of the Human Nucleolus. <i>Current Biology</i> , 2002, 12, 1-11.	1.8	962
115	Analysis of protein-nucleic acid interactions by photochemical cross-linking and mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2002, 21, 163-182.	2.8	67
116	A new derivatization strategy for the analysis of phosphopeptides by precursor ion scanning in positive ion mode. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 996-1003.	1.2	104
117	Detection of Tyrosine Phosphorylated Peptides by Precursor Ion Scanning Quadrupole TOF Mass Spectrometry in Positive Ion Mode. <i>Analytical Chemistry</i> , 2001, 73, 1440-1448.	3.2	306
118	Similarity between condensed phase and gas phase chemistry: Fragmentation of peptides containing oxidized cysteine residues and its implications for proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 228-232.	1.2	59
119	Investigation of tyrosine nitration in proteins by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2001, 36, 616-625.	0.7	141
120	Quadrupole time-of-flight versus triple-quadrupole mass spectrometry for the determination of phosphopeptides by precursor ion scanning. <i>Journal of Mass Spectrometry</i> , 2001, 36, 782-790.	0.7	141
121	Labile sulfogroup allows differentiation of sulfotyrosine and phosphotyrosine in peptides. <i>Journal of Mass Spectrometry</i> , 2001, 36, 832-833.	0.7	28
122	Mass spectrometric analysis of a UV-cross-linked protein-DNA complex: Tryptophans 54 and 88 of E. coliSSB cross-link to DNA. <i>Protein Science</i> , 2001, 10, 1989-2001.	3.1	43
123	Detection and Quantification of Neuropeptide Y in Human Brain Tissue by Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 3320-3326.	3.2	84
124	Using plasma proteomics to investigate viral infections of the central nervous system including patients with HIV-associated neurocognitive disorders. <i>Journal of NeuroVirology</i> , 0, , .	1.0	0