

# 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	Directed Proteomic Analysis of the Human Nucleolus. <i>Current Biology</i> , 2002, 12, 1-11.	1.8	962
2	The abc's (and xyz's) of peptide sequencing. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 699-711.	16.1	948
3	Tau PTM Profiles Identify Patient Heterogeneity and Stages of Alzheimer's Disease. <i>Cell</i> , 2020, 183, 1699-1713.e13.	13.5	354
4	Phosphorylation Analysis by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 172-181.	2.5	313
5	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
6	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
7	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
8	A Specific LSD1/KDM1A Isoform Regulates Neuronal Differentiation through H3K9 Demethylation. <i>Molecular Cell</i> , 2015, 57, 957-970.	4.5	221
9	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
10	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
11	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. <i>Journal of Biological Chemistry</i> , 2002, 277, 1031-1039.	1.6	175
12	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
13	Investigation of tyrosine nitration in proteins by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2001, 36, 616-625.	0.7	141
14	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
15	Tiki1 Is Required for Head Formation via Wnt Cleavage-Oxidation and Inactivation. <i>Cell</i> , 2012, 149, 1565-1577.	13.5	125
16	Urine proteomics for profiling of human disease using high accuracy mass spectrometry. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1052-1061.	0.8	117
17	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
18	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

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19	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
20	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
21	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
22	Urine proteomics for discovery of improved diagnostic markers of Kawasaki disease. <i>EMBO Molecular Medicine</i> , 2013, 5, 210-220.	3.3	80
23	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
24	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
25	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
26	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
27	BCG vaccination-induced emergency granulopoiesis provides rapid protection from neonatal sepsis. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	76
28	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
29	When less can yield more – Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	1.3	73
30	Co-regulation proteomics reveals substrates and mechanisms of APC/C-dependent degradation. <i>EMBO Journal</i> , 2014, 33, 385-399.	3.5	72
31	PCBD5 promotes site-specific oncogenic mutations in human tumors. <i>Nature Genetics</i> , 2017, 49, 1005-1014.	9.4	69
32	Optimizing Sample Handling for Urinary Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 4022-4030.	1.8	68
33	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
34	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
35	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
36	NITPICK: peak identification for mass spectrometry data. <i>BMC Bioinformatics</i> , 2008, 9, 355.	1.2	66

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37	Proteomics goes quantitative: measuring protein abundance. Trends in Biotechnology, 2002, 20, 361-364.	4.9	64
38	Similarity between condensed phase and gas phase chemistry: Fragmentation of peptides containing oxidized cysteine residues and its implications for proteomics. Journal of the American Society for Mass Spectrometry, 2001, 12, 228-232.	1.2	59
39	Multisystem Analysis of <i>Mycobacterium tuberculosis</i> Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. MBio, 2018, 9, .	1.8	57
40	mz5: Space- and Time-efficient Storage of Mass Spectrometry Data Sets. Molecular and Cellular Proteomics, 2012, 11, O111.011379.	2.5	56
41	Quantitative profiling of peptides from RNAs classified as noncoding. Nature Communications, 2014, 5, 5429.	5.8	55
42	Detection and Diagnostic Value of Urine Leucine-Rich $\alpha$ 2-Glycoprotein in Children With Suspected Acute Appendicitis. Annals of Emergency Medicine, 2012, 60, 78-83.e1.	0.3	50
43	Etiology of limb girdle muscular dystrophy 1D/1E determined by laser capture microdissection proteomics. Annals of Neurology, 2012, 71, 141-145.	2.8	49
44	Phosphotyrosine Mapping in Bcr/Abl Oncoprotein Using Phosphotyrosine-specific Immonium Ion Scanning. Molecular and Cellular Proteomics, 2003, 2, 138-145.	2.5	46
45	Mass spectrometric analysis of a UV-cross-linked protein-DNA complex: Tryptophans 54 and 88 of E. coliSSB cross-link to DNA. Protein Science, 2001, 10, 1989-2001.	3.1	43
46	Brainstem Deficiency of the 14-3-3 Regulator of Serotonin Synthesis: A Proteomics Analysis in the Sudden Infant Death Syndrome. Molecular and Cellular Proteomics, 2012, 11, M111.009530.	2.5	42
47	Analysis of Bromotryptophan and Hydroxyproline Modifications by High-Resolution, High-Accuracy Precursor Ion Scanning Utilizing Fragment Ions with Mass-Deficient Mass Tags. Analytical Chemistry, 2002, 74, 6230-6236.	3.2	41
48	Phosphoproteomics. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 255-276.	6.6	41
49	Optimization of cell lysis and protein digestion protocols for the analysis of HeLa S3 cells by LC-MS/MS. Proteomics, 2011, 11, 4726-4730.	1.3	41
50	A Cost-Effective High-Throughput Plasma and Serum Proteomics Workflow Enables Mapping of the Molecular Impact of Total Pancreatectomy with Islet Autotransplantation. Journal of Proteome Research, 2018, 17, 1983-1992.	1.8	39
51	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. Science Signaling, 2002, 2002, pl16-pl16.	1.6	38
52	Comparative analysis of Erk phosphorylation suggests a mixed strategy for measuring phosphoform distributions. Molecular Systems Biology, 2011, 7, 482.	3.2	38
53	Proteomic Analysis of an Immortalized Mouse Pancreatic Stellate Cell Line Identifies Differentially-Expressed Proteins in Activated vs Nonproliferating Cell States. Journal of Proteome Research, 2011, 10, 4835-4844.	1.8	36
54	Protein kinases PknA and PknB independently and coordinately regulate essential Mycobacterium tuberculosis physiologies and antimicrobial susceptibility. PLoS Pathogens, 2020, 16, e1008452.	2.1	33

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55	Optimized sample preparation of endoscopic collected pancreatic fluid for SDS-PAGE analysis. <i>Electrophoresis</i> , 2010, 31, 2377-2387.	1.3	31
56	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
57	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
58	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
59	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
60	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
61	Labile sulfogroup allows differentiation of sulfotyrosine and phosphotyrosine in peptides. <i>Journal of Mass Spectrometry</i> , 2001, 36, 832-833.	0.7	28
62	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
63	Temporal variations of the postnatal rat urinary proteome as a reflection of systemic maturation. <i>Proteomics</i> , 2008, 8, 1097-1112.	1.3	26
64	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
65	FLEXIQinase, a mass spectrometry-based assay, to unveil multikinase mechanisms. <i>Nature Methods</i> , 2012, 9, 504-508.	9.0	26
66	A High-Efficiency Cellular Extraction System for Biological Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 3403-3408.	1.8	26
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	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
69	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
70	Estimating the Confidence of Peptide Identifications without Decoy Databases. <i>Analytical Chemistry</i> , 2010, 82, 4314-4318.	3.2	23
71	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
72	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

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73	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
74	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
75	Nonparametric Bayesian Evaluation of Differential Protein Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 4556-4565.	1.8	22
76	Standard Operating Procedures for Biospecimen Collection, Processing, and Storage. <i>Pancreas</i> , 2018, 47, 1213-1221.	0.5	22
77	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
78	Prohibitin is a prognostic marker and therapeutic target to block chemotherapy resistance in Wilms tumor. <i>JCI Insight</i> , 2019, 4, .	2.3	21
79	Cross-species analysis of nicotine-induced proteomic alterations in pancreatic cells. <i>Proteomics</i> , 2013, 13, 1499-1512.	1.3	20
80	Immunophenotyping assessment in a COVID-19 cohort (IMPACC): A prospective longitudinal study. <i>Science Immunology</i> , 2021, 6, .	5.6	20
81	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
82	A Practical Guide to the FLEXIQuant Method. <i>Methods in Molecular Biology</i> , 2012, 893, 295-319.	0.4	19
83	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
84	Proteomics and Opportunities for Clinical Translation in Urological Disease. <i>Journal of Urology</i> , 2009, 182, 835-843.	0.2	17
85	Placental Proteomics Reveal Insights into Fetal Alcohol Spectrum Disorders. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 1551-1558.	1.4	17
86	Fetal regional brain protein signature in FASD rat model. <i>Reproductive Toxicology</i> , 2018, 76, 84-92.	1.3	17
87	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
88	Urinary Proteomics Yield Pathological Insights for Ureteropelvic Junction Obstruction. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2607-2615.	2.5	16
89	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
90	Influence of Plasmodium falciparum Calcium-Dependent Protein Kinase 5 (PfCDPK5) on the Late Schizont Stage Phosphoproteome. <i>MSphere</i> , 2020, 5, .	1.3	16

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91	Biomarkers of Chronic Pancreatitis: A systematic literature review. <i>Pancreatology</i> , 2021, 21, 323-333.	0.5	16
92	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
93	Bacille Calmette-Guérin vaccine reprograms human neonatal lipid metabolism <i>in vivo</i> and <i>in vitro</i> . <i>Cell Reports</i> , 2022, 39, 110772.	2.9	13
94	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
95	Antioxidant functions of DHHC3 suppress anti-cancer drug activities. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2341-2353.	2.4	12
96	Urine Proteomics for Noninvasive Monitoring of Biomarkers in Bronchopulmonary Dysplasia. <i>Neonatology</i> , 2022, 119, 193-203.	0.9	12
97	A Non-parametric Cutout Index for Robust Evaluation of Identified Proteins. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 807-812.	2.5	11
98	Difference gel electrophoresis identifies differentially expressed proteins in endoscopically collected pancreatic fluid. <i>Electrophoresis</i> , 2011, 32, 1939-1951.	1.3	10
99	Precision Medicine in Pancreatic Disease—Knowledge Gaps and Research Opportunities. <i>Pancreas</i> , 2019, 48, 1250-1258.	0.5	9
100	A simple and effective method for detecting phosphopeptides for phosphoproteomic analysis. <i>Journal of Proteomics</i> , 2009, 72, 831-835.	1.2	8
101	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
102	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
103	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
104	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
105	Sample Handling of Body Fluids for Proteomics. , 2011, , 327-360.		6
106	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
107	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
108	Plasma Proteomic Analysis Distinguishes Severity Outcomes of Human Ebola Virus Disease. <i>MBio</i> , 2022, 13, e0056722.	1.8	5

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109	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
110	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
111	FLEXIQuant-LF to quantify protein modification extent in label-free proteomics data. <i>ELife</i> , 2020, 9, .	2.8	4
112	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
113	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
114	Proteomics based markers of clinical pain severity in juvenile idiopathic arthritis. <i>Pediatric Rheumatology</i> , 2022, 20, 3.	0.9	3
115	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
116	Tyrosine Phosphorylation of Runx1 In Megakaryocytes by Src Family Kinases. <i>Blood</i> , 2010, 116, 742-742.	0.6	2
117	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
118	Multi-Protein Complexes Studied by Mass Spectrometry. <i>Scientific World Journal, The</i> , 2002, 2, 91-92.	0.8	1
119	[O4â€“O2â€“O3]: MAPPING THE TAUOPATHYâ€“SPECIFIC MODIFICATION LANDSCAPE ON TAU. <i>Alzheimer's and Dementia</i> , 2017, 13, P1229.	0.4	1
120	Proteomic Analysis of Palmitoylated Platelet Proteins. <i>Blood</i> , 2010, 116, 2017-2017.	0.6	1
121	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
122	Abstract IA8: A new class of drugs active in T-ALL is revealed in a zebrafish screen. , 2014, , .		0
123	Increased phosphorylation of ACTN4 leads to podocyte vulnerability and proteinuric kidney disease and is stimulated by high glucose and TGFâ€“b. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	0
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