

Jyoti S Choudhary

List of Publications by Year in descending order

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Version: 2024-02-01

138
papers

16,620
citations

34016

52
h-index

19136

118
g-index

154
all docs

154
docs citations

154
times ranked

29792
citing authors

#	ARTICLE	IF	CITATIONS
1	DIPG Harbors Alterations Targetable by MEK Inhibitors, with Acquired Resistance Mechanisms Overcome by Combinatorial Inhibition. <i>Cancer Discovery</i> , 2022, 12, 712-729.	7.7	15
2	The type III secretion system effector network hypothesis. <i>Trends in Microbiology</i> , 2022, 30, 524-533.	3.5	21
3	The ubiquitin-dependent ATPase p97 removes cytotoxic trapped PARP1 from chromatin. <i>Nature Cell Biology</i> , 2022, 24, 62-73.	4.6	66
4	Citrobacter rodentium Infection Induces Persistent Molecular Changes and Interferon Gamma-Dependent Major Histocompatibility Complex Class II Expression in the Colonic Epithelium. <i>MBio</i> , 2022, 13, e0323321.	1.8	3
5	Aneuploidy tolerance caused by BRG1 loss allows chromosome gains and recovery of fitness. <i>Nature Communications</i> , 2022, 13, 1731.	5.8	9
6	EPECâ€œinduced activation of the Ca ²⁺ transporter TRPV2 leads to pyroptotic cell death. <i>Molecular Microbiology</i> , 2022, 117, 480-492.	1.2	7
7	SimPLIT: Simplified Sample Preparation for Large-Scale Isobaric Tagging Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1842-1856.	1.8	9
8	Proteomic characterisation of triple negative breast cancer cells following CDK4/6 inhibition. <i>Scientific Data</i> , 2022, 9, .	2.4	4
9	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	6.5	633
10	3D Functional Genomics Screens Identify CREBBP as a Targetable Driver in Aggressive Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021, 81, 847-859.	0.4	7
11	A molecular quantitative trait locus map for osteoarthritis. <i>Nature Communications</i> , 2021, 12, 1309.	5.8	53
12	Type III secretion system effectors form robust and flexible intracellular virulence networks. <i>Science</i> , 2021, 371, .	6.0	50
13	CRISPR activation screen in mice identifies novel membrane proteins enhancing pulmonary metastatic colonisation. <i>Communications Biology</i> , 2021, 4, 395.	2.0	12
14	A systematic CRISPR screen defines mutational mechanisms underpinning signatures caused by replication errors and endogenous DNA damage. <i>Nature Cancer</i> , 2021, 2, 643-657.	5.7	94
15	Ubiquitylation of MLKL at lysine 219 positively regulates necroptosis-induced tissue injury and pathogen clearance. <i>Nature Communications</i> , 2021, 12, 3364.	5.8	43
16	The type III secretion system effector EspO of enterohaemorrhagic <i>Escherichia coli</i> inhibits apoptosis through an interaction with HAX1. <i>Cellular Microbiology</i> , 2021, 23, e13366.	1.1	3
17	HMGB1 Protein Interactions in Prostate and Ovary Cancer Models Reveal Links to RNA Processing and Ribosome Biogenesis through NuRD, THOC and Septin Complexes. <i>Cancers</i> , 2021, 13, 4686.	1.7	4
18	A commercial antibody to the human condensin II subunit NCAPH2 cross-reacts with a SWI/SNF complex component. <i>Wellcome Open Research</i> , 2021, 6, 3.	0.9	2

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19	<i>Citrobacter rodentium</i> induces rapid and unique metabolic and inflammatory responses in mice suffering from severe disease. Cellular Microbiology, 2020, 22, e13126.	1.1	22
20	Cell-type-specific visualisation and biochemical isolation of endogenous synaptic proteins in mice. European Journal of Neuroscience, 2020, 51, 793-805.	1.2	18
21	Faecal neutrophil elastase-antiprotease balance reflects colitis severity. Mucosal Immunology, 2020, 13, 322-333.	2.7	29
22	Mutations in FAM50A suggest that Armfield XLID syndrome is a spliceosomopathy. Nature Communications, 2020, 11, 3698.	5.8	38
23	Using Deep Learning to Extrapolate Protein Expression Measurements. Proteomics, 2020, 20, e2000009.	1.3	9
24	Phosphorylation-Dependent Assembly of a 14-3-3 Mediated Signaling Complex during Red Blood Cell Invasion by Plasmodium falciparum Merozoites. MBio, 2020, 11, .	1.8	13
25	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. BMC Genetics, 2020, 21, 25.	2.7	30
26	Proteogenomics of Non-smoking Lung Cancer in East Asia Delineates Molecular Signatures of Pathogenesis and Progression. Cell, 2020, 182, 226-244.e17.	13.5	178
27	Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. Nature Communications, 2020, 11, 1801.	5.8	153
28	Cyclin B1-Cdk1 facilitates MAD1 release from the nuclear pore to ensure a robust spindle checkpoint. Journal of Cell Biology, 2020, 219, .	2.3	35
29	Clustering of Tir during enteropathogenic E. coli infection triggers calcium influx-dependent pyroptosis in intestinal epithelial cells. PLoS Biology, 2020, 18, e3000986.	2.6	18
30	Landscape of the Plasmodium Interactome Reveals Both Conserved and Species-Specific Functionality. Cell Reports, 2019, 28, 1635-1647.e5.	2.9	49
31	Autoinhibition Mechanism of the Ubiquitin-Conjugating Enzyme UBE2S by Autoubiquitination. Structure, 2019, 27, 1195-1210.e7.	1.6	20
32	The flagellotropic bacteriophage YSD1 targets <i>Salmonella</i> Typhi with a Chi-like protein tail fibre. Molecular Microbiology, 2019, 112, 1831-1846.	1.2	24
33	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. Nature Communications, 2019, 10, 4513.	5.8	69
34	Intestinal Epithelial Cells and the Microbiome Undergo Swift Reprogramming at the Inception of Colonic <i>Citrobacter rodentium</i> Infection. MBio, 2019, 10, .	1.8	38
35	Proteomic navigation using proximity-labeling. Methods, 2019, 164-165, 67-72.	1.9	6
36	Overexpression of Claspin and Timeless protects cancer cells from replication stress in a checkpoint-independent manner. Nature Communications, 2019, 10, 910.	5.8	105

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37	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	2.4	52
38	Precision Medicine in Pancreatic Disease—Knowledge Gaps and Research Opportunities. <i>Pancreas</i> , 2019, 48, 1250-1258.	0.5	9
39	Evaluation of a Dual Isolation Width Acquisition Method for Isobaric Labeling Ratio Decompression. <i>Journal of Proteome Research</i> , 2019, 18, 1433-1440.	1.8	13
40	C9orf72 arginine-rich dipeptide proteins interact with ribosomal proteins in vivo to induce a toxic translational arrest that is rescued by eIF1A. <i>Acta Neuropathologica</i> , 2019, 137, 487-500.	3.9	94
41	The BAF and PRC2 Complex Subunits Dpf2 and Eed Antagonistically Converge on Tbx3 to Control ESC Differentiation. <i>Cell Stem Cell</i> , 2019, 24, 138-152.e8.	5.2	30
42	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	6.5	2,350
43	Broad-Spectrum Regulation of Nonreceptor Tyrosine Kinases by the Bacterial ADP-Ribosyltransferase EspJ. <i>MBio</i> , 2018, 9, .	1.8	21
44	Nbeal2 interacts with Dock7, Sec16a, and Vac14. <i>Blood</i> , 2018, 131, 1000-1011.	0.6	29
45	An E2-ubiquitin thioester-driven approach to identify substrates modified with ubiquitin and ubiquitin-like molecules. <i>Nature Communications</i> , 2018, 9, 4776.	5.8	25
46	The <i>Citrobacter rodentium</i> type III secretion system effector EspO affects mucosal damage repair and antimicrobial responses. <i>PLoS Pathogens</i> , 2018, 14, e1007406.	2.1	23
47	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. <i>Rheumatology</i> , 2018, 57, 1481-1489.	0.9	19
48	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. <i>Nature Genetics</i> , 2018, 50, 883-894.	9.4	117
49	A Fast and Quantitative Method for Post-translational Modification and Variant Enabled Mapping of Peptides to Genomes. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	3
50	Inhibition of somatosensory mechanotransduction by annexin A6. <i>Science Signaling</i> , 2018, 11, .	1.6	10
51	Delineating the HMGB1 and HMGB2 interactome in prostate and ovary epithelial cells and its relationship with cancer. <i>Oncotarget</i> , 2018, 9, 19050-19064.	0.8	9
52	A Knockout Screen of ApiAP2 Genes Reveals Networks of Interacting Transcriptional Regulators Controlling the Plasmodium Life Cycle. <i>Cell Host and Microbe</i> , 2017, 21, 11-22.	5.1	177
53	Evolution of complexity in the zebrafish synapse proteome. <i>Nature Communications</i> , 2017, 8, 14613.	5.8	112
54	Exploiting induced pluripotent stem cell-derived macrophages to unravel host factors influencing <i>Chlamydia trachomatis</i> pathogenesis. <i>Nature Communications</i> , 2017, 8, 15013.	5.8	50

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55	Eros is a novel transmembrane protein that controls the phagocyte respiratory burst and is essential for innate immunity. <i>Journal of Experimental Medicine</i> , 2017, 214, 1111-1128.	4.2	50
56	<i>Citrobacter rodentium</i> Subverts ATP Flux and Cholesterol Homeostasis in Intestinal Epithelial Cells In Vivo. <i>Cell Metabolism</i> , 2017, 26, 738-752.e6.	7.2	67
57	Crosstalk between PKA and PKG controls pH-dependent host cell egress of <i>Toxoplasma gondii</i> . <i>EMBO Journal</i> , 2017, 36, 3250-3267.	3.5	111
58	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. <i>Cell Reports</i> , 2017, 21, 679-691.	2.9	79
59	Fast, Quantitative and Variant Enabled Mapping of Peptides to Genomes. <i>Cell Systems</i> , 2017, 5, 152-156.e4.	2.9	10
60	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	2.9	95
61	Myst2/Kat7 histone acetyltransferase interaction proteomics reveals tumour-suppressor Niam as a novel binding partner in embryonic stem cells. <i>Scientific Reports</i> , 2017, 7, 8157.	1.6	12
62	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. <i>Scientific Reports</i> , 2017, 7, 8935.	1.6	90
63	Molecular phenotyping of patient chondrocytes reveals genes and pathways involved in osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2017, 25, S209-S210.	0.6	0
64	Resolving Affinity Purified Protein Complexes by Blue Native PAGE and Protein Correlation Profiling. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	8
65	Sub-minute Phosphoregulation of Cell Cycle Systems during Plasmodium Gamete Formation. <i>Cell Reports</i> , 2017, 21, 2017-2029.	2.9	59
66	Activation of the Aryl Hydrocarbon Receptor Interferes with Early Embryonic Development. <i>Stem Cell Reports</i> , 2017, 9, 1377-1386.	2.3	39
67	Global, site-specific analysis of neuronal protein S-acylation. <i>Scientific Reports</i> , 2017, 7, 4683.	1.6	80
68	Targeted Feature Detection for Data-Dependent Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 2964-2974.	1.8	43
69	A quantitative proteomic screen of the <i>Campylobacter jejuni</i> flagellar-dependent secretome. <i>Journal of Proteomics</i> , 2017, 152, 181-187.	1.2	10
70	Transcriptome and proteome analysis of <i>Salmonella enterica</i> serovar Typhimurium systemic infection of wild type and immune-deficient mice. <i>PLoS ONE</i> , 2017, 12, e0181365.	1.1	6
71	Multiple short windows of calcium-dependent protein kinase 4 activity coordinate distinct cell cycle events during Plasmodium gametogenesis. <i>ELife</i> , 2017, 6, .	2.8	62
72	DecoyPyrat: Fast Non-redundant Hybrid Decoy Sequence Generation for Large Scale Proteomics. <i>Journal of Proteomics and Bioinformatics</i> , 2016, 09, 176-180.	0.4	24

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73	Interferon-driven alterations of the host's amino acid metabolism in the pathogenesis of typhoid fever. <i>Journal of Experimental Medicine</i> , 2016, 213, 1061-1077.	4.2	45
74	Role of Eros, a novel transmembrane protein, in regulation of host defence. <i>Lancet, The</i> , 2016, 387, S12.	6.3	0
75	Study of <i>Plasmodium falciparum</i> DHHC palmitoyl transferases identifies a role for PfDHHC9 in gametocytogenesis. <i>Cellular Microbiology</i> , 2016, 18, 1596-1610.	1.1	15
76	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	9.0	537
77	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	5.8	68
78	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. <i>Journal of Proteome Research</i> , 2016, 15, 4686-4695.	1.8	11
79	Expression Atlas update—an integrated database of gene and protein expression in humans, animals and plants. <i>Nucleic Acids Research</i> , 2016, 44, D746-D752.	6.5	526
80	Quantitative proteomic analysis of <i>Shigella flexneri</i> and <i>Shigella sonnei</i> Generalized Modules for Membrane Antigens (GMMA) reveals highly pure preparations. <i>International Journal of Medical Microbiology</i> , 2016, 306, 99-108.	1.5	19
81	Characterization of Two Distinct Nucleosome Remodeling and Deacetylase (NuRD) Complex Assemblies in Embryonic Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 878-891.	2.5	42
82	Chapter 4. PSM Scoring and Validation. <i>New Developments in Mass Spectrometry</i> , 2016, , 69-92.	0.2	1
83	Palmitoylation and palmitoyl-transferases in <i>Plasmodium</i> parasites. <i>Biochemical Society Transactions</i> , 2015, 43, 240-245.	1.6	17
84	Identification of protein complexes that bind to histone H3 combinatorial modifications using super-SILAC and weighted correlation network analysis. <i>Nucleic Acids Research</i> , 2015, 43, 1418-1432.	6.5	35
85	Cyclic diGMP Regulates Production of Sortase Substrates of <i>Clostridium difficile</i> and Their Surface Exposure through ZmpI Protease-mediated Cleavage. <i>Journal of Biological Chemistry</i> , 2015, 290, 24453-24469.	1.6	74
86	Phosphoinositide Metabolism Links cGMP-Dependent Protein Kinase G to Essential Ca ²⁺ Signals at Key Decision Points in the Life Cycle of Malaria Parasites. <i>PLoS Biology</i> , 2014, 12, e1001806.	2.6	185
87	The OMSSAP ercolator: an automated tool to validate OMSSA results. <i>Proteomics</i> , 2014, 14, 1011-1014.	1.3	13
88	A New Method To Determine <i>In Vivo</i> Interactomes Reveals Binding of the <i>Legionella pneumophila</i> Effector PieE to Multiple Rab GTPases. <i>MBio</i> , 2014, 5, .	1.8	29
89	Human post-mortem synapse proteome integrity screening for proteomic studies of postsynaptic complexes. <i>Molecular Brain</i> , 2014, 7, 88.	1.3	49
90	Genome-wide analysis of the heat stress response in Zebu (Sahiwal) cattle. <i>Gene</i> , 2014, 533, 500-507.	1.0	51

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91	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	13.7	1,305
92	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	1.2	145
93	Confident and sensitive phosphoproteomics using combinations of collision induced dissociation and electron transfer dissociation. <i>Journal of Proteomics</i> , 2014, 103, 1-14.	1.2	34
94	Nuclear receptor binding protein 1 regulates intestinal progenitor cell homeostasis and tumour formation. <i>EMBO Journal</i> , 2012, 31, 2486-2497.	3.5	40
95	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 478-491.	2.5	34
96	A <i>Plasmodium</i> Calcium-Dependent Protein Kinase Controls Zygote Development and Transmission by Translationally Activating Repressed mRNAs. <i>Cell Host and Microbe</i> , 2012, 12, 9-19.	5.1	163
97	Analysis of Protein Palmitoylation Reveals a Pervasive Role in <i>Plasmodium</i> Development and Pathogenesis. <i>Cell Host and Microbe</i> , 2012, 12, 246-258.	5.1	177
98	SynGAP isoforms exert opposing effects on synaptic strength. <i>Nature Communications</i> , 2012, 3, 900.	5.8	65
99	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. <i>Molecular Psychiatry</i> , 2012, 17, 142-153.	4.1	775
100	Assignment of Protein Interactions from Affinity Purification/Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2012, 11, 1462-1474.	1.8	52
101	Comparative Study of Human and Mouse Postsynaptic Proteomes Finds High Compositional Conservation and Abundance Differences for Key Synaptic Proteins. <i>PLoS ONE</i> , 2012, 7, e46683.	1.1	179
102	APC15 drives the turnover of MCC-CDC20 to make the spindle assembly checkpoint responsive to kinetochore attachment. <i>Nature Cell Biology</i> , 2011, 13, 1234-1243.	4.6	139
103	Quantitative Proteomics Reveals the Basis for the Biochemical Specificity of the Cell-Cycle Machinery. <i>Molecular Cell</i> , 2011, 43, 406-417.	4.5	127
104	Characterization of the proteome, diseases and evolution of the human postsynaptic density. <i>Nature Neuroscience</i> , 2011, 14, 19-21.	7.1	449
105	Coordinating cell cycle progression via cyclin specificity. <i>Cell Cycle</i> , 2011, 10, 4195-4196.	1.3	6
106	<i>Citrobacter rodentium</i> is an Unstable Pathogen Showing Evidence of Significant Genomic Flux. <i>PLoS Pathogens</i> , 2011, 7, e1002018.	2.1	35
107	Shotgun proteomics aids discovery of novel protein-coding genes, alternative splicing, and resurrected pseudogenes in the mouse genome. <i>Genome Research</i> , 2011, 21, 756-767.	2.4	113
108	Quantitative RNA-seq analysis of the <i>Campylobacter jejuni</i> transcriptome. <i>Microbiology (United Kingdom)</i> , 2011, 155, 1000-1010.	0.7	44

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109	A Conserved Acetyl Esterase Domain Targets Diverse Bacteriophages to the Vi Capsular Receptor of <i>Salmonella enterica</i> Serovar Typhi. <i>Journal of Bacteriology</i> , 2010, 192, 5746-5754.	1.0	79
110	Prmt5 is essential for early mouse development and acts in the cytoplasm to maintain ES cell pluripotency. <i>Genes and Development</i> , 2010, 24, 2772-2777.	2.7	287
111	An Expanded Oct4 Interaction Network: Implications for Stem Cell Biology, Development, and Disease. <i>Cell Stem Cell</i> , 2010, 6, 382-395.	5.2	338
112	Scoring and Validation of Tandem MS Peptide Identification Methods. <i>Methods in Molecular Biology</i> , 2010, 604, 43-53.	0.4	7
113	Targeted tandem affinity purification of PSD-95 recovers core postsynaptic complexes and schizophrenia susceptibility proteins. <i>Molecular Systems Biology</i> , 2009, 5, 269.	3.2	245
114	Neurotransmitters Drive Combinatorial Multistate Postsynaptic Density Networks. <i>Science Signaling</i> , 2009, 2, ra19.	1.6	116
115	Proteomic and Genomic Characterization of Highly Infectious <i>Clostridium difficile</i> 630 Spores. <i>Journal of Bacteriology</i> , 2009, 191, 5377-5386.	1.0	210
116	A Strand-Specific RNA-Seq Analysis of the Transcriptome of the Typhoid Bacillus <i>Salmonella Typhi</i> . <i>PLoS Genetics</i> , 2009, 5, e1000569.	1.5	202
117	Accurate and Sensitive Peptide Identification with Mascot Percolator. <i>Journal of Proteome Research</i> , 2009, 8, 3176-3181.	1.8	399
118	Mapping multiprotein complexes by affinity purification and mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2008, 19, 324-330.	3.3	118
119	Evolutionary expansion and anatomical specialization of synapse proteome complexity. <i>Nature Neuroscience</i> , 2008, 11, 799-806.	7.1	171
120	Molecular Characterization of the <i>Salmonella enterica</i> Serovar Typhi Vi-Typing Bacteriophage E1. <i>Journal of Bacteriology</i> , 2008, 190, 2580-2587.	1.0	41
121	Phosphoproteomic Analysis of the Mouse Brain Cytosol Reveals a Predominance of Protein Phosphorylation in Regions of Intrinsic Sequence Disorder. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1331-1348.	2.5	157
122	Comparison of Mascot and X!Tandem Performance for Low and High Accuracy Mass Spectrometry and the Development of an Adjusted Mascot Threshold. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 962-970.	2.5	58
123	Analysis of protein phosphorylation on a proteome-scale. <i>Proteomics</i> , 2007, 7, 2751-2768.	1.3	153
124	Molecular characterization and comparison of the components and multiprotein complexes in the postsynaptic proteome. <i>Journal of Neurochemistry</i> , 2006, 97, 16-23.	2.1	397
125	Robust Enrichment of Phosphorylated Species in Complex Mixtures by Sequential Protein and Peptide Metal-Affinity Chromatography and Analysis by Tandem Mass Spectrometry. <i>Science Signaling</i> , 2005, p16-pl6.	1.6	25
126	Proteomic Analysis of in Vivo Phosphorylated Synaptic Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 5972-5982.	1.6	300

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127	Proteomics in postgenomic neuroscience: the end of the beginning. <i>Nature Neuroscience</i> , 2004, 7, 440-445.	7.1	134
128	The Three-Dimensional Structure and X-Ray Sequence Reveal that Trichomaglin Is a Novel S-like Ribonuclease. <i>Structure</i> , 2004, 12, 1015-1025.	1.6	6
129	Paxillin Associates with Poly(A)-binding Protein 1 at the Dense Endoplasmic Reticulum and the Leading Edge of Migrating Cells. <i>Journal of Biological Chemistry</i> , 2002, 277, 6428-6437.	1.6	87
130	Interrogating the human genome using uninterpreted mass spectrometry data. <i>Proteomics</i> , 2001, 1, 651-667.	1.3	80
131	Matching peptide mass spectra to EST and genomic DNA databases. <i>Trends in Biotechnology</i> , 2001, 19, 17-22.	4.9	48
132	Matching peptide mass spectra to EST and genomic DNA databases. <i>Trends in Biotechnology</i> , 2001, 19, S17-S22.	4.9	56
133	Proteomics Characterization of Abundant Golgi Membrane Proteins. <i>Journal of Biological Chemistry</i> , 2001, 276, 5152-5165.	1.6	217
134	Proteomic analysis of NMDA receptor-adhesion protein signaling complexes. <i>Nature Neuroscience</i> , 2000, 3, 661-669.	7.1	1,122
135	Applications of Protein Mass Spectrometry in Cell Biology. <i>Methods</i> , 2000, 20, 383-397.	1.9	35
136	Proteomic analysis of extracellular vesicles from a <i>Plasmodium falciparum</i> Kenyan clinical isolate defines a core parasite secretome. <i>Wellcome Open Research</i> , 0, 2, 50.	0.9	25
137	Identifying and characterising Thrap3, Bclaf1 and Erh interactions using cross-linking mass spectrometry. <i>Wellcome Open Research</i> , 0, 6, 260.	0.9	2
138	Landscape of the <i>Plasmodium</i> Interactome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1