

# Jyoti S Choudhary

## List of Publications by Year in descending order

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Version: 2024-02-01

138  
papers

16,620  
citations

34105

52  
h-index

19190

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.	9.4	15
2	The type III secretion system effector network hypothesis. <i>Trends in Microbiology</i> , 2022, 30, 524-533.	7.7	21
3	The ubiquitin-dependent ATPase p97 removes cytotoxic trapped PARP1 from chromatin. <i>Nature Cell Biology</i> , 2022, 24, 62-73.	10.3	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.	4.1	3
5	Aneuploidy tolerance caused by BRG1 loss allows chromosome gains and recovery of fitness. <i>Nature Communications</i> , 2022, 13, 1731.	12.8	9
6	EPECâ€induced activation of the Ca <sup>2+</sup> transporter TRPV2 leads to pyroptotic cell death. <i>Molecular Microbiology</i> , 2022, 117, 480-492.	2.5	7
7	SimPLIT: Simplified Sample Preparation for Large-Scale Isobaric Tagging Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1842-1856.	3.7	9
8	Proteomic characterisation of triple negative breast cancer cells following CDK4/6 inhibition. <i>Scientific Data</i> , 2022, 9, .	5.3	4
9	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	14.5	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.	0.9	7
11	A molecular quantitative trait locus map for osteoarthritis. <i>Nature Communications</i> , 2021, 12, 1309.	12.8	53
12	Type III secretion system effectors form robust and flexible intracellular virulence networks. <i>Science</i> , 2021, 371, .	12.6	50
13	CRISPR activation screen in mice identifies novel membrane proteins enhancing pulmonary metastatic colonisation. <i>Communications Biology</i> , 2021, 4, 395.	4.4	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.	13.2	94
15	Ubiquitylation of MLKL at lysine 219 positively regulates necroptosis-induced tissue injury and pathogen clearance. <i>Nature Communications</i> , 2021, 12, 3364.	12.8	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.	2.1	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.	3.7	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.	1.8	2

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19	<i>Citrobacter rodentium</i> induces rapid and unique metabolic and inflammatory responses in mice suffering from severe disease. <i>Cellular Microbiology</i> , 2020, 22, e13126.	2.1	22
20	Cell-type-specific visualisation and biochemical isolation of endogenous synaptic proteins in mice. <i>European Journal of Neuroscience</i> , 2020, 51, 793-805.	2.6	18
21	Faecal neutrophil elastase-antiprotease balance reflects colitis severity. <i>Mucosal Immunology</i> , 2020, 13, 322-333.	6.0	29
22	Mutations in FAM50A suggest that Armfield XLID syndrome is a spliceosomopathy. <i>Nature Communications</i> , 2020, 11, 3698.	12.8	38
23	Using Deep Learning to Extrapolate Protein Expression Measurements. <i>Proteomics</i> , 2020, 20, e2000009.	2.2	9
24	Phosphorylation-Dependent Assembly of a 14-3-3 Mediated Signaling Complex during Red Blood Cell Invasion by <i>Plasmodium falciparum</i> Merozoites. <i>MBio</i> , 2020, 11, .	4.1	13
25	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. <i>BMC Genetics</i> , 2020, 21, 25.	2.7	30
26	Proteogenomics of Non-smoking Lung Cancer in East Asia Delineates Molecular Signatures of Pathogenesis and Progression. <i>Cell</i> , 2020, 182, 226-244.e17.	28.9	178
27	Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. <i>Nature Communications</i> , 2020, 11, 1801.	12.8	153
28	Cyclin B1-Cdk1 facilitates MAD1 release from the nuclear pore to ensure a robust spindle checkpoint. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	35
29	Clustering of Tir during enteropathogenic <i>E. coli</i> infection triggers calcium influx-dependent pyroptosis in intestinal epithelial cells. <i>PLoS Biology</i> , 2020, 18, e3000986.	5.6	18
30	Landscape of the <i>Plasmodium</i> Interactome Reveals Both Conserved and Species-Specific Functionality. <i>Cell Reports</i> , 2019, 28, 1635-1647.e5.	6.4	49
31	Autoinhibition Mechanism of the Ubiquitin-Conjugating Enzyme UBE2S by Autoubiquitination. <i>Structure</i> , 2019, 27, 1195-1210.e7.	3.3	20
32	The flagellotropic bacteriophage YSD1 targets <i>Salmonella</i> Typhi with a Chi-like protein tail fibre. <i>Molecular Microbiology</i> , 2019, 112, 1831-1846.	2.5	24
33	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019, 10, 4513.	12.8	69
34	Intestinal Epithelial Cells and the Microbiome Undergo Swift Reprogramming at the Inception of Colonic <i>Citrobacter rodentium</i> Infection. <i>MBio</i> , 2019, 10, .	4.1	38
35	Proteomic navigation using proximity-labeling. <i>Methods</i> , 2019, 164-165, 67-72.	3.8	6
36	Overexpression of Claspin and Timeless protects cancer cells from replication stress in a checkpoint-independent manner. <i>Nature Communications</i> , 2019, 10, 910.	12.8	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.	5.5	52
38	Precision Medicine in Pancreatic Disease—Knowledge Gaps and Research Opportunities. <i>Pancreas</i> , 2019, 48, 1250-1258.	1.1	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.	3.7	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.	7.7	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.	11.1	30
42	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
43	Broad-Spectrum Regulation of Nonreceptor Tyrosine Kinases by the Bacterial ADP-Ribosyltransferase EspJ. <i>MBio</i> , 2018, 9, .	4.1	21
44	Nbeal2 interacts with Dock7, Sec16a, and Vac14. <i>Blood</i> , 2018, 131, 1000-1011.	1.4	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.	12.8	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.	4.7	23
47	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. <i>Rheumatology</i> , 2018, 57, 1481-1489.	1.9	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.	21.4	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, , .	0.3	3
50	Inhibition of somatosensory mechanotransduction by annexin A6. <i>Science Signaling</i> , 2018, 11, .	3.6	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.	1.8	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.	11.0	177
53	Evolution of complexity in the zebrafish synapse proteome. <i>Nature Communications</i> , 2017, 8, 14613.	12.8	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.	12.8	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.	8.5	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.	16.2	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.	7.8	111
58	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. <i>Cell Reports</i> , 2017, 21, 679-691.	6.4	79
59	Fast, Quantitative and Variant Enabled Mapping of Peptides to Genomes. <i>Cell Systems</i> , 2017, 5, 152-156.e4.	6.2	10
60	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	6.4	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.	3.3	12
62	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. <i>Scientific Reports</i> , 2017, 7, 8935.	3.3	90
63	Molecular phenotyping of patient chondrocytes reveals genes and pathways involved in osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2017, 25, S209-S210.	1.3	0
64	Resolving Affinity Purified Protein Complexes by Blue Native PAGE and Protein Correlation Profiling. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	8
65	Sub-minute Phosphoregulation of Cell Cycle Systems during Plasmodium Gamete Formation. <i>Cell Reports</i> , 2017, 21, 2017-2029.	6.4	59
66	Activation of the Aryl Hydrocarbon Receptor Interferes with Early Embryonic Development. <i>Stem Cell Reports</i> , 2017, 9, 1377-1386.	4.8	39
67	Global, site-specific analysis of neuronal protein S-acylation. <i>Scientific Reports</i> , 2017, 7, 4683.	3.3	80
68	Targeted Feature Detection for Data-Dependent Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 2964-2974.	3.7	43
69	A quantitative proteomic screen of the <i>Campylobacter jejuni</i> flagellar-dependent secretome. <i>Journal of Proteomics</i> , 2017, 152, 181-187.	2.4	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.	2.5	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, .	6.0	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.	8.5	45
74	Role of Eros, a novel transmembrane protein, in regulation of host defence. <i>Lancet, The</i> , 2016, 387, S12.	13.7	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.	2.1	15
76	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
77	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	12.8	68
78	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. <i>Journal of Proteome Research</i> , 2016, 15, 4686-4695.	3.7	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.	14.5	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.	3.6	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.	3.8	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.	3.4	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.	14.5	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.	3.4	74
86	Phosphoinositide Metabolism Links cGMP-Dependent Protein Kinase G to Essential Ca <sup>2+</sup> Signals at Key Decision Points in the Life Cycle of Malaria Parasites. <i>PLoS Biology</i> , 2014, 12, e1001806.	5.6	185
87	The OMSSAP ercolator: an automated tool to validate OMSSA results. <i>Proteomics</i> , 2014, 14, 1011-1014.	2.2	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, .	4.1	29
89	Human post-mortem synapse proteome integrity screening for proteomic studies of postsynaptic complexes. <i>Molecular Brain</i> , 2014, 7, 88.	2.6	49
90	Genome-wide analysis of the heat stress response in Zebu (Sahiwal) cattle. <i>Gene</i> , 2014, 533, 500-507.	2.2	51

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91	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	27.8	1,305
92	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	2.8	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.	2.4	34
94	Nuclear receptor binding protein 1 regulates intestinal progenitor cell homeostasis and tumour formation. <i>EMBO Journal</i> , 2012, 31, 2486-2497.	7.8	40
95	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 478-491.	3.8	34
96	A Plasmodium Calcium-Dependent Protein Kinase Controls Zygote Development and Transmission by Translationally Activating Repressed mRNAs. <i>Cell Host and Microbe</i> , 2012, 12, 9-19.	11.0	163
97	Analysis of Protein Palmitoylation Reveals a Pervasive Role in Plasmodium Development and Pathogenesis. <i>Cell Host and Microbe</i> , 2012, 12, 246-258.	11.0	177
98	SynGAP isoforms exert opposing effects on synaptic strength. <i>Nature Communications</i> , 2012, 3, 900.	12.8	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.	7.9	775
100	Assignment of Protein Interactions from Affinity Purification/Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2012, 11, 1462-1474.	3.7	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.	2.5	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.	10.3	139
103	Quantitative Proteomics Reveals the Basis for the Biochemical Specificity of the Cell-Cycle Machinery. <i>Molecular Cell</i> , 2011, 43, 406-417.	9.7	127
104	Characterization of the proteome, diseases and evolution of the human postsynaptic density. <i>Nature Neuroscience</i> , 2011, 14, 19-21.	14.8	449
105	Coordinating cell cycle progression via cyclin specificity. <i>Cell Cycle</i> , 2011, 10, 4195-4196.	2.6	6
106	<i>Citrobacter rodentium</i> is an Unstable Pathogen Showing Evidence of Significant Genomic Flux. <i>PLoS Pathogens</i> , 2011, 7, e1002018.	4.7	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.	5.5	113
108	Quantitative RNA-seq analysis of the <i>Campylobacter jejuni</i> transcriptome. <i>Microbiology (United Kingdom)</i> , 2011, 155, 118-124.	1.8	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.	2.2	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.	5.9	287
111	An Expanded Oct4 Interaction Network: Implications for Stem Cell Biology, Development, and Disease. <i>Cell Stem Cell</i> , 2010, 6, 382-395.	11.1	338
112	Scoring and Validation of Tandem MS Peptide Identification Methods. <i>Methods in Molecular Biology</i> , 2010, 604, 43-53.	0.9	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.	7.2	245
114	Neurotransmitters Drive Combinatorial Multistate Postsynaptic Density Networks. <i>Science Signaling</i> , 2009, 2, ra19.	3.6	116
115	Proteomic and Genomic Characterization of Highly Infectious <i>Clostridium difficile</i> 630 Spores. <i>Journal of Bacteriology</i> , 2009, 191, 5377-5386.	2.2	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.	3.5	202
117	Accurate and Sensitive Peptide Identification with Mascot Percolator. <i>Journal of Proteome Research</i> , 2009, 8, 3176-3181.	3.7	399
118	Mapping multiprotein complexes by affinity purification and mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2008, 19, 324-330.	6.6	118
119	Evolutionary expansion and anatomical specialization of synapse proteome complexity. <i>Nature Neuroscience</i> , 2008, 11, 799-806.	14.8	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.	2.2	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.	3.8	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.	3.8	58
123	Analysis of protein phosphorylation on a proteome-scale. <i>Proteomics</i> , 2007, 7, 2751-2768.	2.2	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.	3.9	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, pl6-pl6.	3.6	25
126	Proteomic Analysis of in Vivo Phosphorylated Synaptic Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 5972-5982.	3.4	300



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127	Proteomics in postgenomic neuroscience: the end of the beginning. <i>Nature Neuroscience</i> , 2004, 7, 440-445.	14.8	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.	3.3	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.	3.4	87
130	Interrogating the human genome using uninterpreted mass spectrometry data. <i>Proteomics</i> , 2001, 1, 651-667.	2.2	80
131	Matching peptide mass spectra to EST and genomic DNA databases. <i>Trends in Biotechnology</i> , 2001, 19, 17-22.	9.3	48
132	Matching peptide mass spectra to EST and genomic DNA databases. <i>Trends in Biotechnology</i> , 2001, 19, S17-S22.	9.3	56
133	Proteomics Characterization of Abundant Golgi Membrane Proteins. <i>Journal of Biological Chemistry</i> , 2001, 276, 5152-5165.	3.4	217
134	Proteomic analysis of NMDA receptor-adhesion protein signaling complexes. <i>Nature Neuroscience</i> , 2000, 3, 661-669.	14.8	1,122
135	Applications of Protein Mass Spectrometry in Cell Biology. <i>Methods</i> , 2000, 20, 383-397.	3.8	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.	1.8	25
137	Identifying and characterising Thrap3, Bclaf1 and Erh interactions using cross-linking mass spectrometry. <i>Wellcome Open Research</i> , 0, 6, 260.	1.8	2
138	Landscape of the &lt;i>Plasmodium</i> Interactome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1