

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	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
2	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	27.8	1,305
3	Proteomic analysis of NMDA receptor–adhesion protein signaling complexes. <i>Nature Neuroscience</i> , 2000, 3, 661-669.	14.8	1,122
4	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
5	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	14.5	633
6	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
7	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
8	Characterization of the proteome, diseases and evolution of the human postsynaptic density. <i>Nature Neuroscience</i> , 2011, 14, 19-21.	14.8	449
9	Accurate and Sensitive Peptide Identification with Mascot Percolator. <i>Journal of Proteome Research</i> , 2009, 8, 3176-3181.	3.7	399
10	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
11	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
12	Proteomic Analysis of in Vivo Phosphorylated Synaptic Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 5972-5982.	3.4	300
13	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
14	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
15	Proteomics Characterization of Abundant Golgi Membrane Proteins. <i>Journal of Biological Chemistry</i> , 2001, 276, 5152-5165.	3.4	217
16	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
17	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
18	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.	5.6	185

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19	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
20	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
21	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
22	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
23	Evolutionary expansion and anatomical specialization of synapse proteome complexity. <i>Nature Neuroscience</i> , 2008, 11, 799-806.	14.8	171
24	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
25	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
26	Analysis of protein phosphorylation on a proteome scale. <i>Proteomics</i> , 2007, 7, 2751-2768.	2.2	153
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	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	2.8	145
29	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
30	Proteomics in postgenomic neuroscience: the end of the beginning. <i>Nature Neuroscience</i> , 2004, 7, 440-445.	14.8	134
31	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
32	Mapping multiprotein complexes by affinity purification and mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2008, 19, 324-330.	6.6	118
33	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
34	Neurotransmitters Drive Combinatorial Multistate Postsynaptic Density Networks. <i>Science Signaling</i> , 2009, 2, ra19.	3.6	116
35	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
36	Evolution of complexity in the zebrafish synapse proteome. <i>Nature Communications</i> , 2017, 8, 14613.	12.8	112

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37	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
38	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
39	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	6.4	95
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	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
42	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
43	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
44	Interrogating the human genome using uninterpreted mass spectrometry data. <i>Proteomics</i> , 2001, 1, 651-667.	2.2	80
45	Global, site-specific analysis of neuronal protein S-acylation. <i>Scientific Reports</i> , 2017, 7, 4683.	3.3	80
46	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
47	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
48	Cyclic diGMP Regulates Production of Sortase Substrates of <i>Clostridium difficile</i> and Their Surface Exposure through Zmpl Protease-mediated Cleavage. <i>Journal of Biological Chemistry</i> , 2015, 290, 24453-24469.	3.4	74
49	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019, 10, 4513.	12.8	69
50	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	12.8	68
51	<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
52	The ubiquitin-dependent ATPase p97 removes cytotoxic trapped PARP1 from chromatin. <i>Nature Cell Biology</i> , 2022, 24, 62-73.	10.3	66
53	SynGAP isoforms exert opposing effects on synaptic strength. <i>Nature Communications</i> , 2012, 3, 900.	12.8	65
54	Multiple short windows of calcium-dependent protein kinase 4 activity coordinate distinct cell cycle events during <i>Plasmodium</i> gametogenesis. <i>ELife</i> , 2017, 6, .	6.0	62

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55	Sub-minute Phosphoregulation of Cell Cycle Systems during Plasmodium Gamete Formation. Cell Reports, 2017, 21, 2017-2029.	6.4	59
56	Comparison of Mascot and X!Tandem Performance for Low and High Accuracy Mass Spectrometry and the Development of an Adjusted Mascot Threshold. Molecular and Cellular Proteomics, 2008, 7, 962-970.	3.8	58
57	Matching peptide mass spectra to EST and genomic DNA databases. Trends in Biotechnology, 2001, 19, S17-S22.	9.3	56
58	A molecular quantitative trait locus map for osteoarthritis. Nature Communications, 2021, 12, 1309.	12.8	53
59	Assignment of Protein Interactions from Affinity Purification/Mass Spectrometry Data. Journal of Proteome Research, 2012, 11, 1462-1474.	3.7	52
60	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	5.5	52
61	Genome-wide analysis of the heat stress response in Zebu (Sahiwal) cattle. Gene, 2014, 533, 500-507.	2.2	51
62	Exploiting induced pluripotent stem cell-derived macrophages to unravel host factors influencing Chlamydia trachomatis pathogenesis. Nature Communications, 2017, 8, 15013.	12.8	50
63	Eros is a novel transmembrane protein that controls the phagocyte respiratory burst and is essential for innate immunity. Journal of Experimental Medicine, 2017, 214, 1111-1128.	8.5	50
64	Type III secretion system effectors form robust and flexible intracellular virulence networks. Science, 2021, 371, .	12.6	50
65	Human post-mortem synapse proteome integrity screening for proteomic studies of postsynaptic complexes. Molecular Brain, 2014, 7, 88.	2.6	49
66	Landscape of the Plasmodium Interactome Reveals Both Conserved and Species-Specific Functionality. Cell Reports, 2019, 28, 1635-1647.e5.	6.4	49
67	Matching peptide mass spectra to EST and genomic DNA databases. Trends in Biotechnology, 2001, 19, 17-22.	9.3	48
68	Interferon-driven alterations of the host's amino acid metabolism in the pathogenesis of typhoid fever. Journal of Experimental Medicine, 2016, 213, 1061-1077.	8.5	45
69	Quantitative RNA-seq analysis of the Campylobacter jejuni transcriptome. Microbiology (United Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	44
70	Targeted Feature Detection for Data-Dependent Shotgun Proteomics. Journal of Proteome Research, 2017, 16, 2964-2974.	3.7	43
71	Ubiquitylation of MLKL at lysine 219 positively regulates necroptosis-induced tissue injury and pathogen clearance. Nature Communications, 2021, 12, 3364.	12.8	43
72	Characterization of Two Distinct Nucleosome Remodeling and Deacetylase (NuRD) Complex Assemblies in Embryonic Stem Cells. Molecular and Cellular Proteomics, 2016, 15, 878-891.	3.8	42

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73	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
74	Nuclear receptor binding protein 1 regulates intestinal progenitor cell homeostasis and tumour formation. <i>EMBO Journal</i> , 2012, 31, 2486-2497.	7.8	40
75	Activation of the Aryl Hydrocarbon Receptor Interferes with Early Embryonic Development. <i>Stem Cell Reports</i> , 2017, 9, 1377-1386.	4.8	39
76	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
77	Mutations in FAM50A suggest that Armfield XLID syndrome is a spliceosomopathy. <i>Nature Communications</i> , 2020, 11, 3698.	12.8	38
78	Applications of Protein Mass Spectrometry in Cell Biology. <i>Methods</i> , 2000, 20, 383-397.	3.8	35
79	<i>Citrobacter rodentium</i> is an Unstable Pathogen Showing Evidence of Significant Genomic Flux. <i>PLoS Pathogens</i> , 2011, 7, e1002018.	4.7	35
80	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
81	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
82	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
83	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
84	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
85	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
86	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
87	Nbeal2 interacts with Dock7, Sec16a, and Vac14. <i>Blood</i> , 2018, 131, 1000-1011.	1.4	29
88	Faecal neutrophil elastase-antiprotease balance reflects colitis severity. <i>Mucosal Immunology</i> , 2020, 13, 322-333.	6.0	29
89	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.	3.6	25
90	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

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91	Proteomic analysis of extracellular vesicles from a Plasmodium falciparum Kenyan clinical isolate defines a core parasite secretome. Wellcome Open Research, 0, 2, 50.	1.8	25
92	DecoyPyrat: Fast Non-redundant Hybrid Decoy Sequence Generation for Large Scale Proteomics. Journal of Proteomics and Bioinformatics, 2016, 09, 176-180.	0.4	24
93	The flagellotropic bacteriophage YSD1 targets <i>Salmonella</i> Typhi with a Chiâ€like protein tailâ€fibre. Molecular Microbiology, 2019, 112, 1831-1846.	2.5	24
94	The Citrobacter rodentium type III secretion system effector EspO affects mucosal damage repair and antimicrobial responses. PLoS Pathogens, 2018, 14, e1007406.	4.7	23
95	<i>Citrobacter rodentium</i> induces rapid and unique metabolic and inflammatory responses in mice suffering from severe disease. Cellular Microbiology, 2020, 22, e13126.	2.1	22
96	Broad-Spectrum Regulation of Nonreceptor Tyrosine Kinases by the Bacterial ADP-Ribosyltransferase EspJ. MBio, 2018, 9, .	4.1	21
97	The type III secretion system effector network hypothesis. Trends in Microbiology, 2022, 30, 524-533.	7.7	21
98	Autoinhibition Mechanism of the Ubiquitin-Conjugating Enzyme UBE2S by Autoubiquitination. Structure, 2019, 27, 1195-1210.e7.	3.3	20
99	Quantitative proteomic analysis of Shigella flexneri and Shigella sonnei Generalized Modules for Membrane Antigens (GMMAs) reveals highly pure preparations. International Journal of Medical Microbiology, 2016, 306, 99-108.	3.6	19
100	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. Rheumatology, 2018, 57, 1481-1489.	1.9	19
101	Cellâ€typeâ€specific visualisation and biochemical isolation of endogenous synaptic proteins in mice. European Journal of Neuroscience, 2020, 51, 793-805.	2.6	18
102	Clustering of Tir during enteropathogenic E. coli infection triggers calcium influxâ€dependent pyroptosis in intestinal epithelial cells. PLoS Biology, 2020, 18, e3000986.	5.6	18
103	Palmitoylation and palmitoyl-transferases in <i>Plasmodium</i> parasites. Biochemical Society Transactions, 2015, 43, 240-245.	3.4	17
104	Study of Plasmodium falciparum DHHC palmitoyl transferases identifies a role for PfDHHC9 in gametocytogenesis. Cellular Microbiology, 2016, 18, 1596-1610.	2.1	15
105	DIPG Harbors Alterations Targetable by MEK Inhibitors, with Acquired Resistance Mechanisms Overcome by Combinatorial Inhibition. Cancer Discovery, 2022, 12, 712-729.	9.4	15
106	The <sc>OMSSAP</sc>erator: <sc>A</sc>n automated tool to validate <sc>OMSSA</sc> results. Proteomics, 2014, 14, 1011-1014.	2.2	13
107	Evaluation of a Dual Isolation Width Acquisition Method for Isobaric Labeling Ratio Decompression. Journal of Proteome Research, 2019, 18, 1433-1440.	3.7	13
108	Phosphorylation-Dependent Assembly of a 14-3-3 Mediated Signaling Complex during Red Blood Cell Invasion by Plasmodium falciparum Merozoites. MBio, 2020, 11, .	4.1	13

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109	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
110	CRISPR activation screen in mice identifies novel membrane proteins enhancing pulmonary metastatic colonisation. <i>Communications Biology</i> , 2021, 4, 395.	4.4	12
111	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. <i>Journal of Proteome Research</i> , 2016, 15, 4686-4695.	3.7	11
112	Fast, Quantitative and Variant Enabled Mapping of Peptides to Genomes. <i>Cell Systems</i> , 2017, 5, 152-156.e4.	6.2	10
113	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
114	Inhibition of somatosensory mechanotransduction by annexin A6. <i>Science Signaling</i> , 2018, 11, .	3.6	10
115	Precision Medicine in Pancreatic Disease—Knowledge Gaps and Research Opportunities. <i>Pancreas</i> , 2019, 48, 1250-1258.	1.1	9
116	Using Deep Learning to Extrapolate Protein Expression Measurements. <i>Proteomics</i> , 2020, 20, e2000009.	2.2	9
117	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
118	Aneuploidy tolerance caused by BRG1 loss allows chromosome gains and recovery of fitness. <i>Nature Communications</i> , 2022, 13, 1731.	12.8	9
119	SimPLIT: Simplified Sample Preparation for Large-Scale Isobaric Tagging Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1842-1856.	3.7	9
120	Resolving Affinity Purified Protein Complexes by Blue Native PAGE and Protein Correlation Profiling. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	8
121	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
122	Scoring and Validation of Tandem MS Peptide Identification Methods. <i>Methods in Molecular Biology</i> , 2010, 604, 43-53.	0.9	7
123	EPEC-induced activation of the Ca ²⁺ transporter TRPV2 leads to pyroptotic cell death. <i>Molecular Microbiology</i> , 2022, 117, 480-492.	2.5	7
124	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
125	Coordinating cell cycle progression via cyclin specificity. <i>Cell Cycle</i> , 2011, 10, 4195-4196.	2.6	6
126	Proteomic navigation using proximity-labeling. <i>Methods</i> , 2019, 164-165, 67-72.	3.8	6

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127	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
128	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
129	Proteomic characterisation of triple negative breast cancer cells following CDK4/6 inhibition. <i>Scientific Data</i> , 2022, 9, .	5.3	4
130	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
131	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
132	<i>Citrobacter rodentium</i> 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
133	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
134	Identifying and characterising Thrap3, Bclaf1 and Erh interactions using cross-linking mass spectrometry. <i>Wellcome Open Research</i> , 0, 6, 260.	1.8	2
135	Chapter 4. PSM Scoring and Validation. <i>New Developments in Mass Spectrometry</i> , 2016, , 69-92.	0.2	1
136	Landscape of the <i>Plasmodium</i> Interactome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
137	Role of Eros, a novel transmembrane protein, in regulation of host defence. <i>Lancet</i> , The, 2016, 387, S12.	13.7	0
138	Molecular phenotyping of patient chondrocytes reveals genes and pathways involved in osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2017, 25, S209-S210.	1.3	0