Paula Meleady

List of Publications by Year
in descending order

86 papers	2,285 citations	201385 27 h-index	253896 43 g-index
86 all docs	86 docs citations	86 times ranked	2976 citing authors

#	Article	IF	Citations
1	Î±-1 Antitrypsin regulates human neutrophil chemotaxis induced by soluble immune complexes and IL-8. Journal of Clinical Investigation, 2010, 120, 4236-4250.	3.9	264
2	A neutrophil intrinsic impairment affecting Rab27a and degranulation in cystic fibrosis is corrected by CFTR potentiator therapy. Blood, 2014, 124, 999-1009.	0.6	138
3	Microarray and proteomics expression profiling identifies several candidates, including the valosinâ€containing protein (VCP), involved in regulating high cellular growth rate in production CHO cell lines. Biotechnology and Bioengineering, 2010, 106, 42-56.	1.7	72
4	Integrated miRNA, mRNA and protein expression analysis reveals the role of post-transcriptional regulation in controlling CHO cell growth rate. BMC Genomics, 2012, 13, 656.	1.2	70
5	Differential protein expression following low temperature culture of suspension CHO-K1 cells. BMC Biotechnology, 2008, 8, 42.	1.7	63
6	Identification of the metabolic alterations associated with the multidrug resistant phenotype in cancer and their intercellular transfer mediated by extracellular vesicles. Scientific Reports, 2017, 7, 44541.	1.6	61
7	Two-Dimensional Gel Electrophoresis and 2D-DIGE. Methods in Molecular Biology, 2018, 1664, 3-14.	0.4	61
8	Sustained productivity in recombinant Chinese Hamster Ovary (CHO) cell lines: proteome analysis of the molecular basis for a process-related phenotype. BMC Biotechnology, 2011, 11, 78.	1.7	59
9	Impact of miR-7 over-expression on the proteome of Chinese hamster ovary cells. Journal of Biotechnology, 2012, 160, 251-262.	1.9	56
10	Labelâ€free mass spectrometric analysis of the mdxâ€4cv diaphragm identifies the matricellular protein periostin as a potential factor involved in dystrophinopathyâ€related fibrosis. Proteomics, 2015, 15, 2318-2331.	1.3	51
11	Proteomic profiling of CHO cells with enhanced rhBMPâ€2 productivity following coâ€expression of PACEsol. Proteomics, 2008, 8, 2611-2624.	1.3	49
12	Multidrug resistant tumour cells shed more microvesicle-like EVs and less exosomes than their drug-sensitive counterpart cells. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 618-627.	1.1	47
13	Utilization and evaluation of CHOâ€specific sequence databases for mass spectrometry based proteomics. Biotechnology and Bioengineering, 2012, 109, 1386-1394.	1.7	46
14	Proteomic analysis of dystrophin deficiency and associated changes in the aged mdx-4cv heart model of dystrophinopathy-related cardiomyopathy. Journal of Proteomics, 2016, 145, 24-36.	1.2	46
15	Comparative Label-Free Mass Spectrometric Analysis of Mildly versus Severely Affected mdx Mouse Skeletal Muscles Identifies Annexin, Lamin, and Vimentin as Universal Dystrophic Markers. Molecules, 2015, 20, 11317-11344.	1.7	44
16	Reâ€programming CHO cell metabolism using miRâ€23 tips the balance towards a highly productive phenotype. Biotechnology Journal, 2015, 10, 1029-1040.	1.8	42
17	Simultaneous Pathoproteomic Evaluation of the Dystrophin-Glycoprotein Complex and Secondary Changes in the mdx-4cv Mouse Model of Duchenne Muscular Dystrophy. Biology, 2015, 4, 397-423.	1.3	37
18	Proteomic analysis of the sarcolemma-enriched fraction from dystrophic mdx-4cv skeletal muscle. Journal of Proteomics, 2019, 191, 212-227.	1.2	37

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19	Proteomic profiling of mdx-4cv serum reveals highly elevated levels of the inflammation-induced plasma marker haptoglobin in muscular dystrophy. International Journal of Molecular Medicine, 2017, 39, 1357-1370.	1.8	34
20	Proteomic profiling of the dystrophin complex and membrane fraction from dystrophic mdx muscle reveals decreases in the cytolinker desmoglein and increases in the extracellular matrix stabilizers biglycan and fibronectin. Journal of Muscle Research and Cell Motility, 2017, 38, 251-268.	0.9	34
21	Glycosylation Repurposes Alpha-1 Antitrypsin for Resolution of Community-acquired Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1346-1349.	2.5	33
22	Rapid charge variant analysis of monoclonal antibodies to support lead candidate biopharmaceutical development. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1095, 166-176.	1.2	32
23	Proteomic profiling of the mouse diaphragm and refined mass spectrometric analysis of the dystrophic phenotype. Journal of Muscle Research and Cell Motility, 2019, 40, 9-28.	0.9	32
24	Residual urinary extracellular vesicles in ultracentrifugation supernatants after hydrostatic filtration dialysis enrichment. Journal of Extracellular Vesicles, 2017, 6, 1267896.	5.5	30
25	Concurrent Label-Free Mass Spectrometric Analysis of Dystrophin Isoform Dp427 and the Myofibrosis Marker Collagen in Crude Extracts from mdx-4cv Skeletal Muscles. Proteomes, 2015, 3, 298-327.	1.7	29
26	Proteomic differences in recombinant CHO cells producing two similar antibody fragments. Biotechnology and Bioengineering, 2016, 113, 1902-1912.	1.7	29
27	Processâ€relevant concentrations of the leachable b<scp>D</scp>t<scp>BPP</scp> impact negatively on C<scp>HO</scp> cell production characteristics. Biotechnology Progress, 2016, 32, 1547-1558.	1.3	29
28	Filter-Aided Sample Preparation (FASP) for Improved Proteome Analysis of Recombinant Chinese Hamster Ovary Cells. Methods in Molecular Biology, 2017, 1603, 187-194.	0.4	29
29	Elevated levels of 14-3-3 proteins, serotonin, gamma enolase and pyruvate kinase identified in clinical samples from patients diagnosed with colorectal cancer. Clinica Chimica Acta, 2015, 441, 133-141.	0.5	28
30	Neutrophil Membrane Cholesterol Content is a Key Factor in Cystic Fibrosis Lung Disease. EBioMedicine, 2017, 23, 173-184.	2.7	28
31	Label-free mass spectrometric analysis reveals complex changes in the brain proteome from the mdx-4cv mouse model of Duchenne muscular dystrophy. Clinical Proteomics, 2015, 12, 27.	1.1	27
32	The iron-responsive microsomal proteome of Aspergillus fumigatus. Journal of Proteomics, 2016, 136, 99-111.	1.2	24
33	Proteomic profiling of liver tissue from the mdx-4cv mouse model of Duchenne muscular dystrophy. Clinical Proteomics, 2018, 15, 34.	1.1	24
34	Glycosylation patterns of kidney proteins differ in rat diabetic nephropathy. Kidney International, 2015, 87, 963-974.	2.6	23
35	Increased Outer Arm and Core Fucose Residues on the N-Glycans of Mutated Alpha-1 Antitrypsin Protein from Alpha-1 Antitrypsin Deficient Individuals. Journal of Proteome Research, 2014, 13, 596-605.	1.8	22
36	Label-free LC-MS analysis of HER2+ breast cancer cell line response to HER2 inhibitor treatment. DARU, Journal of Pharmaceutical Sciences, 2015, 23, 40.	0.9	21

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37	A Comparative Quantitative LC-MS/MS Profiling Analysis of Human Pancreatic Adenocarcinoma, Adjacent-Normal Tissue, and Patient-Derived Tumour Xenografts. Proteomes, 2018, 6, 45.	1.7	21
38	Proteome-wide Changes in the mdx-4cv Spleen due to Pathophysiological Cross Talk with Dystrophin-Deficient Skeletal Muscle. IScience, 2020, 23, 101500.	1.9	21
39	The Expression Pattern of the Phosphoproteome Is Significantly Changed During the Growth Phases of Recombinant CHO Cell Culture. Biotechnology Journal, 2018, 13, e1700221.	1.8	20
40	Circulating Truncated Alpha-1 Antitrypsin Glycoprotein in Patient Plasma Retains Anti-Inflammatory Capacity. Journal of Immunology, 2019, 202, 2240-2253.	0.4	20
41	Protocol for the Bottom-Up Proteomic Analysis of Mouse Spleen. STAR Protocols, 2020, 1, 100196.	0.5	20
42	Novel panel of protein biomarkers to predict response to bortezomib-containing induction regimens in multiple myeloma patients. BBA Clinical, 2017, 8, 28-34.	4.1	19
43	Proteomic and cell biological profiling of the renal phenotype of the mdx-4cv mouse model of Duchenne muscular dystrophy. European Journal of Cell Biology, 2020, 99, 151059.	1.6	19
44	Transferrin-bound proteins as potential biomarkers for advanced breast cancer patients. BBA Clinical, 2014, 2, 24-30.	4.1	18
45	Proteomics in uveal melanoma. Experimental Eye Research, 2014, 118, 1-12.	1.2	18
46	Metabolomic and proteomic analysis of breast cancer patient samples suggests that glutamate and 12-HETE in combination with CA15-3 may be useful biomarkers reflecting tumour burden. Metabolomics, 2015, 11, 620-635.	1.4	17
47	Differential Phosphoproteomic Analysis of Recombinant Chinese Hamster Ovary Cells Following Temperature Shift. Journal of Proteome Research, 2017, 16, 2339-2358.	1.8	17
48	Nanoparticle Biomolecular Corona-Based Enrichment of Plasma Glycoproteins for N-Glycan Profiling and Application in Biomarker Discovery. ACS Nano, 2022, 16, 5463-5475.	7.3	17
49	Parallel mRNA, proteomics and miRNA expression analysis in cell line models of the intestine. World Journal of Gastroenterology, 2017, 23, 7369-7386.	1.4	16
50	Purification and Identification of Membrane Proteins from Urinary Extracellular Vesicles using Triton X-114 Phase Partitioning. Journal of Proteome Research, 2018, 17, 86-96.	1.8	15
51	Proteogenomic Annotation of Chinese Hamsters Reveals Extensive Novel Translation Events and Endogenous Retroviral Elements. Journal of Proteome Research, 2019, 18, 2433-2445.	1.8	15
52	Mass Spectrometric Profiling of Extraocular Muscle and Proteomic Adaptations in the mdx-4cv Model of Duchenne Muscular Dystrophy. Life, 2021, 11, 595.	1.1	14
53	The emerging role of cellular post-translational modifications in modulating growth and productivity of recombinant Chinese hamster ovary cells. Biotechnology Advances, 2021, 49, 107757.	6.0	14
54	2D Gel Electrophoresis and Mass Spectrometry Identification and Analysis of Proteins. Methods in Molecular Biology, 2011, 784, 123-137.	0.4	14

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55	Zinc is a key regulator of gastrointestinal development, microbiota composition and inflammation with relevance for autism spectrum disorders. Cellular and Molecular Life Sciences, 2022, 79, 1.	2.4	14
56	Quantitative label-free mass spectrometry analysis of formalin-fixed, paraffin-embedded tissue representing the invasive cutaneous malignant melanoma proteome. Oncology Letters, 2016, 12, 3296-3304.	0.8	13
57	Transcriptomic analysis of IgG4 Fcâ€fusion protein degradation in a panel of clonallyâ€derived CHO cell lines using RNASeq. Biotechnology and Bioengineering, 2019, 116, 1556-1562.	1.7	13
58	Î±₁ Antitrypsin therapy modulates the neutrophil membrane proteome and secretome. European Respiratory Journal, 2020, 55, 1901678.	3.1	13
59	Intricate effects of primary motor neuronopathy on contractile proteins and metabolic muscle enzymes as revealed by label-free mass spectrometry. Bioscience Reports, 2014, 34, .	1.1	12
60	Depletion of endogenous miRNA-378-3p increases peak cell density of CHO DP12 cells and is correlated with elevated levels of ubiquitin carboxyl-terminal hydrolase 14. Journal of Biotechnology, 2018, 288, 30-40.	1.9	12
61	Increased mAb production in amplified CHO cell lines is associated with increased interaction of CREB1 with transgene promoter. Current Research in Biotechnology, 2019, 1, 49-57.	1.9	12
62	Increased growth rate and productivity following stable depletion of miR-7 in a mAb producing CHO cell line causes an increase in proteins associated with the Akt pathway and ribosome biogenesis. Journal of Proteomics, 2019, 195, 23-32.	1.2	12
63	Proteomic profiling of recombinant cells from large-scale mammalian cell culture processes. Cytotechnology, 2007, 53, 23-31.	0.7	11
64	Clonal variation in productivity and proteolytic clipping of an Fc-fusion protein in CHO cells: Proteomic analysis suggests a role for defective protein folding and the UPR. Journal of Biotechnology, 2018, 281, 21-30.	1.9	10
65	Data supporting the shedding of larger extracellular vesicles by multidrug resistant tumour cells. Data in Brief, 2016, 6, 1023-1027.	0.5	9
66	Improvements in singleâ€use bioreactor film material composition leads to robust and reliable Chinese hamster ovary cell performance. Biotechnology Progress, 2019, 35, e2824.	1.3	9
67	LC-MS/MS-based quantitative proteomic and phosphoproteomic analysis of CHO-K1 cells adapted to growth in glutamine-free media. Biotechnology Letters, 2020, 42, 2523-2536.	1.1	9
68	Proteomic strategies in the search for novel pancreatic cancer biomarkers and drug targets: recent advances and clinical impact. Expert Review of Proteomics, 2016, 13, 383-394.	1.3	7
69	Proteomic profiling of the interface between the stomach wall and the pancreas in dystrophinopathy. European Journal of Translational Myology, 2021, 31, .	0.8	7
70	Utilization of dried and long-term stored polyacrylamide gels for the advanced proteomic profiling of mitochondrial contact sites from rat liver. Biology Methods and Protocols, 2018, 3, bpy008.	1.0	6
71	Subproteomic profiling of sarcolemma from dystrophic mdx-4cv skeletal muscle. Data in Brief, 2018, 17, 980-993.	0.5	6
72	Proteomic analysis of pancreatic ductal adenocarcinoma. Expert Review of Proteomics, 2020, 17, 453-467.	1.3	5

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73	Copper toxicity of inflection point in human intestinal cell line Caco-2 dissected: influence of temporal expression patterns. In Vitro Cellular and Developmental Biology - Animal, 2021, 57, 359-371.	0.7	5
74	Phosphopeptide Enrichment and LC-MS/MS Analysis to Study the Phosphoproteome of Recombinant Chinese Hamster Ovary Cells. Methods in Molecular Biology, 2017, 1603, 195-208.	0.4	4
75	A proteomic profiling dataset of recombinant Chinese hamster ovary cells showing enhanced cellular growth following miR-378 depletion. Data in Brief, 2018, 21, 2679-2688.	0.5	4
76	Transfection of miR-31* boosts oxidative phosphorylation metabolism in the mitochondria and enhances recombinant protein production in Chinese hamster ovary cells. Journal of Biotechnology, 2021, 333, 86-96.	1.9	4
77	Mapping the molecular basis for growth related phenotypes in industrial producer CHO cell lines using differential proteomic analysis. BMC Biotechnology, 2021, 21, 43.	1.7	4
78	Global phosphoproteomic study of high/low specific productivity industrially relevant mAb producing recombinant CHO cell lines. Current Research in Biotechnology, 2021, 3, 49-56.	1.9	4
79	Clinical Proteomics: Liquid Chromatographyâ€“Mass Spectrometry (LCâ€“MS) Purification Systems. Methods in Molecular Biology, 2017, 1485, 375-388.	0.4	3
80	Dataset on the mass spectrometry-based proteomic profiling of the kidney from wild type and the dystrophic mdx-4cv mouse model of X-linked muscular dystrophy. Data in Brief, 2020, 28, 105067.	0.5	3
81	Differential expression of miRNAs and functional role of mir-200a in high and low productivity CHO cells expressing an Fc fusion protein. Biotechnology Letters, 2021, 43, 1551-1563.	1.1	3
82	Phosphoproteomic Analysis of Primary Myeloma Patient Samples Identifies Distinct Phosphorylation Signatures Correlating with Chemo-Sensitivity Profiles in an Ex Vivo Drug Sensitivity Testing Platform. Blood, 2021, 138, 2666-2666.	0.6	2
83	Characterisation and proteomic profiling of continuously exposed Cu-resistant variants of the Caco-2 cell line. Toxicology in Vitro, 2020, 65, 104773.	1.1	1
84	Methods to Study Translated Pseudogenes: Recombinant Expression and Complementation, Targeted Proteomics, and RNA Profiling. Methods in Molecular Biology, 2021, 2324, 239-254.	0.4	1
85	Characterisation of the Tumour Proteome in Primary Extramedullary Multiple Myeloma Identifies Key Proteins Associated with Transendothelial Migration. Blood, 2021, 138, 2665-2665.	0.6	1
86	LC-MS proteomic profiling of Caco-2 human intestinal cells exposed to the copper-chelating agent, triethylenetetramine: A preliminary study. Biochemical and Biophysical Research Communications, 2020, 524, 847-852.	1.0	0