Paula Meleady

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85 1,682 24 37 h-index g-index citations papers 86 1,996 4.5 4.77 L-index avg, IF ext. citations ext. papers

| # | Paper | IF | Citations |
|----|---|-------------------|-----------|
| 85 | El Antitrypsin regulates human neutrophil chemotaxis induced by soluble immune complexes and IL-8. <i>Journal of Clinical Investigation</i> , 2010 , 120, 4236-50 | 15.9 | 191 |
| 84 | A neutrophil intrinsic impairment affecting Rab27a and degranulation in cystic fibrosis is corrected by CFTR potentiator therapy. <i>Blood</i> , 2014 , 124, 999-1009 | 2.2 | 105 |
| 83 | Integrated miRNA, mRNA and protein expression analysis reveals the role of post-transcriptional regulation in controlling CHO cell growth rate. <i>BMC Genomics</i> , 2012 , 13, 656 | 4.5 | 68 |
| 82 | Microarray and proteomics expression profiling identifies several candidates, including the valosin-containing protein (VCP), involved in regulating high cellular growth rate in production CHO cell lines. <i>Biotechnology and Bioengineering</i> , 2010 , 106, 42-56 | 4.9 | 60 |
| 81 | Differential protein expression following low temperature culture of suspension CHO-K1 cells. <i>BMC Biotechnology</i> , 2008 , 8, 42 | 3.5 | 54 |
| 80 | Sustained productivity in recombinant Chinese hamster ovary (CHO) cell lines: proteome analysis of the molecular basis for a process-related phenotype. <i>BMC Biotechnology</i> , 2011 , 11, 78 | 3.5 | 53 |
| 79 | Impact of miR-7 over-expression on the proteome of Chinese hamster ovary cells. <i>Journal of Biotechnology</i> , 2012 , 160, 251-62 | 3.7 | 51 |
| 78 | Identification of the metabolic alterations associated with the multidrug resistant phenotype in cancer and their intercellular transfer mediated by extracellular vesicles. <i>Scientific Reports</i> , 2017 , 7, 445 | 541 ^{.9} | 47 |
| 77 | Proteomic profiling of CHO cells with enhanced rhBMP-2 productivity following co-expression of PACEsol. <i>Proteomics</i> , 2008 , 8, 2611-24 | 4.8 | 43 |
| 76 | Utilization and evaluation of CHO-specific sequence databases for mass spectrometry based proteomics. <i>Biotechnology and Bioengineering</i> , 2012 , 109, 1386-94 | 4.9 | 42 |
| 75 | Two-Dimensional Gel Electrophoresis and 2D-DIGE. <i>Methods in Molecular Biology</i> , 2018 , 1664, 3-14 | 1.4 | 38 |
| 74 | Multidrug resistant tumour cells shed more microvesicle-like EVs and less exosomes than their drug-sensitive counterpart cells. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016 , 1860, 618-27 | 4 | 38 |
| 73 | Label-free mass spectrometric analysis of the mdx-4cv diaphragm identifies the matricellular protein periostin as a potential factor involved in dystrophinopathy-related fibrosis. <i>Proteomics</i> , 2015 , 15, 2318-31 | 4.8 | 37 |
| 72 | Re-programming CHO cell metabolism using miR-23 tips the balance towards a highly productive phenotype. <i>Biotechnology Journal</i> , 2015 , 10, 1029-40 | 5.6 | 37 |
| 71 | Proteomic analysis of dystrophin deficiency and associated changes in the aged mdx-4cv heart model of dystrophinopathy-related cardiomyopathy. <i>Journal of Proteomics</i> , 2016 , 145, 24-36 | 3.9 | 34 |
| 70 | Comparative Label-Free Mass Spectrometric Analysis of Mildly versus Severely Affected mdx Mouse Skeletal Muscles Identifies Annexin, Lamin, and Vimentin as Universal Dystrophic Markers. <i>Molecules</i> , 2015 , 20, 11317-44 | 4.8 | 32 |
| 69 | Proteomic analysis of the sarcolemma-enriched fraction from dystrophic mdx-4cv skeletal muscle. <i>Journal of Proteomics</i> , 2019 , 191, 212-227 | 3.9 | 28 |

(2015-2015)

| 68 | Simultaneous Pathoproteomic Evaluation of the Dystrophin-Glycoprotein Complex and Secondary Changes in the mdx-4cv Mouse Model of Duchenne Muscular Dystrophy. <i>Biology</i> , 2015 , 4, 397-423 | 4.9 | 27 |
|----|---|------|----|
| 67 | Proteomic profiling of mdx-4cv serum reveals highly elevated levels of the inflammation-induced plasma marker haptoglobin in muscular dystrophy. <i>International Journal of Molecular Medicine</i> , 2017 , 39, 1357-1370 | 4.4 | 26 |
| 66 | Elevated levels of 14-3-3 proteins, serotonin, gamma enolase and pyruvate kinase identified in clinical samples from patients diagnosed with colorectal cancer. <i>Clinica Chimica Acta</i> , 2015 , 441, 133-41 | 6.2 | 26 |
| 65 | Glycosylation Repurposes Alpha-1 Antitrypsin for Resolution of Community-acquired Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 197, 1346-1349 | 10.2 | 26 |
| 64 | Concurrent Label-Free Mass Spectrometric Analysis of Dystrophin Isoform Dp427 and the Myofibrosis Marker Collagen in Crude Extracts from Skeletal Muscles. <i>Proteomes</i> , 2015 , 3, 298-327 | 4.6 | 25 |
| 63 | 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. <i>Journal of Muscle Research and Cell Motility</i> , 2017 , 38, 251-268 | 3.5 | 24 |
| 62 | Process-relevant concentrations of the leachable bDtBPP impact negatively on CHO cell production characteristics. <i>Biotechnology Progress</i> , 2016 , 32, 1547-1558 | 2.8 | 24 |
| 61 | Proteomic differences in recombinant CHO cells producing two similar antibody fragments. <i>Biotechnology and Bioengineering</i> , 2016 , 113, 1902-12 | 4.9 | 22 |
| 60 | Glycosylation patterns of kidney proteins differ in rat diabetic nephropathy. <i>Kidney International</i> , 2015 , 87, 963-74 | 9.9 | 21 |
| 59 | Rapid charge variant analysis of monoclonal antibodies to support lead candidate biopharmaceutical development. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018 , 1095, 166-176 | 3.2 | 20 |
| 58 | Increased outer arm and core fucose residues on the N-glycans of mutated alpha-1 antitrypsin protein from alpha-1 antitrypsin deficient individuals. <i>Journal of Proteome Research</i> , 2014 , 13, 596-605 | 5.6 | 20 |
| 57 | Neutrophil Membrane Cholesterol Content is a Key Factor in Cystic Fibrosis Lung Disease. <i>EBioMedicine</i> , 2017 , 23, 173-184 | 8.8 | 20 |
| 56 | Residual urinary extracellular vesicles in ultracentrifugation supernatants after hydrostatic filtration dialysis enrichment. <i>Journal of Extracellular Vesicles</i> , 2017 , 6, 1267896 | 16.4 | 20 |
| 55 | The iron-responsive microsomal proteome of Aspergillus fumigatus. <i>Journal of Proteomics</i> , 2016 , 136, 99-111 | 3.9 | 19 |
| 54 | Label-free mass spectrometric analysis reveals complex changes in the brain proteome from the mdx-4cv mouse model of Duchenne muscular dystrophy. <i>Clinical Proteomics</i> , 2015 , 12, 27 | 5 | 18 |
| 53 | Filter-Aided Sample Preparation (FASP) for Improved Proteome Analysis of Recombinant Chinese Hamster Ovary Cells. <i>Methods in Molecular Biology</i> , 2017 , 1603, 187-194 | 1.4 | 17 |
| 52 | Proteomic profiling of the mouse diaphragm and refined mass spectrometric analysis of the dystrophic phenotype. <i>Journal of Muscle Research and Cell Motility</i> , 2019 , 40, 9-28 | 3.5 | 17 |
| 51 | Label-free LC-MS analysis of HER2+ breast cancer cell line response to HER2 inhibitor treatment. <i>DARU, Journal of Pharmaceutical Sciences</i> , 2015 , 23, 40 | 3.9 | 16 |

| 50 | The Expression Pattern of the Phosphoproteome Is Significantly Changed During the Growth Phases of Recombinant CHO Cell Culture. <i>Biotechnology Journal</i> , 2018 , 13, e1700221 | 5.6 | 15 |
|----|---|-----|----|
| 49 | Transferrin-bound proteins as potential biomarkers for advanced breast cancer patients. <i>BBA Clinical</i> , 2014 , 2, 24-30 | | 15 |
| 48 | Proteomics in uveal melanoma. Experimental Eye Research, 2014, 118, 1-12 | 3.7 | 15 |
| 47 | A Comparative Quantitative LC-MS/MS Profiling Analysis of Human Pancreatic Adenocarcinoma, Adjacent-Normal Tissue, and Patient-Derived Tumour Xenografts. <i>Proteomes</i> , 2018 , 6, | 4.6 | 15 |
| 46 | Proteomic profiling of liver tissue from the - mouse model of Duchenne muscular dystrophy. <i>Clinical Proteomics</i> , 2018 , 15, 34 | 5 | 15 |
| 45 | Differential Phosphoproteomic Analysis of Recombinant Chinese Hamster Ovary Cells Following Temperature Shift. <i>Journal of Proteome Research</i> , 2017 , 16, 2339-2358 | 5.6 | 14 |
| 44 | Circulating Truncated Alpha-1 Antitrypsin Glycoprotein in Patient Plasma Retains Anti-Inflammatory Capacity. <i>Journal of Immunology</i> , 2019 , 202, 2240-2253 | 5.3 | 14 |
| 43 | 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. <i>Metabolomics</i> , 2015 , 11, 620-635 | 4.7 | 14 |
| 42 | Proteogenomic Annotation of Chinese Hamsters Reveals Extensive Novel Translation Events and Endogenous Retroviral Elements. <i>Journal of Proteome Research</i> , 2019 , 18, 2433-2445 | 5.6 | 12 |
| 41 | Novel panel of protein biomarkers to predict response to bortezomib-containing induction regimens in multiple myeloma patients. <i>BBA Clinical</i> , 2017 , 8, 28-34 | | 12 |
| 40 | Parallel mRNA, proteomics and miRNA expression analysis in cell line models of the intestine. <i>World Journal of Gastroenterology</i> , 2017 , 23, 7369-7386 | 5.6 | 12 |
| 39 | 2D gel electrophoresis and mass spectrometry identification and analysis of proteins. <i>Methods in Molecular Biology</i> , 2011 , 784, 123-37 | 1.4 | 11 |
| 38 | Proteomic and cell biological profiling of the renal phenotype of the mdx-4cv mouse model of Duchenne muscular dystrophy. <i>European Journal of Cell Biology</i> , 2020 , 99, 151059 | 6.1 | 11 |
| 37 | Purification and Identification of Membrane Proteins from Urinary Extracellular Vesicles using Triton X-114 Phase Partitioning. <i>Journal of Proteome Research</i> , 2018 , 17, 86-96 | 5.6 | 10 |
| 36 | Proteome-wide Changes in the mdx-4cv Spleen due to Pathophysiological Cross Talk with Dystrophin-Deficient Skeletal Muscle. <i>IScience</i> , 2020 , 23, 101500 | 6.1 | 10 |
| 35 | 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. <i>Journal of Proteomics</i> , 2019 , 195, 23-32 | 3.9 | 9 |
| 34 | Intricate effects of primary motor neuronopathy on contractile proteins and metabolic muscle enzymes as revealed by label-free mass spectrometry. <i>Bioscience Reports</i> , 2014 , 34, | 4.1 | 9 |
| 33 | Proteomic profiling of recombinant cells from large-scale mammalian cell culture processes. <i>Cytotechnology</i> , 2007 , 53, 23-31 | 2.2 | 9 |

| 32 | Protocol for the Bottom-Up Proteomic Analysis of Mouse Spleen. STAR Protocols, 2020, 1, 100196 | 1.4 | 9 |
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| 31 | Quantitative label-free mass spectrometry analysis of formalin-fixed, paraffin-embedded tissue representing the invasive cutaneous malignant melanoma proteome. <i>Oncology Letters</i> , 2016 , 12, 3296-3 | 364 | 9 |
| 30 | 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. <i>Journal of Biotechnology</i> , 2018 , 288, 30-40 | 3.7 | 9 |
| 29 | Proteomic strategies in the search for novel pancreatic cancer biomarkers and drug targets: recent advances and clinical impact. <i>Expert Review of Proteomics</i> , 2016 , 13, 383-94 | 4.2 | 7 |
| 28 | Data supporting the shedding of larger extracellular vesicles by multidrug resistant tumour cells. <i>Data in Brief</i> , 2016 , 6, 1023-7 | 1.2 | 7 |
| 27 | Antitrypsin therapy modulates the neutrophil membrane proteome and secretome. <i>European Respiratory Journal</i> , 2020 , 55, | 13.6 | 7 |
| 26 | Transcriptomic analysis of IgG4 Fc-fusion protein degradation in a panel of clonally-derived CHO cell lines using RNASeq. <i>Biotechnology and Bioengineering</i> , 2019 , 116, 1556-1562 | 4.9 | 6 |
| 25 | 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. <i>Journal of Biotechnology</i> , 2018 , 281, 21-30 | 3.7 | 6 |
| 24 | Improvements in single-use bioreactor film material composition leads to robust and reliable Chinese hamster ovary cell performance. <i>Biotechnology Progress</i> , 2019 , 35, e2824 | 2.8 | 5 |
| 23 | Increased mAb production in amplified CHO cell lines is associated with increased interaction of CREB1 with transgene promoter. <i>Current Research in Biotechnology</i> , 2019 , 1, 49-57 | 4.8 | 4 |
| 22 | LC-MS/MS-based quantitative proteomic and phosphoproteomic analysis of CHO-K1 cells adapted to growth in glutamine-free media. <i>Biotechnology Letters</i> , 2020 , 42, 2523-2536 | 3 | 4 |
| 21 | Subproteomic profiling of sarcolemma from dystrophic skeletal muscle. <i>Data in Brief</i> , 2018 , 17, 980-993 | 1.2 | 4 |
| 20 | Utilization of dried and long-term stored polyacrylamide gels for the advanced proteomic profiling of mitochondrial contact sites from rat liver. <i>Biology Methods and Protocols</i> , 2018 , 3, bpy008 | 2.4 | 4 |
| 19 | Zinc is a key regulator of gastrointestinal development, microbiota composition and inflammation with relevance for autism spectrum disorders <i>Cellular and Molecular Life Sciences</i> , 2021 , 79, 1 | 10.3 | 4 |
| 18 | Phosphopeptide Enrichment and LC-MS/MS Analysis to Study the Phosphoproteome of Recombinant Chinese Hamster Ovary Cells. <i>Methods in Molecular Biology</i> , 2017 , 1603, 195-208 | 1.4 | 3 |
| 17 | Proteomic analysis of pancreatic ductal adenocarcinoma. Expert Review of Proteomics, 2020, 17, 453-46 | 74.2 | 3 |
| 16 | Transfection of miR-31* boosts oxidative phosphorylation metabolism in the mitochondria and enhances recombinant protein production in Chinese hamster ovary cells. <i>Journal of Biotechnology</i> , 2021 , 333, 86-96 | 3.7 | 3 |
| 15 | Mass Spectrometric Profiling of Extraocular Muscle and Proteomic Adaptations in the Model of Duchenne Muscular Dystrophy. <i>Life</i> , 2021 , 11, | 3 | 3 |

| 14 | A proteomic profiling dataset of recombinant Chinese hamster ovary cells showing enhanced cellular growth following miR-378 depletion. <i>Data in Brief</i> , 2018 , 21, 2679-2688 | 1.2 | 3 |
|----|--|------|---|
| 13 | Clinical Proteomics: Liquid Chromatography-Mass Spectrometry (LC-MS) Purification Systems. <i>Methods in Molecular Biology</i> , 2017 , 1485, 375-388 | 1.4 | 2 |
| 12 | Copper toxicity of inflection point in human intestinal cell line Caco-2 dissected: influence of temporal expression patterns. <i>In Vitro Cellular and Developmental Biology - Animal</i> , 2021 , 57, 359-371 | 2.6 | 2 |
| 11 | Proteomic profiling of the interface between the stomach wall and the pancreas in dystrophinopathy. <i>European Journal of Translational Myology</i> , 2021 , 31, | 2.1 | 2 |
| 10 | Global phosphoproteomic study of high/low specific productivity industrially relevant mAb producing recombinant CHO cell lines. <i>Current Research in Biotechnology</i> , 2021 , 3, 49-56 | 4.8 | 2 |
| 9 | Dataset on the mass spectrometry-based proteomic profiling of the kidney from wild type and the dystrophic mouse model of X-linked muscular dystrophy. <i>Data in Brief</i> , 2020 , 28, 105067 | 1.2 | 1 |
| 8 | Characterisation and proteomic profiling of continuously exposed Cu-resistant variants of the Caco-2 cell line. <i>Toxicology in Vitro</i> , 2020 , 65, 104773 | 3.6 | 1 |
| 7 | Differential expression of miRNAs and functional role of mir-200a in high and low productivity CHO cells expressing an Fc fusion protein. <i>Biotechnology Letters</i> , 2021 , 43, 1551-1563 | 3 | 1 |
| 6 | The emerging role of cellular post-translational modifications in modulating growth and productivity of recombinant Chinese hamster ovary cells. <i>Biotechnology Advances</i> , 2021 , 49, 107757 | 17.8 | 1 |
| 5 | Mapping the molecular basis for growth related phenotypes in industrial producer CHO cell lines using differential proteomic analysis. <i>BMC Biotechnology</i> , 2021 , 21, 43 | 3.5 | 1 |
| 4 | LC-MS proteomic profiling of Caco-2 human intestinal cells exposed to the copper-chelating agent, triethylenetetramine: A preliminary study. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 524, 847-852 | 3.4 | |
| 3 | Characterisation of the Tumour Proteome in Primary Extramedullary Multiple Myeloma Identifies Key Proteins Associated with Transendothelial Migration. <i>Blood</i> , 2021 , 138, 2665-2665 | 2.2 | |
| 2 | Phosphoproteomic Analysis of Primary Myeloma Patient Samples Identifies Distinct Phosphorylation Signatures Correlating with Chemo-Sensitivity Profiles in an Ex Vivo Drug Sensitivity Testing Platform. <i>Blood</i> , 2021 , 138, 2666-2666 | 2.2 | |
| 1 | Methods to Study Translated Pseudogenes: Recombinant Expression and Complementation, Targeted Proteomics, and RNA Profiling. <i>Methods in Molecular Biology</i> , 2021 , 2324, 239-254 | 1.4 | |