

Caroline A Evans

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

3,355
citations

201674

27
h-index

144013

57
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79
all docs

79
docs citations

79
times ranked

5380
citing authors

#	ARTICLE	IF	CITATIONS
1	Metastasising Fibroblasts Show an HDAC6-Dependent Increase in Migration Speed and Loss of Directionality Linked to Major Changes in the Vimentin Interactome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1961.	4.1	6
2	Quantitative proteomic comparison of salt stress in <i>Chlamydomonas reinhardtii</i> and the snow alga <i>Chlamydomonas nivalis</i> reveals mechanisms for salt-triggered fatty acid accumulation via reallocation of carbon resources. <i>Biotechnology for Biofuels</i> , 2021, 14, 121.	6.2	20
3	Colorectal keratins: Integrating nutrition, metabolism and colorectal health. <i>Seminars in Cell and Developmental Biology</i> , 2021, , .	5.0	4
4	Oral delivery of a functional algal-expressed TGF- β 2 mimic halts colitis in a murine DSS model. <i>Journal of Biotechnology</i> , 2021, 340, 1-12.	3.8	15
5	Seminal fluid protein divergence among populations exhibiting postmating prezygotic reproductive isolation. <i>Molecular Ecology</i> , 2020, 29, 4428-4441.	3.9	12
6	Phosphopeptide enrichment for phosphoproteomic analysis - A tutorial and review of novel materials. <i>Analytica Chimica Acta</i> , 2020, 1129, 158-180.	5.4	41
7	Accelerated directed evolution of dye-decolorizing peroxidase using a bacterial extracellular protein secretion system (BENNY). <i>Bioresources and Bioprocessing</i> , 2019, 6, 20.	4.2	21
8	CyanoFactory, a European consortium to develop technologies needed to advance cyanobacteria as chassis for production of chemicals and fuels. <i>Algal Research</i> , 2019, 41, 101510.	4.6	24
9	Engineering Pathways in Central Carbon Metabolism Help to Increase Glycan Production and Improve N-Type Glycosylation of Recombinant Proteins in <i>E. coli</i> . <i>Bioengineering</i> , 2019, 6, 27.	3.5	10
10	Reducing Complexity? Cysteine Reduction and S-Alkylation in Proteomic Workflows: Practical Considerations. <i>Methods in Molecular Biology</i> , 2019, 1977, 83-97.	0.9	2
11	Application of Proteomics to Inflammatory Bowel Disease Research: Current Status and Future Perspectives. <i>Gastroenterology Research and Practice</i> , 2019, 2019, 1-24.	1.5	20
12	Application of the broadband collision-induced dissociation (bbCID) mass spectrometry approach for protein glycosylation and phosphorylation analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 75-85.	1.5	13
13	Proteomic identification and characterization of hepatic glyoxalase 1 dysregulation in non-alcoholic fatty liver disease. <i>Proteome Science</i> , 2018, 16, 4.	1.7	20
14	A prospective, proteomics study identified potential biomarkers of encapsulating peritoneal sclerosis in peritoneal effluent. <i>Kidney International</i> , 2017, 92, 988-1002.	5.2	24
15	Quantitative definition and monitoring of the host cell protein proteome using iTRAQ "a study of an industrial mAb producing CHO" cell line. <i>Biotechnology Journal</i> , 2016, 11, 1014-1024.	3.5	29
16	Quantitative proteomic analysis of the influence of lignin on biofuel production by <i>Clostridium acetobutylicum</i> ATCC 824. <i>Biotechnology for Biofuels</i> , 2016, 9, 113.	6.2	21
17	Su1897 Keratin 8 Expression Is Reduced in Active Ulcerative Colitis Relative to Proximal Inactive Mucosa. <i>Gastroenterology</i> , 2015, 148, S-547.	1.3	0
18	Quantitative proteomic analysis reveals maturation as a mechanism underlying glucocorticoid resistance in B lineage ALL and re-sensitization by JNK inhibition. <i>British Journal of Haematology</i> , 2015, 171, 595-605.	2.5	15

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19	Reduced keratin expression in colorectal neoplasia and associated fields is reversible by diet and resection. <i>BMJ Open Gastroenterology</i> , 2015, 2, e000022.	2.7	6
20	Inflammation decreases keratin level in ulcerative colitis; inadequate restoration associates with increased risk of colitis-associated cancer. <i>BMJ Open Gastroenterology</i> , 2015, 2, e000024.	2.7	22
21	Differential proteomes of the cyanobacterium <i>Cyanothece</i> sp. CCY 0110 upon exposure to heavy metals. <i>Data in Brief</i> , 2015, 4, 152-158.	1.0	3
22	Quantitation with chemical tagging reagents in biomarker studies. <i>Proteomics - Clinical Applications</i> , 2015, 9, 295-300.	1.6	33
23	Effects of heavy metals on <i>Cyanothece</i> sp. CCY 0110 growth, extracellular polymeric substances (EPS) production, ultrastructure and protein profiles. <i>Journal of Proteomics</i> , 2015, 120, 75-94.	2.4	95
24	Advances in proteomics for production strain analysis. <i>Current Opinion in Biotechnology</i> , 2015, 35, 111-117.	6.6	7
25	Are proteins a redundant ontology? Epistemological limitations in the analysis of multistate species. <i>Molecular BioSystems</i> , 2014, 10, 1228-1235.	2.9	2
26	Making Sense Out of the Proteome: the Utility of iTRAQ and TMT. <i>New Developments in Mass Spectrometry</i> , 2014, , 49-79.	0.2	1
27	Promotion of cancer metastasis: candidate validation using an iTRAQ-based approach. <i>Expert Review of Proteomics</i> , 2013, 10, 321-323.	3.0	2
28	Quantitative proteomics analysis of BMS-214662 effects on CD34 positive cells from chronic myeloid leukaemia patients. <i>Proteomics</i> , 2013, 13, 153-168.	2.2	6
29	Application of the MIDAS Approach for Analysis of Lysine Acetylation Sites. <i>Methods in Molecular Biology</i> , 2013, 981, 25-36.	0.9	6
30	Application of the CIRAD Mass Spectrometry Approach for Lysine Acetylation Site Discovery. <i>Methods in Molecular Biology</i> , 2013, 981, 13-23.	0.9	5
31	Application of High Content Biology to Yield Quantitative Spatial Proteomic Information on Protein Acetylations. <i>Methods in Molecular Biology</i> , 2013, 981, 37-45.	0.9	5
32	Modelling of metabolic control by Short Chain Fatty Acids at the level of the functional proteome – a systems biology model of SCFA metabolism. <i>Proceedings of the Nutrition Society</i> , 2013, 72, .	1.0	0
33	An insight into iTRAQ: where do we stand now?. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1011-1027.	3.7	293
34	Keratins in colorectal epithelial function and disease. <i>International Journal of Experimental Pathology</i> , 2012, 93, 305-318.	1.3	42
35	Proteomic analysis of the impact of static culturing on the expansion of rat bone marrow mesenchymal stem cells. <i>Biotechnology Letters</i> , 2012, 34, 1589-1596.	2.2	4
36	Tu1311 Quantitative Proteomics in Ulcerative Colitis Reveals Mucosal Inflammation Reduces Levels of Keratins in the Insoluble Fraction of the Intermediate Filament Proteome. <i>Gastroenterology</i> , 2012, 142, S-799-S-800.	1.3	1

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37	A proteomic analysis of differential cellular responses to the short-chain fatty acids butyrate, valerate and propionate in colon epithelial cancer cells. <i>Molecular BioSystems</i> , 2012, 8, 1146-1156.	2.9	21
38	Mo1592 Quantitative Proteomic Analysis of Intermediate Filament Profile in Ulcerative Colitis Reveals Increased Levels of Keratins 8, 18 and 19 in Patients With Longstanding Pan Colitis Which are Reduced With Development of Dysplasia. <i>Gastroenterology</i> , 2012, 142, S-636.	1.3	0
39	iTRAQ Identification of Candidate Serum Biomarkers Associated with Metastatic Progression of Human Prostate Cancer. <i>PLoS ONE</i> , 2012, 7, e30885.	2.5	56
40	An integrated workflow for extraction and solubilization of intermediate filaments from colorectal biopsies for proteomic analysis. <i>Electrophoresis</i> , 2012, 33, 1967-1974.	2.4	4
41	Evaluation of the salivary proteome as a surrogate tissue for systems biology approaches to understanding appetite. <i>Journal of Proteomics</i> , 2012, 75, 2916-2923.	2.4	9
42	Abstract 1371: Delineating the function of single VEGF isoforms using both proteomic and molecular approaches. , 2012, , .		0
43	Methods in Quantitative Proteomics: Setting iTRAQ on the Right Track. <i>Current Proteomics</i> , 2011, 8, 17-30.	0.3	42
44	Minimising iTRAQ ratio compression through understanding LC-MS elution dependence and high-resolution HILIC fractionation. <i>Proteomics</i> , 2011, 11, 2341-2346.	2.2	112
45	Assessing the Loss of Information through Application of the "Two-hit Rule"™ in iTRAQ Datasets. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	0
46	Quantitative Proteomic Analysis Reveals Maturation As a Mechanism Underlying Glucocorticoid Resistance in Childhood Acute Lymphoblastic Leukemia and PAX5 As a Re-Sensitising Therapeutic Target. <i>Blood</i> , 2011, 118, 1411-1411.	1.4	0
47	Eightplex iTRAQ analysis of variant metastatic human prostate cancer cells identifies candidate biomarkers of progression: An exploratory study. <i>Prostate</i> , 2010, 70, 1313-1332.	2.3	46
48	Balancing robust quantification and identification for iTRAQ: Application of UHR-TOF MS. <i>Proteomics</i> , 2010, 10, 2205-2213.	2.2	28
49	Assessment of downstream effectors of BCR/ABL protein tyrosine kinase using combined proteomic approaches. <i>Proteomics</i> , 2010, 10, 3321-3342.	2.2	17
50	Nuclear Proteome Dynamics in Differentiating Embryonic Carcinoma (NTERA-2) Cells. <i>Journal of Proteome Research</i> , 2010, 9, 3412-3426.	3.7	9
51	A study protocol to investigate the relationship between dietary fibre intake and fermentation, colon cell turnover, global protein acetylation and early carcinogenesis: the FACT study. <i>BMC Cancer</i> , 2009, 9, 332.	2.6	22
52	Prostate cancer proteomics: The urgent need for clinically validated biomarkers. <i>Proteomics - Clinical Applications</i> , 2009, 3, 197-212.	1.6	9
53	iTRAQ Underestimation in Simple and Complex Mixtures: "The Good, the Bad and the Ugly". <i>Journal of Proteome Research</i> , 2009, 8, 5347-5355.	3.7	469
54	Quantitative Proteomic Analysis Implicates An Altered B-Cell Differentiation State as a Mechanism Underlying GC-Resistance in An Acute Lymphoblastic Leukaemia (ALL) Cell Line Model.. <i>Blood</i> , 2009, 114, 1736-1736.	1.4	7

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55	Proteomic analyses of intermediate filaments reveals cytokeratin8 is highly acetylated â€“ implications for colorectal epithelial homeostasis. <i>Proteomics</i> , 2008, 8, 279-288.	2.2	31
56	Eight-channel iTRAQ Enables Comparison of the Activity of Six Leukemogenic Tyrosine Kinases. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 853-863.	3.8	224
57	The application of a hypothesis-driven strategy to the sensitive detection and location of acetylated lysine residues. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 1423-1428.	2.8	29
58	Quantitative proteomics reveals posttranslational control as a regulatory factor in primary hematopoietic stem cells. <i>Blood</i> , 2006, 107, 4687-4694.	1.4	162
59	Guanidination chemistry for qualitative and quantitative proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 3245-3256.	1.5	37
60	Relative quantification in proteomics: new approaches for biochemistry. <i>Trends in Biochemical Sciences</i> , 2006, 31, 473-484.	7.5	54
61	A proteomic analysis of murine bone marrow and its response to ionizing radiation. <i>Proteomics</i> , 2005, 5, 4254-4263.	2.2	34
62	Application of Two-Dimensional Difference Gel Electrophoresis to Studying Bone Marrow Macrophages and Their in Vivo Responses to Ionizing Radiation. <i>Journal of Proteome Research</i> , 2005, 4, 1371-1380.	3.7	24
63	Activation of protein kinase A (PKA) by 8-Cl-cAMP as a novel approach for antileukaemic therapy. <i>British Journal of Cancer</i> , 2004, 91, 186-192.	6.4	18
64	PEDRo: A database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004, 5, 68.	2.8	58
65	A small proportion of mesenchymal stem cells strongly expresses functionally active CXCR4 receptor capable of promoting migration to bone marrow. <i>Blood</i> , 2004, 104, 2643-2645.	1.4	700
66	Comparative proteomics of primitive hematopoietic cell populations reveals differences in expression of proteins regulating motility. <i>Blood</i> , 2004, 103, 3751-3759.	1.4	63
67	The potential for proteomic definition of stem cell populations. <i>Experimental Hematology</i> , 2003, 31, 1147-1159.	0.4	49
68	Proteomic Analysis of Chronic Lymphocytic Leukemia Subtypes with Mutated or Unmutated Ig VH Genes. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1331-1341.	3.8	32
69	Changes in the Proteome Associated with the Action of Bcr-Abl Tyrosine Kinase Are Not Related to Transcriptional Regulation. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 876-884.	3.8	28
70	Identification of primary structural features that define the differential actions of IL-3 and GM-CSF receptors. <i>Blood</i> , 2002, 100, 3164-3174.	1.4	23
71	Activation of Granulocyte-Macrophage Colony-Stimulating Factor and Interleukin-3 Receptor Subunits in a Multipotential Hematopoietic Progenitor Cell Line Leads to Differential Effects on Development. <i>Blood</i> , 1999, 94, 1504-1514.	1.4	34
72	Activation of Granulocyte-Macrophage Colony-Stimulating Factor and Interleukin-3 Receptor Subunits in a Multipotential Hematopoietic Progenitor Cell Line Leads to Differential Effects on Development. <i>Blood</i> , 1999, 94, 1504-1514.	1.4	6

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73	Cytokine-mediated protein kinase C activation is a signal for lineage determination in bipotential granulocyte macrophage colony-forming cells.. Journal of Cell Biology, 1994, 125, 651-659.	5.2	57
74	Cellular signalling events stimulated by myeloid haemopoietic growth factors. Best Practice and Research: Clinical Haematology, 1992, 5, 653-679.	1.1	3