

Caroline A Evans

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

3,355
citations

201658

27
h-index

144002

57
g-index

79
all docs

79
docs citations

79
times ranked

5380
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	An insight into iTRAQ: where do we stand now?. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1011-1027.	3.7	293
4	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
5	Quantitative proteomics reveals posttranslational control as a regulatory factor in primary hematopoietic stem cells. <i>Blood</i> , 2006, 107, 4687-4694.	1.4	162
6	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
7	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
8	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
9	PEDRo: A database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004, 5, 68.	2.8	58
10	Cytokine-mediated protein kinase C activation is a signal for lineage determination in bipotential granulocyte macrophage colony-forming cells.. <i>Journal of Cell Biology</i> , 1994, 125, 651-659.	5.2	57
11	iTRAQ Identification of Candidate Serum Biomarkers Associated with Metastatic Progression of Human Prostate Cancer. <i>PLoS ONE</i> , 2012, 7, e30885.	2.5	56
12	Relative quantification in proteomics: new approaches for biochemistry. <i>Trends in Biochemical Sciences</i> , 2006, 31, 473-484.	7.5	54
13	The potential for proteomic definition of stem cell populations. <i>Experimental Hematology</i> , 2003, 31, 1147-1159.	0.4	49
14	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
15	Methods in Quantitative Proteomics: Setting iTRAQ on the Right Track. <i>Current Proteomics</i> , 2011, 8, 17-30.	0.3	42
16	Keratins in colorectal epithelial function and disease. <i>International Journal of Experimental Pathology</i> , 2012, 93, 305-318.	1.3	42
17	Phosphopeptide enrichment for phosphoproteomic analysis - A tutorial and review of novel materials. <i>Analitica Chimica Acta</i> , 2020, 1129, 158-180.	5.4	41
18	Guanidination chemistry for qualitative and quantitative proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 3245-3256.	1.5	37

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19	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
20	A proteomic analysis of murine bone marrow and its response to ionizing radiation. <i>Proteomics</i> , 2005, 5, 4254-4263.	2.2	34
21	Quantitation with chemical tagging reagents in biomarker studies. <i>Proteomics - Clinical Applications</i> , 2015, 9, 295-300.	1.6	33
22	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
23	Proteomic analyses of intermediate filaments reveals cytookeratin8 is highly acetylated – implications for colorectal epithelial homeostasis. <i>Proteomics</i> , 2008, 8, 279-288.	2.2	31
24	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
25	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
26	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
27	Balancing robust quantification and identification for iTRAQ: Application of UHR-TOF MS. <i>Proteomics</i> , 2010, 10, 2205-2213.	2.2	28
28	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
29	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
30	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
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	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
39	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
40	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
41	Assessment of downstream effectors of BCR/ABL protein tyrosine kinase using combined proteomic approaches. <i>Proteomics</i> , 2010, 10, 3321-3342.	2.2	17
42	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
43	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
44	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
45	Seminal fluid protein divergence among populations exhibiting postmating prezygotic reproductive isolation. <i>Molecular Ecology</i> , 2020, 29, 4428-4441.	3.9	12
46	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
47	Prostate cancer proteomics: The urgent need for clinically validated biomarkers. <i>Proteomics - Clinical Applications</i> , 2009, 3, 197-212.	1.6	9
48	Nuclear Proteome Dynamics in Differentiating Embryonic Carcinoma (NTERA-2) Cells. <i>Journal of Proteome Research</i> , 2010, 9, 3412-3426.	3.7	9
49	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
50	Advances in proteomics for production strain analysis. <i>Current Opinion in Biotechnology</i> , 2015, 35, 111-117.	6.6	7
51	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
52	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
53	Application of the MIDAS Approach for Analysis of Lysine Acetylation Sites. <i>Methods in Molecular Biology</i> , 2013, 981, 25-36.	0.9	6
54	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

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55	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
56	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
57	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
58	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
59	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
60	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
61	Colorectal keratins: Integrating nutrition, metabolism and colorectal health. <i>Seminars in Cell and Developmental Biology</i> , 2021, , .	5.0	4
62	Cellular signalling events stimulated by myeloid haemopoietic growth factors. <i>Best Practice and Research: Clinical Haematology</i> , 1992, 5, 653-679.	1.1	3
63	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
64	Promotion of cancer metastasis: candidate validation using an iTRAQ-based approach. <i>Expert Review of Proteomics</i> , 2013, 10, 321-323.	3.0	2
65	Are proteins a redundant ontology? Epistemological limitations in the analysis of multistate species. <i>Molecular BioSystems</i> , 2014, 10, 1228-1235.	2.9	2
66	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
67	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
68	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
69	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
70	Modelling of metabolic control by Short Chain Fatty Acids at the level of the functional proteome â€“ II: <i>systems biology model of SCFA metabolism</i>. <i>Proceedings of the Nutrition Society</i> , 2013, 72, .	1.0	0
71	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
72	Assessing the Loss of Information through Application of the â€“Two-hit Ruleâ€™ in iTRAQ Datasets. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	0

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73	Quantitative Proteomic Analysis Reveals Maturation As a Mechanism Underlying Glucocorticoid Resistance in Childhood Acute Lymphoblastic Leukemia and PAX5 As a Re-Sensitising Therapeutic Target. Blood, 2011, 118, 1411-1411.	1.4	0
74	Abstract 1371: Delineating the function of single VEGF isoforms using both proteomic and molecular approaches. , 2012, , .		0