Astrid Slany

List of Publications by Year in descending order

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ASTRID SLANV

#	Article	IF	CITATIONS
1	Cell Characterization by Proteome Profiling Applied to Primary Hepatocytes and Hepatocyte Cell Lines Hep-G2 and Hep-3B. Journal of Proteome Research, 2010, 9, 6-21.	3.7	88
2	Proteomics and transcriptomics of peripheral nerve tissue and cells unravel new aspects of the human Schwann cell repair phenotype. Glia, 2016, 64, 2133-2153.	4.9	77
3	Proteome profiling in IL-1Î ² and VEGF-activated human umbilical vein endothelial cells delineates the interlink between inflammation and angiogenesis. PLoS ONE, 2017, 12, e0179065.	2.5	64
4	Proteomics and metabolomics identify molecular mechanisms of aging potentially predisposing for chronic lymphocytic leukemia. Molecular and Cellular Proteomics, 2018, 17, 290-303.	3.8	62
5	Entering a New Era of Rational Biomarker Discovery for Early Detection of Melanoma Metastases: Secretome Analysis of Associated Stroma Cells. Journal of Proteome Research, 2009, 8, 2501-2510.	3.7	51
6	Comprehensive Assessment of Proteins Regulated by Dexamethasone Reveals Novel Effects in Primary Human Peripheral Blood Mononuclear Cells. Journal of Proteome Research, 2014, 13, 5989-6000.	3.7	50
7	Multi-omics Analysis of Serum Samples Demonstrates Reprogramming of Organ Functions Via Systemic Calcium Mobilization and Platelet Activation in Metastatic Melanoma. Molecular and Cellular Proteomics, 2017, 16, 86-99.	3.8	50
8	Proteome Maps of the Main Human Peripheral Blood Constituents. Journal of Proteome Research, 2009, 8, 3834-3843.	3.7	49
9	Cytoplasmic Proteome and Secretome Profiles of Differently Stimulated Human Dendritic Cells. Journal of Proteome Research, 2009, 8, 2799-2811.	3.7	48
10	Extracellular Matrix Remodeling by Bone Marrow Fibroblast-like Cells Correlates with Disease Progression in Multiple Myeloma. Journal of Proteome Research, 2014, 13, 844-854.	3.7	46
11	Proteome signatures of inflammatory activated primary human peripheral blood mononuclear cells. Journal of Proteomics, 2012, 76, 150-162.	2.4	43
12	Contribution of Human Fibroblasts and Endothelial Cells to the Hallmarks of Inflammation as Determined by Proteome Profiling. Molecular and Cellular Proteomics, 2016, 15, 1982-1997.	3.8	41
13	Neutrophil Extracellular Trap Formation Correlates with Favorable Overall Survival in High Grade Ovarian Cancer. Cancers, 2020, 12, 505.	3.7	37
14	Proteome Profiling of Breast Cancer Biopsies Reveals a Wound Healing Signature of Cancer-Associated Fibroblasts. Journal of Proteome Research, 2014, 13, 4773-4782.	3.7	35
15	Combined Proteome and Eicosanoid Profiling Approach for Revealing Implications of Human Fibroblasts in Chronic Inflammation. Analytical Chemistry, 2017, 89, 1945-1954.	6.5	33
16	Introducing a new parameter for quality control of proteome profiles: Consideration of commonly expressed proteins. Electrophoresis, 2009, 30, 1306-1328.	2.4	31
17	Metabolic, Anti-apoptotic and Immune Evasion Strategies of Primary Human Myeloma Cells Indicate Adaptations to Hypoxia*. Molecular and Cellular Proteomics, 2019, 18, 936-953.	3.8	30
18	Finger sweat analysis enables short interval metabolic biomonitoring in humans. Nature Communications, 2021, 12, 5993.	12.8	28

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19	Plasticity of fibroblasts demonstrated by tissue-specific and function-related proteome profiling. Clinical Proteomics, 2014, 11, 41.	2.1	25
20	Introducing the CPL/MUW proteome database: Interpretation of human liver and liver cancer proteome profiles by referring to isolated primary cells. Electrophoresis, 2009, 30, 2076-2089.	2.4	24
21	Targeting breast cancer-associated fibroblasts to improve anti-cancer therapy. Breast, 2015, 24, 532-538.	2.2	21
22	Myofibroblasts are important contributors to human hepatocellular carcinoma: Evidence for tumor promotion by proteome profiling. Electrophoresis, 2013, 34, 3315-3325.	2.4	19
23	Proteome Analysis Reveals Distinct Mitochondrial Functions Linked to Interferon Response Patterns in Activated CD4+ and CD8+ T Cells. Frontiers in Pharmacology, 2019, 10, 727.	3.5	19
24	Determination of cell typeâ€specific proteome signatures of primary human leukocytes, endothelial cells, keratinocytes, hepatocytes, fibroblasts and melanocytes by comparative proteome profiling. Electrophoresis, 2014, 35, 1428-1438.	2.4	16
25	Curcumin exerts its antitumor effects in a context dependent fashion. Journal of Proteomics, 2018, 182, 65-72.	2.4	16
26	Quantification of cytokines secreted by primary human cells using multiple reaction monitoring: evaluation of analytical parameters. Analytical and Bioanalytical Chemistry, 2015, 407, 6525-6536.	3.7	15
27	Membrane disruption, but not metabolic rewiring, is the key mechanism of anticancer-action of FASN-inhibitors: a multi-omics analysis in ovarian cancer. Scientific Reports, 2020, 10, 14877.	3.3	13
28	EGF Induces Migration Independent of EMT or Invasion in A549 Lung Adenocarcinoma Cells. Frontiers in Cell and Developmental Biology, 2021, 9, 634371.	3.7	13
29	Consequences of Acute and Chronic Oxidative Stress upon the Expression Pattern of Proteins in Peripheral Blood Mononuclear Cells. Journal of Proteome Research, 2008, 7, 5138-5147.	3.7	12
30	Evaluation of inflammation-related signaling events covering phosphorylation and nuclear translocation of proteins based on mass spectrometry data. Journal of Proteomics, 2017, 152, 161-171.	2.4	9
31	A Cellular Proteome Map of Human Multiple Myeloma Blood, 2007, 110, 111-111.	1.4	1
32	Secretome Analyses of Primary Bone Marrow Fibroblasts Isolated From MGUS and Multiple Myeloma Show a Stepwise Occurrence of Alterations Blood, 2009, 114, 1801-1801.	1.4	0
33	Metabolic Reprogramming of Mesenchymal Stem Cells upon Co-Cultivation with Primary CLL Cells Determined By Mass Spectrometry-Based Proteomics. Blood, 2016, 128, 5560-5560.	1.4	0