

Jiri Petrak

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,119
citations

257101

24
h-index

233125

45
g-index

55
all docs

55
docs citations

55
times ranked

3419
citing authors

#	ARTICLE	IF	CITATIONS
1	DÃ©jÃ© vu in proteomics. A hit parade of repeatedly identified differentially expressed proteins. <i>Proteomics</i> , 2008, 8, 1744-1749.	1.3	337
2	Ribosomal protein S17 gene (RPS17) is mutated in Diamond-Blackfan anemia. <i>Human Mutation</i> , 2007, 28, 1178-1182.	1.1	203
3	Myocardial iron content and mitochondrial function in human heart failure: a direct tissue analysis. <i>European Journal of Heart Failure</i> , 2017, 19, 522-530.	2.9	180
4	Hepcidin, the hormone of iron metabolism, is bound specifically to Î±-2-macroglobulin in blood. <i>Blood</i> , 2009, 113, 6225-6236.	0.6	111
5	Identification of mutations in the ribosomal protein L5 (RPL5) and ribosomal protein L11 (RPL11) genes in Czech patients with Diamond-Blackfan anemia. <i>Human Mutation</i> , 2009, 30, 321-327.	1.1	91
6	Hepcidin: A direct link between iron metabolism and immunity. <i>International Journal of Biochemistry and Cell Biology</i> , 2005, 37, 1768-1773.	1.2	83
7	Integral membrane proteins in proteomics. How to break open the black box?. <i>Journal of Proteomics</i> , 2017, 153, 8-20.	1.2	77
8	Hephaestinâ€™s ferroxidase of cellular iron export. <i>International Journal of Biochemistry and Cell Biology</i> , 2005, 37, 1173-1178.	1.2	74
9	A novel iron responsive element in the 3â€™UTR of human MRCKÎ±. <i>Biochemical and Biophysical Research Communications</i> , 2006, 341, 158-166.	1.0	62
10	Translational efficiency in patients with Diamond-Blackfan anemia. <i>Haematologica</i> , 2006, 91, 1456-64.	1.7	58
11	Prion Protein Modulates Cellular Iron Uptake: A Novel Function with Implications for Prion Disease Pathogenesis. <i>PLoS ONE</i> , 2009, 4, e4468.	1.1	52
12	Effect of metformin therapy on cardiac function and survival in a volume-overload model of heart failure in rats. <i>Clinical Science</i> , 2011, 121, 29-41.	1.8	50
13	Metabolic characterization of volume overload heart failure due to aorto-caval fistula in rats. <i>Molecular and Cellular Biochemistry</i> , 2011, 354, 83-96.	1.4	50
14	Skeletal Muscle Abnormalities and Iron Deficiency in Chronic Heart Failure. <i>Circulation: Heart Failure</i> , 2018, 11, e004800.	1.6	44
15	Therapeutic potential of hepcidin â€™ the master regulator of iron metabolism. <i>Pharmacological Research</i> , 2017, 115, 242-254.	3.1	40
16	Proteomic and transcriptomic analysis of heart failure due to volume overload in a rat aorto-caval fistula model provides support for new potential therapeutic targets - monoamine oxidase A and transglutaminase 2. <i>Proteome Science</i> , 2011, 9, 69.	0.7	39
17	Decreased concentrations of retinol-binding protein 4 in sera of epithelial ovarian cancer patients: A potential biomarker identified by proteomics. <i>Oncology Reports</i> , 2011, 27, 318-24.	1.2	35
18	Native proteomic analysis of protein complexes in murine intestinal brush border membranes. <i>Proteomics</i> , 2007, 7, 121-129.	1.3	33

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19	Proteomic analysis of hepatic iron overload in mice suggests dysregulation of urea cycle, impairment of fatty acid oxidation, and changes in the methylation cycle. <i>American Journal of Physiology - Renal Physiology</i> , 2007, 292, G1490-G1498.	1.6	32
20	Identification of heme binding protein complexes in murine erythroleukemic cells: Study by a novel two-dimensional native separation - liquid chromatography and electrophoresis. <i>Proteomics</i> , 2005, 5, 340-350.	1.3	30
21	Downregulation of deoxycytidine kinase in cytarabine-resistant mantle cell lymphoma cells confers cross-resistance to nucleoside analogs gemcitabine, fludarabine and cladribine, but not to other classes of anti-lymphoma agents. <i>Molecular Cancer</i> , 2014, 13, 159.	7.9	30
22	Myocardial Morphological Characteristics and Proarrhythmic Substrate in the Rat Model of Heart Failure Due to Chronic Volume Overload. <i>Anatomical Record</i> , 2011, 294, 102-111.	0.8	29
23	Affinity depletion versus relative protein enrichment: a side-by-side comparison of two major strategies for increasing human cerebrospinal fluid proteome coverage. <i>Clinical Proteomics</i> , 2019, 16, 9.	1.1	27
24	Human MRCK β is regulated by cellular iron levels and interferes with transferrin iron uptake. <i>Biochemical and Biophysical Research Communications</i> , 2010, 395, 163-167.	1.0	26
25	Iron transport in K562 cells: a kinetic study using native gel electrophoresis and ^{59}Fe autoradiography. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 1998, 1403, 179-188.	1.9	25
26	Proteomic analysis of iron overload in human hepatoma cells. <i>American Journal of Physiology - Renal Physiology</i> , 2006, 290, G1059-G1066.	1.6	25
27	Kidney Response to Heart Failure; Proteomic Analysis of Cardiorenal Syndrome. <i>Kidney and Blood Pressure Research</i> , 2018, 43, 1437-1450.	0.9	25
28	Changes in Myocardial Composition and Conduction Properties in Rat Heart Failure Model Induced by Chronic Volume Overload. <i>Frontiers in Physiology</i> , 2016, 7, 367.	1.3	23
29	An activating mutation of GNB1 is associated with resistance to tyrosine kinase inhibitors in ETV6-ABL1-positive leukemia. <i>Oncogene</i> , 2017, 36, 5985-5994.	2.6	21
30	Right versus left ventricular remodeling in heart failure due to chronic volume overload. <i>Scientific Reports</i> , 2021, 11, 17136.	1.6	21
31	Myocardial iron homeostasis and hepcidin expression in a rat model of heart failure at different levels of dietary iron intake. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 703-713.	1.1	20
32	Incorporation of iron into <i>Tritrichomonas foetus</i> cell compartments reveals ferredoxin as a major iron-binding protein in hydrogenosomes. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1911-1921.	0.7	19
33	Detection of iron-containing proteins contributing to the cellular labile iron pool by a native electrophoresis metal blotting technique. <i>Journal of Inorganic Biochemistry</i> , 2001, 86, 669-675.	1.5	17
34	Separation of cellular iron containing compounds by electrophoresis. <i>Biological Trace Element Research</i> , 1998, 61, 263-275.	1.9	15
35	Exosomes released by imatinib-resistant K562 cells contain specific membrane markers, IFITM3, CD146 and CD36 and increase the survival of imatinib-sensitive cells in the presence of imatinib. <i>International Journal of Oncology</i> , 2020, 58, 238-250.	1.4	14
36	Iron-independent specific protein expression pattern in the liver of HFE-deficient mice. <i>International Journal of Biochemistry and Cell Biology</i> , 2007, 39, 1006-1015.	1.2	12

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37	Large-scale identification of membrane proteins based on analysis of trypsin-protected transmembrane segments. <i>Journal of Proteomics</i> , 2016, 149, 15-22.	1.2	12
38	Detection and quantitation of iron in ferritin, transferrin and labile iron pool (LIP) in cardiomyocytes using ⁵⁵ Fe and storage phosphorimaging. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2895-2901.	1.1	12
39	Detailed Functional and Proteomic Characterization of Fludarabine Resistance in Mantle Cell Lymphoma Cells. <i>PLoS ONE</i> , 2015, 10, e0135314.	1.1	9
40	Proteomic analysis of erythroid differentiation induced by hexamethylene bisacetamide in murine erythroleukemia cells. <i>Experimental Hematology</i> , 2007, 35, 193-202.	0.2	7
41	Proteomic analysis of imatinib-resistant CML-T1 cells reveals calcium homeostasis as a potential therapeutic target. <i>Oncology Reports</i> , 2016, 36, 1258-1268.	1.2	7
42	Identification of molecular targets for selective elimination of TRAIL-resistant leukemia cells. From spots to <i>in vitro</i> assays using TOP15 charts. <i>Proteomics</i> , 2009, 9, 5006-5015.	1.3	6
43	Resistance to TRAIL in mantle cell lymphoma cells is associated with the decreased expression of purine metabolism enzymes. <i>International Journal of Molecular Medicine</i> , 2013, 31, 1273-1279.	1.8	6
44	Quantitative proteomic analysis of cerebrospinal fluid of women newly diagnosed with multiple sclerosis. <i>International Journal of Neuroscience</i> , 2022, 132, 724-734.	0.8	6
45	Identification of differentially expressed proteins using automated meta-analysis of proteomic articles. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2009, 3, 10-16.	0.2	4
46	Deep Membrane Proteome Profiling Reveals Overexpression of Prostate-Specific Membrane Antigen (PSMA) in High-Risk Human Paraganglioma and Pheochromocytoma, Suggesting New Theranostic Opportunity. <i>Molecules</i> , 2021, 26, 6567.	1.7	4
47	Detection and Quantitation of ⁵⁹ Fe-Labeled Proteins Using Storage Phosphorimaging. <i>Analytical Biochemistry</i> , 1998, 260, 103-106.	1.1	3
48	Tyrosine 87 is vital for the activity of human protein arginine methyltransferase 3 (PRMT3). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 277-282.	1.1	3
49	Nutritional hepatic iron overload is not prevented by parenteral hepcidin substitution therapy in mice. <i>British Journal of Nutrition</i> , 2012, 108, 1723-1725.	1.2	3
50	A three-pronged "Pitchfork" strategy enables an extensive description of the human membrane proteome and the identification of missing proteins. <i>Journal of Proteomics</i> , 2019, 204, 103411.	1.2	3
51	Native electrophoretic separation and femtomolar detection of ⁶⁵ Zn-containing proteins by storage phosphorimaging. <i>Journal of Proteomics</i> , 2003, 57, 177-182.	2.4	2
52	Flow Cytometry Analysis of Blood Large Extracellular Vesicles in Patients with Multiple Sclerosis Experiencing Relapse of the Disease. <i>Journal of Clinical Medicine</i> , 2022, 11, 2832.	1.0	2
53	Proteomic and mRNA Expression Chip Analysis of Acquired TRAIL-Resistance in Human HL60 Myeloid Leukemia Cells. <i>Blood</i> , 2007, 110, 4155-4155.	0.6	0
54	Multilevel Molecular Profiling to Dissect Resistance to Tyrosine Kinase Inhibitors in TEL/ABL Positive Acute Lymphoblastic Leukemia. <i>Blood</i> , 2014, 124, 3637-3637.	0.6	0

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55	GNB1 K89M Drives TKI Resistance in ETV6-ABL1-Positive Leukemia. Blood, 2016, 128, 751-751.	0.6	0