## Tymon Rubel

List of Publications by Year in descending order

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TVMON PUBEL

#	Article	IF	CITATIONS
1	ApoE4 disrupts interaction of sortilin with fatty acid-binding protein 7 essential to promote lipid signaling. Journal of Cell Science, 2021, 134, .	2.0	11
2	The interactome of multifunctional HAX1 protein suggests its role in the regulation of energy metabolism, de-aggregation, cytoskeleton organization and RNA-processing. Bioscience Reports, 2020, 40, .	2.4	10
3	HAX1 impact on collective cell migration, cell adhesion, and cell shape is linked to the regulation of actomyosin contractility. Molecular Biology of the Cell, 2019, 30, 3024-3036.	2.1	13
4	Mass Spectrometry-Based Comprehensive Analysis of Pancreatic Cyst Fluids. BioMed Research International, 2018, 2018, 1-12.	1.9	9
5	Limited prolonged effects of rifaximin treatment on irritable bowel syndrome-related differences in the fecal microbiome and metabolome. Gut Microbes, 2016, 7, 397-413.	9.8	68
6	Histone H1 Variants in Arabidopsis Are Subject to Numerous Post-Translational Modifications, Both Conserved and Previously Unknown in Histones, Suggesting Complex Functions of H1 in Plants. PLoS ONE, 2016, 11, e0147908.	2.5	36
7	Beads-free protein immunoprecipitation for a mass spectrometry-based interactome and posttranslational modifications analysis. Proteome Science, 2015, 13, 23.	1.7	14
8	The Novel Gene CRNDE Encodes a Nuclear Peptide (CRNDEP) Which Is Overexpressed in Highly Proliferating Tissues. PLoS ONE, 2015, 10, e0127475.	2.5	40
9	The putative oncogene, <i>CRNDE,</i> is a negative prognostic factor in ovarian cancer patients. Oncotarget, 2015, 6, 43897-43910.	1.8	51
10	jChIP: a graphical environment for exploratory ChIP-Seq data analysis. BMC Research Notes, 2014, 7, 676.	1.4	2
11	Urine proteomes of healthy aging humans reveal extracellular matrix (ECM) alterations and immune system dysfunction. Age, 2014, 36, 299-311.	3.0	35
12	Mitochondrial-related proteomic changes during obesity and fasting in mice are greater in the liver than skeletal muscles. Functional and Integrative Genomics, 2014, 14, 245-259.	3.5	25
13	Histone H3 lysine 27 acetylation is altered in colon cancer. Clinical Proteomics, 2014, 11, 24.	2.1	72
14	Pre-analytical-related variability influencing serum peptide profiles demonstrated in a mass spectrometry-based search for colorectal and prostate cancer biomarkers Acta Biochimica Polonica, 2013, 60, .	0.5	11
15	Pre-analytical-related variability influencing serum peptide profiles demonstrated in a mass spectrometry-based search for colorectal and prostate cancer biomarkers. Acta Biochimica Polonica, 2013, 60, 417-25.	0.5	8
16	Diffprot — software for non-parametric statistical analysis of differential proteomics data. Journal of Proteomics, 2012, 75, 4062-4073.	2.4	59
17	Comparative kinome analysis to identify putative colon tumor biomarkers. Journal of Molecular Medicine, 2012, 90, 447-456.	3.9	34
18	Neural Network-Based Method for Peptide Identification in Proteomics. Lecture Notes in Computer Science, 2012, , 437-444.	1.3	1

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19	Integrating proteomic and transcriptomic high-throughput surveys for search of new biomarkers of colon tumors. Functional and Integrative Genomics, 2011, 11, 215-224.	3.5	97
20	Application of Density Based Clustering to Microarray Data Analysis. International Journal of Electronics and Telecommunications, 2010, 56, 281-286.	0.5	8
21	Halogenated imidazole derivatives block RNA polymerase II elongation along mitogen inducible genes. BMC Molecular Biology, 2010, 11, 4.	3.0	7
22	Comprehensive Analysis of the Palindromic Motif TCTCGCGAGA: A Regulatory Element of the HNRNPK Promoter. DNA Research, 2010, 17, 245-260.	3.4	39
23	Modeling Oncogenic Signaling in Colon Tumors by Multidirectional Analyses of Microarray Data Directed for Maximization of Analytical Reliability. PLoS ONE, 2010, 5, e13091.	2.5	320
24	Functional features of gene expression profiles differentiating gastrointestinal stromal tumours according to KITmutations and expression. BMC Cancer, 2009, 9, 413.	2.6	21
25	Yeast prion [PSI] lowers the levels of mitochondrial prohibitins. Biochimica Et Biophysica Acta - Molecular Cell Research, 2009, 1793, 1703-1709.	4.1	8
26	An integrated LCâ€ESIâ€MS platform for quantitation of serum peptide ladders. Application for colon carcinoma study. Proteomics - Clinical Applications, 2009, 3, 932-946.	1.6	45
27	Molecular defense mechanisms of Barrett's metaplasia estimated by an integrative genomics. Journal of Molecular Medicine, 2007, 85, 733-743.	3.9	44
28	Landscape of the hnRNP K protein–protein interactome. Proteomics, 2006, 6, 2395-2406.	2.2	69
29	Casein kinases phosphorylate multiple residues spanning the entire hnRNP K length. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 299-306.	2.3	12
30	Three clinical variants of gastroesophageal reflux disease form two distinct gene expression signatures. Journal of Molecular Medicine, 2006, 84, 872-882.	3.9	11