

Alexandre Zougman

List of Publications by Year in descending order

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36
papers

10,046
citations

318942

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406436

35
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39
all docs

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docs citations

39
times ranked

20782
citing authors

#	ARTICLE	IF	CITATIONS
1	Detergent-Free Simultaneous Sample Preparation Method for Proteomics and Metabolomics. Journal of Proteome Research, 2020, 19, 2838-2844.	1.8	16
2	A simple serum depletion method for proteomics analysis. BioTechniques, 2020, 69, 148-151.	0.8	5
3	Dysregulation at multiple points of the kynurenine pathway is a ubiquitous feature of renal cancer: implications for tumour immune evasion. British Journal of Cancer, 2020, 123, 137-147.	2.9	17
4	Growth Factor-like Gene Regulation Is Separable from Survival and Maturation in Antibody-Secreting Cells. Journal of Immunology, 2019, 202, 1287-1300.	0.4	11
5	Cellular Barcoding Identifies Clonal Substitution as a Hallmark of Local Recurrence in a Surgical Model of Head and Neck Squamous Cell Carcinoma. Cell Reports, 2018, 25, 2208-2222.e7.	2.9	30
6	Network Analysis Identifies Proinflammatory Plasma Cell Polarization for Secretion of ISG15 in Human Autoimmunity. Journal of Immunology, 2016, 197, 1447-1459.	0.4	52
7	C-STrap Sample Preparation Method In-Situ Cysteinyl Peptide Capture for Bottom-Up Proteomics Analysis in the STrap Format. PLoS ONE, 2015, 10, e0138775.	1.1	11
8	Suspension trapping (STrap) sample preparation method for bottom-up proteomics analysis. Proteomics, 2014, 14, 1006-1000.	1.3	280
9	Role of miR-26b in carcinoma-associated fibroblasts and effect on migration and invasion of breast cancer epithelial cells. Lancet, The, 2014, 383, S103.	6.3	1
10	Retinoic acid-induced protein 3: Identification and characterisation of a novel prognostic colon cancer biomarker. European Journal of Cancer, 2013, 49, 531-539.	1.3	39
11	Serum aminoacylase-1 is a novel biomarker with potential prognostic utility for long-term outcome in patients with delayed graft function following renal transplantation. Kidney International, 2013, 84, 1214-1225.	2.6	47
12	Predicting Response to Bevacizumab in Ovarian Cancer: A Panel of Potential Biomarkers Informing Treatment Selection. Clinical Cancer Research, 2013, 19, 5227-5239.	3.2	63
13	MiR-26b is down-regulated in carcinoma-associated fibroblasts from ER-positive breast cancers leading to enhanced cell migration and invasion. Journal of Pathology, 2013, 231, 388-399.	2.1	103
14	Proteomic analysis of formalin-fixed paraffin-embedded renal tissue samples by label-free MS: Assessment of overall technical variability and the impact of block age. Proteomics - Clinical Applications, 2013, 7, 273-282.	0.8	45
15	A systematic analysis of the effects of increasing degrees of serum immunodepletion in terms of depth of coverage and other key aspects in top-down and bottom-up proteomic analyses. Proteomics, 2011, 11, 2222-2235.	1.3	64
16	Identification and characterization of a novel ubiquitous nucleolar protein NARR™ encoded by a gene overlapping the rab34 oncogene. Nucleic Acids Research, 2011, 39, 7103-7113.	6.5	10
17	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. Journal of Proteome Research, 2010, 9, 3280-3289.	1.8	253
18	Immunohistochemical and Proteomic Evaluation of Nuclear Ubiquitous Casein and Cyclin-Dependent Kinases Substrate in Invasive Ductal Carcinoma of the Breast. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-8.	3.0	31

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19	Identification of novel neuropeptides in the ventral nerve cord ganglia and their targets in an annelid worm, <i>Eisenia fetida</i> . Journal of Comparative Neurology, 2009, 514, 415-432.	0.9	14
20	Identification of novel neuropeptides in the ventral nerve cord ganglia and their targets in an annelid worm, <i>Eisenia fetida</i> . Journal of Comparative Neurology, 2009, 514, spc1-spc1.	0.9	0
21	Identification of novel neuropeptides in the ventral nerve cord ganglia and their targets in an annelid worm, <i>Eisenia fetida</i> . Journal of Comparative Neurology, 2009, 514, spc1-spc1.	0.9	0
22	Universal sample preparation method for proteome analysis. Nature Methods, 2009, 6, 359-362.	9.0	6,678
23	Mapping of Lysine Monomethylation of Linker Histones in Human Breast and Its Cancer. Journal of Proteome Research, 2009, 8, 4207-4215.	1.8	24
24	Combination of FASP and StageTip-Based Fractionation Allows In-Depth Analysis of the Hippocampal Membrane Proteome. Journal of Proteome Research, 2009, 8, 5674-5678.	1.8	507
25	Constitutive and dynamic phosphorylation and acetylation sites on NUCKS, a hypermodified nuclear protein, studied by quantitative proteomics. Proteins: Structure, Function and Bioinformatics, 2008, 73, 710-718.	1.5	43
26	Integrated Analysis of the Cerebrospinal Fluid Peptidome and Proteome. Journal of Proteome Research, 2008, 7, 386-399.	1.8	162
27	Evidence for Insertional RNA Editing in Humans. Current Biology, 2008, 18, 1760-1765.	1.8	12
28	N ^ε -Formylation of lysine is a widespread post-translational modification of nuclear proteins occurring at residues involved in regulation of chromatin function. Nucleic Acids Research, 2008, 36, 570-577.	6.5	152
29	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. Nucleic Acids Research, 2007, 35, D771-D779.	6.5	69
30	Mass Spectrometric Mapping of Linker Histone H1 Variants Reveals Multiple Acetylations, Methylations, and Phosphorylation as Well as Differences between Cell Culture and Tissue. Molecular and Cellular Proteomics, 2007, 6, 72-87.	2.5	205
31	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. Journal of Proteome Research, 2007, 6, 2963-2972.	1.8	83
32	A Proteomic Screen for Presynaptic Terminal N-type Calcium Channel (Ca _v 2.2) Binding Partners. BMB Reports, 2007, 40, 302-314.	1.1	45
33	Beyond Linker Histones and High Mobility Group Proteins: A Global Profiling of Perchloric Acid Soluble Proteins. Journal of Proteome Research, 2006, 5, 925-934.	1.8	19
34	Proteomic, Functional, and Domain-Based Analysis of In Vivo 14-3-3 Binding Proteins Involved in Cytoskeletal Regulation and Cellular Organization. Current Biology, 2004, 14, 1436-1450.	1.8	412
35	Production and characterization of bioactive peptides from soy hydrolysate and soy-fermented food. Food Research International, 2004, 37, 123-131.	2.9	339
36	RAM: A Conserved Signaling Network That Regulates Ace2p Transcriptional Activity and Polarized Morphogenesis. Molecular Biology of the Cell, 2003, 14, 3782-3803.	0.9	203