

Amina A Qutub

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

2,018
citations

304368

22
h-index

253896

43
g-index

69
all docs

69
docs citations

69
times ranked

3544
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical relevance of proteomic profiling in de novo pediatric acute myeloid leukemia: a Children's Oncology Group study. <i>Haematologica</i> , 2022, , .	1.7	7
2	cytoNet: Spatiotemporal network analysis of cell communities. <i>PLoS Computational Biology</i> , 2022, 18, e1009846.	1.5	3
3	Integrins and extracellular matrix proteins modulate adipocyte thermogenic capacity. <i>Scientific Reports</i> , 2021, 11, 5442.	1.6	23
4	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 705627.	1.3	7
5	Differential proteome profile, biological pathways, and network relationships of osteogenic proteins in calcified human aortic valves. <i>Heart and Vessels</i> , 2021, , 1.	0.5	2
6	A novel self-organizing embryonic stem cell system reveals signaling logic underlying the patterning of human ectoderm. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	44
7	Image-based Classification of Tumor Type and Growth Rate using Machine Learning: a preclinical study. <i>Scientific Reports</i> , 2019, 9, 12529.	1.6	32
8	Proteomic Profiling of Acute Promyelocytic Leukemia Identifies Two Protein Signatures Associated with Relapse. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800133.	0.8	7
9	LGALS3 is connected to CD74 in a previously unknown protein network that is associated with poor survival in patients with AML. <i>EBioMedicine</i> , 2019, 44, 126-137.	2.7	14
10	A quantitative analysis of heterogeneities and hallmarks in acute myelogenous leukaemia. <i>Nature Biomedical Engineering</i> , 2019, 3, 889-901.	11.6	27
11	Proteomic Landscape of Acute Leukemia: A Comparison between ALL and AML in Adults. <i>Blood</i> , 2019, 134, 1461-1461.	0.6	0
12	Histone Modification Patterns Using RPPA-Based Profiling Predict Outcome in Acute Myeloid Leukemia Patients. <i>Proteomics</i> , 2018, 18, e1700379.	1.3	11
13	Recognition of Recurrent Protein Expression Patterns in Pediatric Acute Myeloid Leukemia Identified New Therapeutic Targets. <i>Molecular Cancer Research</i> , 2018, 16, 1275-1286.	1.5	16
14	Recurrent Patterns of Protein Expression Signatures in Pediatric Acute Lymphoblastic Leukemia: Recognition and Therapeutic Guidance. <i>Molecular Cancer Research</i> , 2018, 16, 1263-1274.	1.5	12
15	Mycoplasma contamination of leukemic cell lines alters protein expression determined by reverse phase protein arrays. <i>Cytotechnology</i> , 2018, 70, 1529-1535.	0.7	7
16	Proteomics in Acute Myeloid Leukemia. , 2018, , .		1
17	Advances in Glioblastoma Multiforme Treatment: New Models for Nanoparticle Therapy. <i>Frontiers in Physiology</i> , 2018, 9, 170.	1.3	110
18	Shrinkage Clustering: a fast and size-constrained clustering algorithm for biomedical applications. <i>BMC Bioinformatics</i> , 2018, 19, 19.	1.2	27

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19	Shining a light on cell signaling in leukemia through proteomics: relevance for the clinic. <i>Expert Review of Proteomics</i> , 2018, 15, 613-622.	1.3	3
20	Classification of brain tumors using texture based analysis of T1-post contrast MR scans in a preclinical model. , 2018, , .		0
21	IDENTIFYING CANCER SPECIFIC METABOLIC SIGNATURES USING CONSTRAINT-BASED MODELS. , 2017, 22, 485-496.		4
22	GAIN: A graphical method to automatically analyze individual neurite outgrowth. <i>Journal of Neuroscience Methods</i> , 2017, 283, 62-71.	1.3	6
23	Evolutionâ€informed modeling improves outcome prediction for cancers. <i>Evolutionary Applications</i> , 2017, 10, 68-76.	1.5	13
24	p53 pathway dysfunction is highly prevalent in acute myeloid leukemia independent of TP53 mutational status. <i>Leukemia</i> , 2017, 31, 1296-1305.	3.3	87
25	Reconstruction of Tissue-Specific Metabolic Networks Using CORDA. <i>PLoS Computational Biology</i> , 2016, 12, e1004808.	1.5	113
26	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016, 13, 310-318.	9.0	209
27	Endothelial cells decode VEGF-mediated Ca ²⁺ signaling patterns to produce distinct functional responses. <i>Science Signaling</i> , 2016, 9, ra20.	1.6	85
28	A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. <i>PLoS Computational Biology</i> , 2016, 12, e1004890.	1.5	28
29	Functional Proteomic Profiling of Myelodysplastic Syndromes Reveals Distinct Protein Expression Signatures and Identifies Candidate Therapeutic Targets. <i>Blood</i> , 2016, 128, 1975-1975.	0.6	0
30	Recurrent Patterns of Protein Expression Signatures in Pediatric Acute Lymphoblastic Leukemia: Recognition and Therapeutic Guidance. <i>Blood</i> , 2016, 128, 4089-4089.	0.6	0
31	Recognition of Recurrent Protein Expression Patterns in Pediatric Acute Myeloid Leukemia Suggests New Therapeutic Targets. <i>Blood</i> , 2016, 128, 1712-1712.	0.6	0
32	Progeny Clustering: A Method to Identify Biological Phenotypes. <i>Scientific Reports</i> , 2015, 5, 12894.	1.6	36
33	Recapitulation and Modulation of the Cellular Architecture of a User-Chosen Cell of Interest Using Cell-Derived, Biomimetic Patterning. <i>ACS Nano</i> , 2015, 9, 6128-6138.	7.3	20
34	Angiogenesis, Computational Modeling Perspective. , 2015, , 58-67.		2
35	Simulation Predicts IGFBP2-HIF1Î± Interaction Drives Glioblastoma Growth. <i>PLoS Computational Biology</i> , 2015, 11, e1004169.	1.5	19
36	Predicting internal cell fluxes at sub-optimal growth. <i>BMC Systems Biology</i> , 2015, 9, 18.	3.0	10

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37	CREB/ATF Family Protein Expression States in AML: Active CREB1, but Not ATF Is an Adverse Prognostic Factor. <i>Blood</i> , 2014, 124, 2344-2344.	0.6	2
38	Adhesion Signaling States in AML. <i>Blood</i> , 2014, 124, 2386-2386.	0.6	1
39	Cells as state machines: Cell behavior patterns arise during capillary formation as a function of BDNF and VEGF. <i>Journal of Theoretical Biology</i> , 2013, 326, 43-57.	0.8	18
40	Systems approaches for synthetic biology: a pathway toward mammalian design. <i>Frontiers in Physiology</i> , 2013, 4, 285.	1.3	8
41	Predicting Endothelial Cell Phenotypes in Angiogenesis. , 2013, , .		3
42	Proteomic Profiling Identifies Distinct Protein Patterns in Acute Myelogenous Leukemia CD34+CD38-Stem-Like Cells. <i>PLoS ONE</i> , 2013, 8, e78453.	1.1	48
43	Hippo Pathway (HP) Activity In Acute Myelogenous Leukemia (AML): Different Prognostic Implications Of TAZ versus YAP Inactivation By Phosphorylation. <i>Blood</i> , 2013, 122, 1337-1337.	0.6	3
44	A Global Proteomic Pathway Map In Acute Myeloid Leukemia (AML). <i>Blood</i> , 2013, 122, 1302-1302.	0.6	0
45	Classification Of Acute Myelogenous Leukemia (AML) Based On Functionally Related Proteins Groups. <i>Blood</i> , 2013, 122, 492-492.	0.6	0
46	Recurrent Patterns Of Histone Methylation and Acetylation Regulating Protein Expression In Acute Myelogenous Leukemia (AML). <i>Blood</i> , 2013, 122, 3733-3733.	0.6	0
47	Multiplexed Inâ€¦Situ Immunofluorescence Using Dynamic DNA Complexes. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 9292-9296.	7.2	57
48	Network analysis of reverse phase protein expression data: Characterizing protein signatures in acute myeloid leukemia cytogenetic categories t(8;21) and inv(16). <i>Proteomics</i> , 2012, 12, 2084-2093.	1.3	10
49	Computational models of VEGF-associated angiogenic processes in cancer. <i>Mathematical Medicine and Biology</i> , 2012, 29, 85-94.	0.8	22
50	Abnormal expression of FLI1 protein is an adverse prognostic factor in acute myeloid leukemia. <i>Blood</i> , 2011, 118, 5604-5612.	0.6	58
51	Module-based multiscale simulation of angiogenesis in skeletal muscle. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 6.	2.1	60
52	Systems biology of proâ€¦angiogenic therapies targeting the VEGF system. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 694-707.	6.6	80
53	Patient-Specific Modeling of Hypoxic Response and Microvasculature Dynamics. , 2010, , 183-201.		1
54	Elongation, proliferation & migration differentiate endothelial cell phenotypes and determine capillary sprouting. <i>BMC Systems Biology</i> , 2009, 3, 13.	3.0	103

#	ARTICLE	IF	CITATIONS
55	Multiscale models of angiogenesis. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 14-31.	1.1	139
56	Integration of angiogenesis modules at multiple scales: from molecular to tissue. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 316-27.	0.7	14
57	Reactive Oxygen Species Regulate Hypoxia-Inducible Factor 1 α Differentially in Cancer and Ischemia. Molecular and Cellular Biology, 2008, 28, 5106-5119.	1.1	167
58	INTEGRATION OF ANGIOGENESIS MODULES AT MULTIPLE SCALES: FROM MOLECULAR TO TISSUE. , 2008, , .		9
59	Three autocrine feedback loops determine HIF1 α expression in chronic hypoxia. Biochimica Et Biophysica Acta - Molecular Cell Research, 2007, 1773, 1511-1525.	1.9	40
60	Three autocrine feedback loops determine HIF1 α expression in chronic hypoxia. FASEB Journal, 2007, 21, A857.	0.2	4
61	A computational model of intracellular oxygen sensing by hypoxia-inducible factor HIF1 α . Journal of Cell Science, 2006, 119, 3467-3480.	1.2	88
62	Glucose transport to the brain: A systems model. Brain Research Reviews, 2005, 49, 595-617.	9.1	81
63	cytoNet: Network Analysis of Cell Communities. SSRN Electronic Journal, 0, , .	0.4	0