Amina A Qutub

List of Publications by Year
in descending order

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	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	9.0	209
2	Reactive Oxygen Species Regulate Hypoxia-Inducible Factor 1Î± Differentially in Cancer and Ischemia. Molecular and Cellular Biology, 2008, 28, 5106-5119.	1.1	167
3	Multiscale models of angiogenesis. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 14-31.	1.1	139
4	Reconstruction of Tissue-Specific Metabolic Networks Using CORDA. PLoS Computational Biology, 2016, 12, e1004808.	1.5	113
5	Advances in Glioblastoma Multiforme Treatment: New Models for Nanoparticle Therapy. Frontiers in Physiology, 2018, 9, 170.	1.3	110
6	Elongation, proliferation & migration differentiate endothelial cell phenotypes and determine capillary sprouting. BMC Systems Biology, 2009, 3, 13.	3.0	103
7	A computational model of intracellular oxygen sensing by hypoxia-inducible factor HIF1Î±. Journal of Cell Science, 2006, 119, 3467-3480.	1.2	88
8	p53 pathway dysfunction is highly prevalent in acute myeloid leukemia independent of TP53 mutational status. Leukemia, 2017, 31, 1296-1305.	3.3	87
9	Endothelial cells decode VEGF-mediated Ca $^{2+}$ signaling patterns to produce distinct functional responses. Science Signaling, 2016, 9, ra20.	1.6	85
10	Glucose transport to the brain: A systems model. Brain Research Reviews, 2005, 49, 595-617.	9.1	81
11	Systems biology of proâ€angiogenic therapies targeting the VEGF system. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 694-707.	6.6	80
12	Module-based multiscale simulation of angiogenesis in skeletal muscle. Theoretical Biology and Medical Modelling, 2011, 8, 6.	2.1	60
13	Abnormal expression of FLI1 protein is an adverse prognostic factor in acute myeloid leukemia. Blood, 2011, 118, 5604-5612.	0.6	58
14	Multiplexed Inâ€¦Situ Immunofluorescence Using Dynamic DNA Complexes. Angewandte Chemie - International Edition, 2012, 51, 9292-9296.	7.2	57
15	Proteomic Profiling Identifies Distinct Protein Patterns in Acute Myelogenous Leukemia CD34+CD38-Stem-Like Cells. PLoS ONE, 2013, 8, e78453.	1.1	48
16	A novel self-organizing embryonic stem cell system reveals signaling logic underlying the patterning of human ectoderm. Development (Cambridge), 2019, 146, .	1.2	44
17	Three autocrine feedback loops determine HIF1Î± expression in chronic hypoxia. Biochimica Et Biophysica Acta - Molecular Cell Research, 2007, 1773, 1511-1525.	1.9	40
18	Progeny Clustering: A Method to Identify Biological Phenotypes. Scientific Reports, 2015, 5, 12894.	1.6	36

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19	Image-based Classification of Tumor Type and Growth Rate using Machine Learning: a preclinical study. Scientific Reports, 2019, 9, 12529.	1.6	32
20	A Crowdsourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. PLoS Computational Biology, 2016, 12, e1004890.	1.5	28
21	Shrinkage Clustering: a fast and size-constrained clustering algorithm for biomedical applications. BMC Bioinformatics, 2018, 19, 19.	1.2	27
22	A quantitative analysis of heterogeneities and hallmarks in acute myelogenous leukaemia. Nature Biomedical Engineering, 2019, 3, 889-901.	11.6	27
23	Integrins and extracellular matrix proteins modulate adipocyte thermogenic capacity. Scientific Reports, 2021, 11, 5442.	1.6	23
24	Computational models of VEGF-associated angiogenic processes in cancer. Mathematical Medicine and Biology, 2012, 29, 85-94.	0.8	22
25	Recapitulation and Modulation of the Cellular Architecture of a User-Chosen Cell of Interest Using Cell-Derived, Biomimetic Patterning. ACS Nano, 2015, 9, 6128-6138.	7.3	20
26	Simulation Predicts IGFBP2-HIF1α Interaction Drives Glioblastoma Growth. PLoS Computational Biology, 2015, 11, e1004169.	1.5	19
27	Cells as state machines: Cell behavior patterns arise during capillary formation as a function of BDNF and VEGF. Journal of Theoretical Biology, 2013, 326, 43-57.	0.8	18
28	Recognition of Recurrent Protein Expression Patterns in Pediatric Acute Myeloid Leukemia Identified New Therapeutic Targets. Molecular Cancer Research, 2018, 16, 1275-1286.	1.5	16
29	LGALS3 is connected to CD74 in a previously unknown protein network that is associated with poor survival in patients with AML. EBioMedicine, 2019, 44, 126-137.	2.7	14
30	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
31	Evolution–informed modeling improves outcome prediction for cancers. Evolutionary Applications, 2017, 10, 68-76.	1.5	13
32	Recurrent Patterns of Protein Expression Signatures in Pediatric Acute Lymphoblastic Leukemia: Recognition and Therapeutic Guidance. Molecular Cancer Research, 2018, 16, 1263-1274.	1.5	12
33	Histone Modification Patterns Using RPPA–Based Profiling Predict Outcome in Acute Myeloid Leukemia Patients. Proteomics, 2018, 18, e1700379.	1.3	11
34	Network analysis of reverse phase protein expression data: Characterizing protein signatures in acute myeloid leukemia cytogenetic categories t(8;21) and inv(16). Proteomics, 2012, 12, 2084-2093.	1.3	10
35	Predicting internal cell fluxes at sub-optimal growth. BMC Systems Biology, 2015, 9, 18.	3.0	10
36	INTEGRATION OF ANGIOGENESIS MODULES AT MULTIPLE SCALES: FROM MOLECULAR TO TISSUE. , 2008, , .		9

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37	Systems approaches for synthetic biology: a pathway toward mammalian design. Frontiers in Physiology, 2013, 4, 285.	1.3	8
38	Mycoplasma contamination of leukemic cell lines alters protein expression determined by reverse phase protein arrays. Cytotechnology, 2018, 70, 1529-1535.	0.7	7
39	Proteomic Profiling of Acute Promyelocytic Leukemia Identifies Two Protein Signatures Associated with Relapse. Proteomics - Clinical Applications, 2019, 13, 1800133.	0.8	7
40	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. Frontiers in Oncology, 2021, 11, 705627.	1.3	7
41	Clinical relevance of proteomic profiling in de novo pediatric acute myeloid leukemia: a Children's Oncology Group study. Haematologica, 2022, , .	1.7	7
42	GAIN: A graphical method to automatically analyze individual neurite outgrowth. Journal of Neuroscience Methods, 2017, 283, 62-71.	1.3	6
43	IDENTIFYING CANCER SPECIFIC METABOLIC SIGNATURES USING CONSTRAINT-BASED MODELS. , 2017, 22, 485-496.		4
44	Three autocrine feedback loops determine HIF1α expression in chronic hypoxia. FASEB Journal, 2007, 21, A857.	0.2	4
45	Predicting Endothelial Cell Phenotypes in Angiogenesis. , 2013, , .		3
46	Shining a light on cell signaling in leukemia through proteomics: relevance for the clinic. Expert Review of Proteomics, 2018, 15, 613-622.	1.3	3
47	Hippo Pathway (HP) Activity In Acute Myelogenous Leukemia (AML): Different Prognostic Implications Of TAZ versus YAP Inactivation By Phosphorylation. Blood, 2013, 122, 1337-1337.	0.6	3
48	cytoNet: Spatiotemporal network analysis of cell communities. PLoS Computational Biology, 2022, 18, e1009846.	1.5	3
49	Angiogenesis, Computational Modeling Perspective. , 2015, , 58-67.		2
50	CREB/ATF Family Protein Expression States in AML: Active CREB1, but Not ATF Is an Adverse Prognostic Factor. Blood, 2014, 124, 2344-2344.	0.6	2
51	Differential proteome profile, biological pathways, and network relationships of osteogenic proteins in calcified human aortic valves. Heart and Vessels, 2021, , 1.	0.5	2
52	Proteomics in Acute Myeloid Leukemia. , 2018, , .		1
53	Patient-Specific Modeling of Hypoxic Response and Microvasculature Dynamics. , 2010, , 183-201.		1
54	Adhesion Signaling States in AML. Blood, 2014, 124, 2386-2386.	0.6	1

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55	A Global Proteomic Pathway Map In Acute Myeloid Leukemia (AML). Blood, 2013, 122, 1302-1302.	0.6	0
56	Classification Of Acute Myelogenous Leukemia (AML) Based On Functionally Related Proteins Groups. Blood, 2013, 122, 492-492.	0.6	0
57	Recurrent Patterns Of Histone Methylation and Acetylation Regulating Protein Expression In Acute Myelogenous Leukemia (AML). Blood, 2013, 122, 3733-3733.	0.6	0
58	Functional Proteomic Profiling of Myelodysplastic Syndromes Reveals Distinct Protein Expression Signatures and Identifies Candidate Therapeutic Targets. Blood, 2016, 128, 1975-1975.	0.6	0
59	Recurrent Patterns of Protein Expression Signatures in Pediatric Acute Lymphoblastic Leukemia: Recognition and Therapeutic Guidance. Blood, 2016, 128, 4089-4089.	0.6	0
60	Recognition of Recurrent Protein Expression Patterns in Pediatric Acute Myeloid Leukemia Suggests New Therapeutic Targets. Blood, 2016, 128, 1712-1712.	0.6	0
61	Classification of brain tumors using texture based analysis of T1-post contrast MR scans in a preclinical model. , 2018, , .		0
62	cytoNet: Network Analysis of Cell Communities. SSRN Electronic Journal, 0, , .	0.4	0
63	Proteomic Landscape of Acute Leukemia: A Comparison between ALL and AML in Adults. Blood, 2019, 134, 1461-1461.	0.6	0