Hasan H Otu

List of Publications by Year
in descending order

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87	4,811	101384	98622
papers	citations	36 h-index	67 g-index

89	89	89	7906
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Patterns and Persistence of Perioperative Plasma and Cerebrospinal Fluid Neuroinflammatory Protein Biomarkers After Elective Orthopedic Surgery Using SOMAscan. Anesthesia and Analgesia, 2023, 136, 163-175.	1.1	6
2	Proteome-Wide Analysis Using SOMAscan Identifies and Validates Chitinase-3-Like Protein 1 as a Risk and Disease Marker of Delirium Among Older Adults Undergoing Major Elective Surgery. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 484-493.	1.7	27
3	Identifying large-scale interaction atlases using probabilistic graphs and external knowledge. Journal of Clinical and Translational Science, 2022, 6, e27.	0.3	1
4	Serum Protein Signatures Using Aptamer-Based Proteomics for Minimal Change Disease and Membranous Nephropathy. Kidney International Reports, 2022, 7, 1539-1556.	0.4	8
5	Parenteral lipid emulsions induce unique ileal fatty acid and metabolomic profiles but do not increase the risk of necrotizing enterocolitis in preterm pigs. American Journal of Physiology - Renal Physiology, 2021, 320, G227-G239.	1.6	5
6	Identification of Plasma Proteome Signatures Associated With Surgery Using SOMAscan. Annals of Surgery, 2021, 273, 732-742.	2.1	41
7	Targeted metabolomics analysis of postoperative delirium. Scientific Reports, 2021, 11, 1521.	1.6	24
8	KEGG2Net: Deducing gene interaction networks and acyclic graphs from KEGG pathways. EMBnet Journal, 2021, 26, e949.	0.2	7
9	An Unbiased Predictive Model to Detect DNA Methylation Propensity of CpG Islands in the Human Genome. Current Bioinformatics, 2021, 16, 179-196.	0.7	8
10	Integration of Multi-omics Data Using Probabilistic Graph Models and External Knowledge. Current Bioinformatics, 2021, 16, .	0.7	2
11	Comparative analysis of single-cell transcriptomics in human and zebrafish oocytes. BMC Genomics, 2020, 21, 471.	1.2	14
12	Unexpected effects of systemic steroids on the CRSwNP proteome: is protein upregulation more important than inhibition?. International Forum of Allergy and Rhinology, 2020, 10, 334-342.	1.5	6
13	Placenta accreta spectrum: biomarker discovery using plasma proteomics. American Journal of Obstetrics and Gynecology, 2020, 223, 433.e1-433.e14.	0.7	41
14	FQStat: a parallel architecture for very high-speed assessment of sequencing quality metrics. BMC Bioinformatics, 2019, 20, 424.	1.2	7
15	Identification of Genes Differentially Expressed in Simvastatinâ€Induced Alveolar Bone Formation. JBMR Plus, 2019, 3, e10122.	1.3	9
16	Neutrophil activation in systemic capillary leak syndrome (Clarkson disease). Journal of Cellular and Molecular Medicine, 2019, 23, 5119-5127.	1.6	18
17	Translating transcription: proteomics in chronic rhinosinusitis with nasal polyps reveals significant discordance with messenger RNA expression. International Forum of Allergy and Rhinology, 2019, 9, 776-786.	1.5	18
18	The Role of Inflammation after Surgery for Elders (RISE) study: Study design, procedures, and cohort profile. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2019, 11, 752-762.	1.2	11

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19	Noninvasive exosomal proteomic biosignatures, including cystatin SN, peroxiredoxinâ€5, and glycoprotein VI, accurately predict chronic rhinosinusitis with nasal polyps. International Forum of Allergy and Rhinology, 2019, 9, 177-186.	1.5	33
20	Development of a Dynamic Multi-Protein Signature of Postoperative Delirium. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 261-268.	1.7	31
21	Higher C-Reactive Protein Levels Predict Postoperative Delirium in Older Patients Undergoing Major Elective Surgery: A Longitudinal Nested Case-Control Study. Biological Psychiatry, 2017, 81, 145-153.	0.7	100
22	Comparative analysis of human and mouse CpG islands using dbCGI. , 2017, , .		1
23	Distinct and Shared Determinants of Cardiomyocyte Contractility in Multi-Lineage Competent Ethnically Diverse Human iPSCs. Scientific Reports, 2016, 6, 37637.	1.6	20
24	Nicotine Exposure During Pregnancy Results in Persistent Midline Epithelial Seam With Improper Palatal Fusion. Nicotine and Tobacco Research, 2016, 18, 604-612.	1.4	20
25	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. Cell Reports, 2016, 14, 945-955.	2.9	49
26	Bioinformatics approaches to single-cell analysis in developmental biology. Molecular Human Reproduction, 2016, 22, 182-192.	1.3	18
27	Meta-analysis of transcriptome data identifies a novel 5-gene pancreatic adenocarcinoma classifier. Oncotarget, 2016, 7, 23263-23281.	0.8	49
28	Whole Genome Sequence of a Turkish Individual. PLoS ONE, 2014, 9, e85233.	1.1	22
29	Bayesian Pathway Analysis of Cancer Microarray Data. PLoS ONE, 2014, 9, e102803.	1.1	13
30	Bayesian network prior: network analysis of biological data using external knowledge. Bioinformatics, 2014, 30, 860-867.	1.8	39
31	Histone chaperone ASF1A is required for maintenance of pluripotency and cellular reprogramming. Science, 2014, 345, 822-825.	6.0	72
32	Gene expression profiling of granulosa cells from PCOS patients following varying doses of human chorionic gonadotropin. Journal of Assisted Reproduction and Genetics, 2013, 30, 341-352.	1.2	13
33	Testing robustness of relative complexity measure method constructing robust phylogenetic trees for Galanthus L. Using the relative complexity measure. BMC Bioinformatics, 2013, 14, 20.	1.2	5
34	A dynamic Bayesian framwork to learn temporal gene interactions using external knowledge. , 2013, , .		0
35	Identification of a novel gene set in human cumulus cells predictive of an oocyte's pregnancy potential. Fertility and Sterility, 2013, 99, 745-752.e6.	0.5	56
36	Detecting gene interactions within a Bayesian Network framework using external knowledge. , 2012, , .		3

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37	Pathway analysis of high-throughput biological data within a Bayesian network framework. Bioinformatics, 2011, 27, 1667-1674.	1.8	37
38	Reprogrammed Transcriptome in Rhesus-Bovine Interspecies Somatic Cell Nuclear Transfer Embryos. PLoS ONE, 2011, 6, e22197.	1.1	25
39	An exquisite cross-control mechanism among endothelial cell fate regulators directs the plasticity and heterogeneity of lymphatic endothelial cells. Blood, 2010, 116, 140-150.	0.6	87
40	Clustering of protein families into functional subtypes using Relative Complexity Measure with reduced amino acid alphabets. BMC Bioinformatics, 2010, 11, 428.	1.2	19
41	Bioinformatic identification and characterization of human endothelial cell-restricted genes. BMC Genomics, 2010, 11, 342.	1.2	54
42	Sequencing, Analysis, and Annotation of Expressed Sequence Tags for Camelus dromedarius. PLoS ONE, 2010, 5, e10720.	1.1	40
43	Tob1 is a constitutively expressed repressor of liver regeneration. Journal of Experimental Medicine, 2010, 207, 1197-1208.	4.2	38
44	Physico-chemical properties of DNA in phylogeny construction. , 2010, , .		0
45	Tob1 is a constitutively expressed repressor of liver regeneration. Journal of Cell Biology, 2010, 189, i14-i14.	2.3	0
46	Tissue permeability associated with chemokine-class inflammatory response following cardiac surgery. Journal of the American College of Surgeons, 2009, 209, S29-S30.	0.2	0
47	Differential gene expression of bone marrow-derived CD34+ cells is associated with survival of patients suffering from myelodysplastic syndrome. International Journal of Hematology, 2009, 89, 173-187.	0.7	25
48	Aprotinin Attenuates Genomic Expression Variability Following Cardiac Surgery. Journal of Cardiac Surgery, 2009, 24, 772-780.	0.3	1
49	Gene expression profile of mouse prostate tumors reveals dysregulations in major biological processes and identifies potential murine targets for preclinical development of human prostate cancer therapy. Prostate, 2008, 68, 1517-1530.	1.2	47
50	Differential expression of GADD45Î² in normal and osteoarthritic cartilage: Potential role in homeostasis of articular chondrocytes. Arthritis and Rheumatism, 2008, 58, 2075-2087.	6.7	91
51	Grammar-based distance in progressive multiple sequence alignment. BMC Bioinformatics, 2008, 9, 306.	1.2	38
52	Gene expression analysis of embryonic stem cells expressing VE-cadherin (CD144) during endothelial differentiation. BMC Genomics, 2008, 9, 240.	1.2	21
53	Proteomic Identification of Interleukin-2 Therapy Response in Metastatic Renal Cell Cancer. Journal of Urology, 2008, 179, 730-736.	0.2	11
54	Genomic Counter-Stress Changes Induced by the Relaxation Response. PLoS ONE, 2008, 3, e2576.	1.1	198

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55	Serum Proteomics and Biomarkers in Hepatocellular Carcinoma and Chronic Liver Disease. Clinical Cancer Research, 2008, 14, 470-477.	3.2	191
56	Gene Expression of Purified Î²-Cell Tissue Obtained from Human Pancreas with Laser Capture Microdissection. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 1046-1053.	1.8	73
57	Restoration of Liver Mass after Injury Requires Proliferative and Not Embryonic Transcriptional Patterns. Journal of Biological Chemistry, 2007, 282, 11197-11204.	1.6	77
58	From the cover: Serum proteome profiling detects myelodysplastic syndromes and identifies CXC chemokine ligands 4 and 7 as markers for advanced disease. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1307-1312.	3.3	91
59	Computational Analysis of Transcriptional Profiling in Dysmorphic Syndrome. , 2007, , .		0
60	Reduced PDEF Expression Increases Invasion and Expression of Mesenchymal Genes in Prostate Cancer Cells. Cancer Research, 2007, 67, 4219-4226.	0.4	86
61	A high-fat, ketogenic diet induces a unique metabolic state in mice. American Journal of Physiology - Endocrinology and Metabolism, 2007, 292, E1724-E1739.	1.8	343
62	c-Fos as a Proapoptotic Agent in TRAIL-Induced Apoptosis in Prostate Cancer Cells. Cancer Research, 2007, 67, 9425-9434.	0.4	85
63	Prediction of Diabetic Nephropathy Using Urine Proteomic Profiling 10 Years Prior to Development of Nephropathy. Diabetes Care, 2007, 30, 638-643.	4.3	118
64	Oxidative Stress and Atrial Fibrillation After Cardiac Surgery: A Case-Control Study. Annals of Thoracic Surgery, 2007, 84, 1166-1173.	0.7	111
65	Genomic expression pathways associated with brain injury after cardiopulmonary bypass. Journal of Thoracic and Cardiovascular Surgery, 2007, 134, 996-1005.e4.	0.4	22
66	Dysregulated Notch signaling induces pathological arterialization of developing lymphatics in Down syndrome fetus.. FASEB Journal, 2007, 21, A15.	0.2	1
67	A Novel Pathway Involving Melanoma Differentiation Associated Gene-7/Interleukin-24 Mediates Nonsteroidal Anti-inflammatory Drugâ€“Induced Apoptosis and Growth Arrest of Cancer Cells. Cancer Research, 2006, 66, 11922-11931.	0.4	54
68	Proteomic Analysis of the Allograft Response. Transplantation, 2006, 82, 267-274.	0.5	12
69	Essential role of Jun family transcription factors in PU.1 knockdownâ€“induced leukemic stem cells. Nature Genetics, 2006, 38, 1269-1277.	9.4	167
70	A Novel Class of Vascular Endothelial Growth Factor-responsive Genes That Require Forkhead Activity for Expression. Journal of Biological Chemistry, 2006, 281, 35544-35553.	1.6	50
71	The transcriptome of human oocytes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14027-14032.	3.3	177
72	Differential Gene Expression Analysis Reveals Generation of an Autocrine Loop by a Mutant Epidermal Growth Factor Receptor in Glioma Cells. Cancer Research, 2006, 66, 867-874.	0.4	149

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73	A Novel Role for GADD45Î² as a Mediator of MMP-13 Gene Expression during Chondrocyte Terminal Differentiation. Journal of Biological Chemistry, 2005, 280, 38544-38555.	1.6	93
74	Unique Gene Expression Profile Based on Pathologic Response in Epithelial Ovarian Cancer. Journal of Clinical Oncology, 2005, 23, 7911-7918.	0.8	133
75	Preconditioning of primary human endothelial cells with inflammatory mediators alters the â€œset pointâ€•of the cell. FASEB Journal, 2005, 19, 1914-1916.	0.2	24
76	Gene Signatures of Progression and Metastasis in Renal Cell Cancer. Clinical Cancer Research, 2005, 11, 5730-5739.	3.2	386
77	Optimization and evaluation of surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF MS) with reversed-phase protein arrays for protein profiling. Clinical Chemistry and Laboratory Medicine, 2005, 43, 133-40.	1.4	41
78	Essential Role of Jun Family Transcription Factors in PU.1-Induced Leukemic Stem Cell Transformation.. Blood, 2005, 106, 463-463.	0.6	4
79	Differences in Gene Expression Profiles of Diabetic and Nondiabetic Patients Undergoing Cardiopulmonary Bypass and Cardioplegic Arrest. Circulation, 2004, 110, II-280-II-286.	1.6	43
80	Differential transcriptional effects of PTH and estrogen during anabolic bone formation. Journal of Cellular Biochemistry, 2004, 93, 476-490.	1.2	27
81	Utilization of the relative complexity measure to construct a phylogenetic tree for fungi. Mycological Research, 2004, 108, 117-125.	2.5	18
82	Serum Protein Profiling with Mass Spectrometry for the Diagnosis of Myelodysplastic Syndromes.. Blood, 2004, 104, 2362-2362.	0.6	0
83	A divide-and-conquer approach to fragment assembly. Bioinformatics, 2003, 19, 22-29.	1.8	24
84	A new sequence distance measure for phylogenetic tree construction. Bioinformatics, 2003, 19, 2122-2130.	1.8	286
85	Comment on " 'Stemness': Transcriptional Profiling of Embryonic and Adult Stem Cells" and "A Stem Cell Molecular Signature" (I). Science, 2003, 302, 393b-393.	6.0	297
86	Joint source/channel coding for variable length codes. IEEE Transactions on Communications, 2000, 48, 787-794.	4.9	88
87	A joint source/channel coder with block constraints. IEEE Transactions on Communications, 1999, 47, 1615-1618.	4.9	9