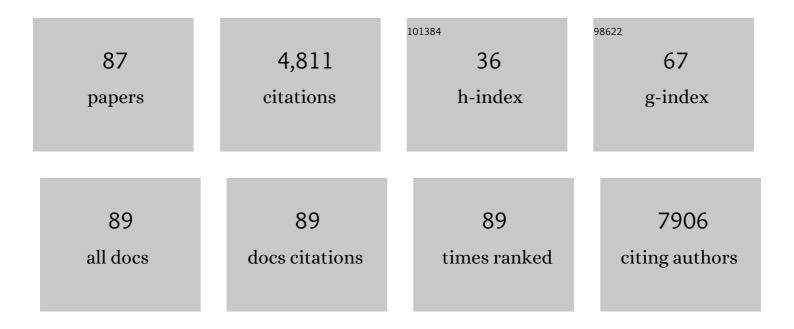
## Hasan H Otu

List of Publications by Year in descending order

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ΗΛΩΛΝΗ ΟΤΙΙ

#	Article	IF	CITATIONS
1	Gene Signatures of Progression and Metastasis in Renal Cell Cancer. Clinical Cancer Research, 2005, 11, 5730-5739.	3.2	386
2	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
3	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
4	A new sequence distance measure for phylogenetic tree construction. Bioinformatics, 2003, 19, 2122-2130.	1.8	286
5	Genomic Counter-Stress Changes Induced by the Relaxation Response. PLoS ONE, 2008, 3, e2576.	1.1	198
6	Serum Proteomics and Biomarkers in Hepatocellular Carcinoma and Chronic Liver Disease. Clinical Cancer Research, 2008, 14, 470-477.	3.2	191
7	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
8	Essential role of Jun family transcription factors in PU.1 knockdown–induced leukemic stem cells. Nature Genetics, 2006, 38, 1269-1277.	9.4	167
9	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
10	Unique Gene Expression Profile Based on Pathologic Response in Epithelial Ovarian Cancer. Journal of Clinical Oncology, 2005, 23, 7911-7918.	0.8	133
11	Prediction of Diabetic Nephropathy Using Urine Proteomic Profiling 10 Years Prior to Development of Nephropathy. Diabetes Care, 2007, 30, 638-643.	4.3	118
12	Oxidative Stress and Atrial Fibrillation After Cardiac Surgery: A Case-Control Study. Annals of Thoracic Surgery, 2007, 84, 1166-1173.	0.7	111
13	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
14	A Novel Role for GADD45Î <sup>2</sup> as a Mediator of MMP-13 Gene Expression during Chondrocyte Terminal Differentiation. Journal of Biological Chemistry, 2005, 280, 38544-38555.	1.6	93
15	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
16	Differential expression of GADD45β in normal and osteoarthritic cartilage: Potential role in homeostasis of articular chondrocytes. Arthritis and Rheumatism, 2008, 58, 2075-2087.	6.7	91
17	Joint source/channel coding for variable length codes. IEEE Transactions on Communications, 2000, 48, 787-794.	4.9	88
18	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

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19	Reduced PDEF Expression Increases Invasion and Expression of Mesenchymal Genes in Prostate Cancer Cells. Cancer Research, 2007, 67, 4219-4226.	0.4	86
20	c-Fos as a Proapoptotic Agent in TRAIL-Induced Apoptosis in Prostate Cancer Cells. Cancer Research, 2007, 67, 9425-9434.	0.4	85
21	Restoration of Liver Mass after Injury Requires Proliferative and Not Embryonic Transcriptional Patterns. Journal of Biological Chemistry, 2007, 282, 11197-11204.	1.6	77
22	Gene Expression of Purified β-Cell Tissue Obtained from Human Pancreas with Laser Capture Microdissection. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 1046-1053.	1.8	73
23	Histone chaperone ASF1A is required for maintenance of pluripotency and cellular reprogramming. Science, 2014, 345, 822-825.	6.0	72
24	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
25	A Novel Pathway Involving Melanoma Differentiation Associated Gene-7/Interleukin-24 Mediates Nonsteroidal Anti-inflammatory Drug–Induced Apoptosis and Growth Arrest of Cancer Cells. Cancer Research, 2006, 66, 11922-11931.	0.4	54
26	Bioinformatic identification and characterization of human endothelial cell-restricted genes. BMC Genomics, 2010, 11, 342.	1.2	54
27	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
28	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
29	Meta-analysis of transcriptome data identifies a novel 5-gene pancreatic adenocarcinoma classifier. Oncotarget, 2016, 7, 23263-23281.	0.8	49
30	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
31	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
32	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
33	Placenta accreta spectrum: biomarker discovery using plasma proteomics. American Journal of Obstetrics and Gynecology, 2020, 223, 433.e1-433.e14.	0.7	41
34	Identification of Plasma Proteome Signatures Associated With Surgery Using SOMAscan. Annals of Surgery, 2021, 273, 732-742.	2.1	41
35	Sequencing, Analysis, and Annotation of Expressed Sequence Tags for Camelus dromedarius. PLoS ONE, 2010, 5, e10720.	1.1	40
36	Bayesian network prior: network analysis of biological data using external knowledge. Bioinformatics, 2014, 30, 860-867.	1.8	39

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37	Grammar-based distance in progressive multiple sequence alignment. BMC Bioinformatics, 2008, 9, 306.	1.2	38
38	Tob1 is a constitutively expressed repressor of liver regeneration. Journal of Experimental Medicine, 2010, 207, 1197-1208.	4.2	38
39	Pathway analysis of high-throughput biological data within a Bayesian network framework. Bioinformatics, 2011, 27, 1667-1674.	1.8	37
40	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
41	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
42	Differential transcriptional effects of PTH and estrogen during anabolic bone formation. Journal of Cellular Biochemistry, 2004, 93, 476-490.	1.2	27
43	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
44	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
45	Reprogrammed Transcriptome in Rhesus-Bovine Interspecies Somatic Cell Nuclear Transfer Embryos. PLoS ONE, 2011, 6, e22197.	1.1	25
46	A divide-and-conquer approach to fragment assembly. Bioinformatics, 2003, 19, 22-29.	1.8	24
47	Preconditioning of primary human endothelial cells with inflammatory mediators alters the "set point―of the cell. FASEB Journal, 2005, 19, 1914-1916.	0.2	24
48	Targeted metabolomics analysis of postoperative delirium. Scientific Reports, 2021, 11, 1521.	1.6	24
49	Genomic expression pathways associated with brain injury after cardiopulmonary bypass. Journal of Thoracic and Cardiovascular Surgery, 2007, 134, 996-1005.e4.	0.4	22
50	Whole Genome Sequence of a Turkish Individual. PLoS ONE, 2014, 9, e85233.	1.1	22
51	Gene expression analysis of embryonic stem cells expressing VE-cadherin (CD144) during endothelial differentiation. BMC Genomics, 2008, 9, 240.	1.2	21
52	Distinct and Shared Determinants of Cardiomyocyte Contractility in Multi-Lineage Competent Ethnically Diverse Human iPSCs. Scientific Reports, 2016, 6, 37637.	1.6	20
53	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
54	Clustering of protein families into functional subtypes using Relative Complexity Measure with reduced amino acid alphabets. BMC Bioinformatics, 2010, 11, 428.	1.2	19

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55	Utilization of the relative complexity measure to construct a phylogenetic tree for fungi. Mycological Research, 2004, 108, 117-125.	2.5	18
56	Bioinformatics approaches to single-cell analysis in developmental biology. Molecular Human Reproduction, 2016, 22, 182-192.	1.3	18
57	Neutrophil activation in systemic capillary leak syndrome (Clarkson disease). Journal of Cellular and Molecular Medicine, 2019, 23, 5119-5127.	1.6	18
58	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
59	Comparative analysis of single-cell transcriptomics in human and zebrafish oocytes. BMC Genomics, 2020, 21, 471.	1.2	14
60	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
61	Bayesian Pathway Analysis of Cancer Microarray Data. PLoS ONE, 2014, 9, e102803.	1.1	13
62	Proteomic Analysis of the Allograft Response. Transplantation, 2006, 82, 267-274.	0.5	12
63	Proteomic Identification of Interleukin-2 Therapy Response in Metastatic Renal Cell Cancer. Journal of Urology, 2008, 179, 730-736.	0.2	11
64	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
65	A joint source/channel coder with block constraints. IEEE Transactions on Communications, 1999, 47, 1615-1618.	4.9	9
66	Identification of Genes Differentially Expressed in Simvastatinâ€Induced Alveolar Bone Formation. JBMR Plus, 2019, 3, e10122.	1.3	9
67	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
68	Serum Protein Signatures Using Aptamer-Based Proteomics for Minimal Change Disease and Membranous Nephropathy. Kidney International Reports, 2022, 7, 1539-1556.	0.4	8
69	FQStat: a parallel architecture for very high-speed assessment of sequencing quality metrics. BMC Bioinformatics, 2019, 20, 424.	1.2	7
70	KEGG2Net: Deducing gene interaction networks and acyclic graphs from KEGG pathways. EMBnet Journal, 2021, 26, e949.	0.2	7
71	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
72	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

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73	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
74	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
75	Essential Role of Jun Family Transcription Factors in PU.1-Induced Leukemic Stem Cell Transformation Blood, 2005, 106, 463-463.	0.6	4
76	Detecting gene interactions within a Bayesian Network framework using external knowledge. , 2012, , .		3
77	Integration of Multi-omics Data Using Probabilistic Graph Models and External Knowledge. Current Bioinformatics, 2021, 16, .	0.7	2
78	Aprotinin Attenuates Genomic Expression Variability Following Cardiac Surgery. Journal of Cardiac Surgery, 2009, 24, 772-780.	0.3	1
79	Comparative analysis of human and mouse CpG islands using dbCGI. , 2017, , .		1
80	Dysregulated Notch signaling induces pathological arterialization of developing lymphatics in Down syndrome fetus FASEB Journal, 2007, 21, A15.	0.2	1
81	Identifying large-scale interaction atlases using probabilistic graphs and external knowledge. Journal of Clinical and Translational Science, 2022, 6, e27.	0.3	1
82	Computational Analysis of Transcriptional Profiling in Dysmorphic Syndrome. , 2007, , .		0
83	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
84	Physico-chemical properties of DNA in phylogeny construction. , 2010, , .		0
85	A dynamic Bayesian framwork to learn temporal gene interactions using external knowledge. , 2013, , .		0
86	Serum Protein Profiling with Mass Spectrometry for the Diagnosis of Myelodysplastic Syndromes Blood, 2004, 104, 2362-2362.	0.6	0
87	Tob1 is a constitutively expressed repressor of liver regeneration. Journal of Cell Biology, 2010, 189, i14-i14.	2.3	Ο