Jacob O Odeberg

List of Publications by Year
in descending order

95 papers	18,479 citations	101543 36 h-index	39675 94 g-index
103 all docs	103 docs citations	103 times ranked	38920 citing authors

#	Article	IF	Citations
1	Proteomics in thrombosis research. Research and Practice in Thrombosis and Haemostasis, 2022, 6, e12706.	2.3	2
2	A human adipose tissue cell-type transcriptome atlas. Cell Reports, 2022, 40, 111046.	6.4	30
3	Xenotropic and polytropic retrovirus receptor 1 regulates procoagulant platelet polyphosphate. Blood, 2021, 137, 1392-1405.	1.4	21
4	Explainable Artificial Neural Network for Recurrent Venous Thromboembolism Based on Plasma Proteomics. Lecture Notes in Computer Science, 2021, , 108-121.	1.3	4
5	A singleâ€“cell type transcriptomics map of human tissues. Science Advances, 2021, 7, .	10.3	632
6	An artificial neural network approach integrating plasma proteomics and genetic data identifies PLXNA4 as a new susceptibility locus for pulmonary embolism. Scientific Reports, 2021, 11, 14015.	3.3	8
7	Affinity Assays for Cardiovascular and Atherosclerotic Disease Biomarkers. Methods in Molecular Biology, 2021, 2344, 163-179.	0.9	1
8	Identification of Endothelial Proteins in Plasma Associated With Cardiovascular Risk Factors. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2990-3004.	2.4	8
9	PCSK6 Is a Key Protease in the Control of Smooth Muscle Cell Function in Vascular Remodeling. Circulation Research, 2020, 126, 571-585.	4.5	38
10	Facets of individual-specific health signatures determined from longitudinal plasma proteome profiling. EBioMedicine, 2020, 57, 102854.	6.1	18
11	Integration of molecular profiles in a longitudinal wellness profiling cohort. Nature Communications, 2020, 11, 4487.	12.8	66
12	Transcriptomic profiling of experimental arterial injury reveals new mechanisms and temporal dynamics in vascular healing response. JVS Vascular Science, 2020, 1, 13-27.	1.1	10
13	Profiles of histidine-rich glycoprotein associate with age and risk of all-cause mortality. Life Science Alliance, 2020, 3, e202000817.	2.8	9
14	A Systems-Based Map of Human Brain Cell-Type Enriched Genes and Malignancy-Associated Endothelial Changes. Cell Reports, 2019, 29, 1690-1706.e4.	6.4	22
15	Correlation of computed tomography with carotid plaque transcriptomes associates calcification with lesion-stabilization. Atherosclerosis, 2019, 288, 175-185.	0.8	52
16	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. Science, 2019, 366, .	12.6	329
17	A systems-approach reveals human nestin is an endothelial-enriched, angiogenesis-independent intermediate filament protein. Scientific Reports, 2018, 8, 14668.	3.3	19
18	Novel Multiomics Profiling of Human Carotid Atherosclerotic Plaques and Plasma Reveals Biliverdin Reductase B asÂa Marker of Intraplaque Hemorrhage. JACC Basic To Translational Science, 2018, 3, 464-480.	4.1	42

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19	A novel cysteine-linked antibacterial surface coating significantly inhibits bacterial colonization of nasal silicone prongs in a phase one pre-clinical trial. Materials Science and Engineering C, 2018, 93, 782-789.	7.3	10
20	Management of rivaroxaban- or apixaban-associated major bleeding with prothrombin complex concentrates: a cohort study. Blood, 2017, 130, 1706-1712.	1.4	258
21	Whole blood ristocetin-activated platelet impedance aggregometry (Multiplate) for the rapid detection of Von Willebrand disease. Thrombosis and Haemostasis, 2017, 117, 1528-1533.	3.4	13
22	F11 is associated with recurrent VTE in women. Thrombosis and Haemostasis, 2016, 115, 406-414.	3.4	9
23	Gene expression signatures, pathways and networks in carotid atherosclerosis. Journal of Internal Medicine, 2016, 279, 293-308.	6.0	114
24	PDGFB, a new candidate plasma biomarker for venous thromboembolism: results from the VEREMA affinity proteomics study. Blood, 2016, 128, e59-e66.	1.4	39
25	Cardiovascular disease and mortality after a first episode of venous thromboembolism in young and middle-aged women. Thrombosis Research, 2016, 138, 80-85.	1.7	12
26	Analysis of Body-wide Unfractionated Tissue Data to Identify a Core Human Endothelial Transcriptome. Cell Systems, 2016, 3, 287-301.e3.	6.2	44
27	Tissue microarray profiling in human heart failure. Proteomics, 2016, 16, 2319-2326.	2.2	9
28	Phenotypic Modulation of Smooth Muscle Cells in Atherosclerosis Is Associated With Downregulation of LMOD1, SYNPO2, PDLIM7, PLN , and SYNM. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1947-1961.	2.4	64
29	GeneiASE: Detection of condition-dependent and static allele-specific expression from RNA-seq data without haplotype information. Scientific Reports, 2016, 6, 21134.	3.3	79
30	Influence of pre-existing inflammation on the outcome of acute coronary syndrome: a cross-sectional study. BMJ Open, 2016, 6, e009968.	1.9	17
31	Tissue-based map of the human proteome. Science, 2015, 347, 1260419.	12.6	10,802
32	The Kidney Transcriptome and Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2014, 9, e116125.	2.5	49
33	The influence of smoking and impaired glucose homoeostasis on the outcome in patients presenting with an acute coronary syndrome: a cross-sectional study. BMJ Open, 2014, 4, e005077-e005077.	1.9	7
34	Association of Venous Thromboembolism With Hormonal Contraception and Thrombophilic Genotypes. Obstetrics and Gynecology, 2014, 124, 600-609.	2.4	64
35	Molecular- and Organelle-Based Predictive Paradigm Underlying Recovery by Left Ventricular Assist Device Support. Circulation: Heart Failure, 2014, 7, 359-366.	3.9	10
36	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. Molecular and Cellular Proteomics, 2014, 13, 397-406.	3.8	2,819

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37	Influence of coronary artery disease-associated genetic variants on risk of venous thromboembolism. Thrombosis Research, 2014, 134, 426-432.	1.7	18
38	Heart Research Advances Using Database Search Engines, Human Protein Atlas and the Sydney Heart Bank. Heart Lung and Circulation, 2013, 22, 819-826.	0.4	18
39	Profiling post-centrifugation delay of serum and plasma with antibody bead arrays. Journal of Proteomics, 2013, 95, 46-54.	2.4	24
40	Contribution of Antibody-based Protein Profiling to the Human Chromosome-centric Proteome Project (C-HPP). Journal of Proteome Research, 2013, 12, 2439-2448.	3.7	48
41	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. Circulation Research, 2013, 113, 1043-1053.	4.5	65
42	Profiling of Atherosclerotic Lesions by Gene and Tissue Microarrays Reveals PCSK6 as a Novel Protease in Unstable Carotid Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2432-2443.	2.4	84
43	Antibody-based Protein Profiling of the Human Chromosome 21. Molecular and Cellular Proteomics, 2012, 11, M111.013458.	3.8	26
44	A case series of five episodes of massive LMWH non-fatal self-induced overdose in a single patient. Thrombosis Research, 2012, 129, 668-670.	1.7	7
45	A Genome-Wide Association Study Identifies KNG1 as a Genetic Determinant of Plasma Factor XI Level and Activated Partial Thromboplastin Time. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 2008-2016.	2.4	33
46	Risk factors for venous thromboembolism in pre-and postmenopausal women. Thrombosis Research, 2012, 130, 596-601.	1.7	33
47	Combined Chromatin and Expression Analysis Reveals Specific Regulatory Mechanisms within Cytokine Genes in the Macrophage Early Immune Response. PLoS ONE, 2012, 7, e32306.	2.5	18
48	Use of the Whole Leucocyte Population in the Study of the NFÎºB Pathway. Scandinavian Journal of Immunology, 2011, 73, 338-343.	2.7	3
49	Linkage Analysis of Autopsy-Confirmed Familial Alzheimer Disease Supports an Alzheimer Disease Locus in 8q24. Dementia and Geriatric Cognitive Disorders, 2011, 31, 109-118.	1.5	4
50	Allele-specific transcription of the PAI-1 gene in human astrocytes. Thrombosis and Haemostasis, 2010, 104, 998-1008.	3.4	14
51	Linkage to 20p13 including the ANGPT4 gene in families with mixed Alzheimer's disease and vascular dementia. Journal of Human Genetics, 2010, 55, 649-655.	2.3	9
52	Intercalated discs: multiple proteins perform multiple functions in non-failing and failing human hearts. Biophysical Reviews, 2009, 1, 43-49.	3.2	49
53	The epitope space of the human proteome. Protein Science, 2008, 17, 606-613.	7.6	39
54	Expanded high-resolution genetic study of 109 Swedish families with Alzheimer's disease. European Journal of Human Genetics, 2008, 16, 202-208.	2.8	18

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55	Validation of a composite score for clinical severity of hemophilia. Journal of Thrombosis and Haemostasis, 2008, 6, 1113-1121.	3.8	84
56	The Asp298 allele of endothelial nitric oxide synthase is a risk factor for myocardial infarction among patients with type 2 diabetes mellitus. BMC Cardiovascular Disorders, 2008, 8, 36.	1.7	14
57	In Silico Detection of Sequence Variations Modifying Transcriptional Regulation. PLoS Computational Biology, 2008, 4, e5.	3.2	94
58	APC resistance during the normal menstrual cycle. Thrombosis and Haemostasis, 2007, 98, 1246-1251.	3.4	8
59	Hormonal and nutritional regulation of alternative CD36 transcripts in rat liver â€“ a role for growth hormone in alternative exon usage. BMC Molecular Biology, 2007, 8, 60.	3.0	39
60	The use of grid computing to drive data-intensive genetic research. European Journal of Human Genetics, 2007, 15, 694-702.	2.8	15
61	Allele-specific MMP-3 transcription under in vivo conditions. Biochemical and Biophysical Research Communications, 2006, 348, 1150-1156.	2.1	39
62	Alternative promoter usage of the membrane glycoprotein CD36. BMC Molecular Biology, 2006, 7, 8.	3.0	49
63	UGT1A polymorphisms in a Swedish cohort and a human diversity panel, and the relation to bilirubin plasma levels in males and females. European Journal of Clinical Pharmacology, 2006, 62, 829-837.	1.9	36
64	Comparison of PrASE and Pyrosequencing for SNP Genotyping. BMC Genomics, 2006, 7, 291.	2.8	5
65	A quality assessment survey of SNP genotyping laboratories. Human Mutation, 2006, 27, 711-714.	2.5	18
66	Applications of Grid Computing in Genetics and Proteomics. , 2006, , 791-798.		3
67	Using Grid technology for computationally intensive applied bioinformatics analyses. In Silico Biology, 2006, 6, 495-504.	0.9	5
68	Serum matrix metalloproteinase-3 concentration is influenced by MMP-3 -1612 5A/6A promoter genotype and associated with myocardial infarction. Journal of Internal Medicine, 2005, 258, 411-419.	6.0	113
69	Expression profiling of adrenocortical neoplasms suggests a molecular signature of malignancy. Surgery, 2005, 138, 1087-1094.	1.9	124
70	A Structural Basis for CD8+ T Cell-dependent Recognition of Non-homologous Peptide Ligands. Journal of Biological Chemistry, 2005, 280, 27069-27075.	3.4	20
71	Pyrosequencing Analysis of Thrombosis-Associated Risk Markers. Clinical Chemistry, 2005, 51, 1549-1552.	3.2	15
72	Vascular Gene Expression in Atherosclerotic Plaque-Prone Regions Analyzed by Representational Difference Analysis. Pathobiology, 2004, 71, 107-114.	3.8	5

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73	Pyrosequencing for Detection of Lamivudine-Resistant Hepatitis B Virus. Journal of Clinical Microbiology, 2004, 42, 4788-4795.	3.9	69
74	Both risk alleles for FcÎ³RIIA and FcÎ³RIIIA are susceptibility factors for SLE: a unifying hypothesis. Genes and Immunity, 2004, 5, 130-137.	4.1	58
75	Polymorphisms of the FcÎ³ receptor type IIB gene are not associated with systemic lupus erythematosus in the Swedish population. Arthritis and Rheumatism, 2004, 50, 1348-1350.	6.7	40
76	Shotgun sequencing and microarray analysis of RDA transcripts. Gene, 2003, 310, 39-47.	2.2	1
77	SNP typing by apyrase-mediated allele-specific primer extension on DNA microarrays. Nucleic Acids Research, 2002, 30, 75e-75.	14.5	48
78	A Structural Basis for LCMV Immune Evasion. Immunity, 2002, 17, 757-768.	14.3	50
79	Gene expression analysis by signature pyrosequencing. Gene, 2002, 289, 31-39.	2.2	24
80	Molecular Haplotyping by PyrosequencingTM. BioTechniques, 2002, 33, 1104-1108.	1.8	18
81	Monitoring of the subtraction process in solid-phase representational difference analysis: characterization of a candidate drug. Gene, 2001, 271, 183-192.	2.2	8
82	Novel Candidate Genes for Atherosclerosis Are Identified by Representational Difference Analysis-Based Transcript Profiling of Cholesterol-Loaded Macrophages. Pathobiology, 2001, 69, 304-314.	3.8	15
83	Genotyping by apyrase-mediated allele-specific extension. Nucleic Acids Research, 2001, 29, 121e-121.	14.5	40
84	A cDNA RDA protocol using solid-phase technology suited for analysis in small tissue samples. New Biotechnology, 2000, 17, 1-9.	2.7	17
85	The C1orf9 Gene Encodes a Putative Transmembrane Member of a Novel Protein Family. Biochemical and Biophysical Research Communications, 2000, 267, 855-862.	2.1	3
86	Differential Cloning of Growth Hormone-Regulated Hepatic Transcripts in the Aged Rat. Endocrinology, 2000, 141, 910-921.	2.8	9
87	Context-dependent Taq-polymerase-mediated nucleotide alterations, as revealed by direct sequencing of the ZNF189 gene: implications for mutation detection. Gene, 1999, 235, 103-109.	2.2	7
88	[28] Solid-phase differential display and bacterial expression systems in selection and functional analysis of cDNAs. Methods in Enzymology, 1999, 303, 495-511.	1.0	8
89	Genetic instability in the 9q22.3 region is a late event in the development of squamous cell carcinoma. Oncogene, 1998, 17, 1837-1843.	5.9	45
90	Variation in the hepatitis C virus NS5a region in relation to hypervariable region 1 heterogeneity during interferon treatment. , 1998, 56, 33-38.		32

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91	Cloning and Characterization of ZNF189, a Novel HumanKrÃ¼ppel-like Zinc Finger Gene Localized to Chromosome 9q22â€“q31. Genomics, 1998, 50, 213-221.	2.9	17
92	Variation of Hepatitis C Virus Hypervariable Region 1 in Immunocompromised Patients. Journal of Infectious Diseases, 1997, 175, 938-943.	4.0	45
93	PR-39, a proline-rich peptide antibiotic from pig, and FALL-39, a tentative human counterpart. Veterinary Immunology and Immunopathology, 1996, 54, 127-131.	1.2	18
94	The Human Gene FALL39 and Processing of the Cathelin Precursor to the Antibacterial Peptide LLâ€37 in Granulocytes. FEBS Journal, 1996, 238, 325-332.	0.2	502
95	FALL-39, a putative human peptide antibiotic, is cysteine-free and expressed in bone marrow and testis.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 195-199.	7.1	472