

Hans-Ulrich Klein

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

7,576
citations

94269

37
h-index

60497

81
g-index

105
all docs

105
docs citations

105
times ranked

13519
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome-Wide Discovery of Cortical Proteins That May Provide Motor Resilience to Offset the Negative Effects of Pathologies in Older Adults. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2023, 78, 494-503.	1.7	4
2	Epigenomic features related to microglia are associated with attenuated effect of <i>APOE</i> ϵ 4 on Alzheimer's disease risk in humans. <i>Alzheimer's and Dementia</i> , 2022, 18, 688-699.	0.4	9
3	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults. <i>Neurology</i> , 2022, 98, .	1.5	22
4	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies <i>DCDC2</i> gene as predictor of episodic memory maintenance. <i>Alzheimer's and Dementia</i> , 2022, 18, 1797-1811.	0.4	5
5	Mitochondrial respiratory chain protein co-regulation in the human brain. <i>Heliyon</i> , 2022, 8, e09353.	1.4	4
6	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. <i>JAMA Neurology</i> , 2021, 78, 102.	4.5	144
7	Cortical proteins may provide motor resilience in older adults. <i>Scientific Reports</i> , 2021, 11, 11311.	1.6	14
8	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. <i>Neurobiology of Disease</i> , 2021, 157, 105428.	2.1	36
9	A cortical immune network map identifies distinct microglial transcriptional programs associated with β -amyloid and Tau pathologies. <i>Translational Psychiatry</i> , 2021, 11, 50.	2.4	19
10	Characterization of mitochondrial DNA quantity and quality in the human aged and Alzheimer's disease brain. <i>Molecular Neurodegeneration</i> , 2021, 16, 75.	4.4	44
11	Atlas of RNA editing events affecting protein expression in aged and Alzheimer's disease human brain tissue. <i>Nature Communications</i> , 2021, 12, 7035.	5.8	19
12	Proximal and distal effects of genetic susceptibility to multiple sclerosis on the T cell epigenome. <i>Nature Communications</i> , 2021, 12, 7078.	5.8	15
13	Multi-region brain transcriptomes uncover two subtypes of aging individuals with differences in the impact of <i>APOE</i> ϵ 4. <i>Alzheimer's and Dementia</i> , 2021, 17, e057240.	0.4	1
14	Cell type-specific Alzheimer's disease polygenic risk scores are associated with distinct disease processes in preclinical Alzheimer's disease.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e055304.	0.4	0
15	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	2.4	75
16	Considerations for integrative multi-omic approaches to explore Alzheimer's disease mechanisms. <i>Brain Pathology</i> , 2020, 30, 984-991.	2.1	11
17	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	2.9	199
18	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. <i>Molecular Neurodegeneration</i> , 2020, 15, 44.	4.4	32

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19	Epigenomic features related to microglia are associated with attenuated effect of APOE ϵ 4 on Alzheimer's disease risk in humans. <i>Alzheimer's and Dementia</i> , 2020, 16, e043533.	0.4	2
20	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. <i>Neuron</i> , 2020, 107, 496-508.e6.	3.8	29
21	Bayesian integrative analysis of epigenomic and transcriptomic data identifies Alzheimer's disease candidate genes and networks. <i>PLoS Computational Biology</i> , 2020, 16, e1007771.	1.5	10
22	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer's human brains. <i>Nature Neuroscience</i> , 2019, 22, 37-46.	7.1	188
23	How do we measure the epigenome(s)? <i>Multiple Sclerosis Journal</i> , 2018, 24, 446-448.	1.4	0
24	MS <i>AH1</i> genetic risk promotes IFN γ CD4 T cells. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2018, 5, e414.	3.1	6
25	P3 ϵ 136: MODULE QUANTITATIVE TRAIT LOCI ANALYSIS IMPLICATES <i>TMEM106B</i> AND <i>RBFOX1</i> AS KEY BRAIN TRANSCRIPTOME REGULATORS IN OLDER ADULTS. <i>Alzheimer's and Dementia</i> , 2018, 14, P1120.	0.4	0
26	A multi-omic atlas of the human frontal cortex for aging and Alzheimer's disease research. <i>Scientific Data</i> , 2018, 5, 180142.	2.4	357
27	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. <i>Nature Neuroscience</i> , 2018, 21, 811-819.	7.1	422
28	Tau Activates Transposable Elements in Alzheimer's Disease. <i>Cell Reports</i> , 2018, 23, 2874-2880.	2.9	216
29	Integrative analysis of multiple genomic variables using a hierarchical Bayesian model. <i>Bioinformatics</i> , 2017, 33, 3220-3227.	1.8	5
30	Diurnal and seasonal molecular rhythms in human neocortex and their relation to Alzheimer's disease. <i>Nature Communications</i> , 2017, 8, 14931.	5.8	51
31	Loss of the histone methyltransferase EZH2 induces resistance to multiple drugs in acute myeloid leukemia. <i>Nature Medicine</i> , 2017, 23, 69-78.	15.2	192
32	<i>UNC5C</i> variants are associated with cerebral amyloid angiopathy. <i>Neurology: Genetics</i> , 2017, 3, e176.	0.9	8
33	AML1-ETO requires enhanced C/D box snoRNA/RNP formation to induce self-renewal and leukaemia. <i>Nature Cell Biology</i> , 2017, 19, 844-855.	4.6	132
34	Identification of genes associated with dissociation of cognitive performance and neuropathological burden: Multistep analysis of genetic, epigenetic, and transcriptional data. <i>PLoS Medicine</i> , 2017, 14, e1002287.	3.9	88
35	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. <i>Nature Neuroscience</i> , 2017, 20, 1418-1426.	7.1	377
36	The epigenome in Alzheimer's disease: current state and approaches for a new path to gene discovery and understanding disease mechanism. <i>Acta Neuropathologica</i> , 2016, 132, 503-514.	3.9	44

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37	Uncovering the Role of the Methylome in Dementia and Neurodegeneration. Trends in Molecular Medicine, 2016, 22, 687-700.	3.5	25
38	Integrative Analysis of Histone ChIP-seq and RNA-seq Data. Current Protocols in Human Genetics, 2016, 90, 20.3.1-20.3.16.	3.5	3
39	Rheumatoid arthritis-associated RBPJ polymorphism alters memory CD4 ⁺ T cells. Human Molecular Genetics, 2016, 25, 404-417.	1.4	8
40	An evaluation of methods to test predefined genomic regions for differential methylation in bisulfite sequencing data. Briefings in Bioinformatics, 2016, 17, 796-807.	3.2	40
41	Epigenetic dysregulation of K _{Ca} 3.1 channels induces poor prognosis in lung cancer. International Journal of Cancer, 2015, 137, 1306-1317.	2.3	75
42	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	1.7	20
43	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	7.7	341
44	Deep Sequencing in Conjunction with Expression and Functional Analyses Reveals Activation of FGFR1 in Ewing Sarcoma. Clinical Cancer Research, 2015, 21, 4935-4946.	3.2	68
45	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	0.6	1
46	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
47	Abstract 4430: Loss of the histone methyltransferase EZH2 induces chemoresistance in acute myeloid leukemia (AML). , 2015, , .		0
48	Abstract A2-20: Integrative study of genomic alterations in liposarcoma. , 2015, , .		0
49	Landscape of genetic lesions in 944 patients with myelodysplastic syndromes. Leukemia, 2014, 28, 241-247.	3.3	1,291
50	A New Workflow for Whole-Genome Sequencing of Single Human Cells. Human Mutation, 2014, 35, 1260-1270.	1.1	19
51	DNA Methyltransferase Inhibition Reverses Epigenetically Embedded Phenotypes in Lung Cancer Preferentially Affecting Polycomb Target Genes. Clinical Cancer Research, 2014, 20, 814-826.	3.2	45
52	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. Bioinformatics, 2014, 30, 1154-1162.	1.8	31
53	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	0.6	1
54	Identification of CAR As a Novel Mediator of Erythroid Differentiation and Migration That Is Specifically Downregulated in Erythropoietic Progenitor Cells in Patients with MDS. Blood, 2014, 124, 1570-1570.	0.6	14

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55	Detection of significantly differentially methylated regions in targeted bisulfite sequencing data. <i>Bioinformatics</i> , 2013, 29, 1647-1653.	1.8	230
56	Genomic instability may originate from imatinib-refractory chronic myeloid leukemia stem cells. <i>Blood</i> , 2013, 121, 4175-4183.	0.6	105
57	DNA methylation changes are a late event in acute promyelocytic leukemia and coincide with loss of transcription factor binding. <i>Blood</i> , 2013, 121, 178-187.	0.6	61
58	Robustness of Amplicon Deep Sequencing Underlines Its Utility in Clinical Applications. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 473-484.	1.2	48
59	Cancer gene prioritization by integrative analysis of mRNA expression and DNA copy number data: a comparative review. <i>Briefings in Bioinformatics</i> , 2013, 14, 27-35.	3.2	31
60	Molecular pathways of early CD105-positive erythroid cells as compared with CD34-positive common precursor cells by flow cytometric cell-sorting and gene expression profiling. <i>Blood Cancer Journal</i> , 2013, 3, e100-e100.	2.8	28
61	Multiple myeloma is affected by multiple and heterogeneous somatic mutations in adhesion- and receptor tyrosine kinase signaling molecules. <i>Blood Cancer Journal</i> , 2013, 3, e102-e102.	2.8	51
62	Characterization of ZC3H15 as a potential TRAF-2-interacting protein implicated in the NF κ B pathway and overexpressed in AML. <i>International Journal of Oncology</i> , 2013, 43, 246-254.	1.4	12
63	Endoplasmic reticulum protein GliPR1 regulates G protein signaling and the cell cycle and is overexpressed in AML. <i>Oncology Reports</i> , 2013, 30, 2254-2262.	1.2	13
64	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. <i>Blood</i> , 2013, 122, 521-521.	0.6	14
65	Abnormal Expression Of The Major Coxsackie-Adenovirus Receptor CAR On Immature Dysplastic CD105+ Erythroid Progenitor Cells In Patients With MDS and Related Bone Marrow Neoplasms. <i>Blood</i> , 2013, 122, 2818-2818.	0.6	0
66	CD34+ gene expression profiling of individual children with very severe aplastic anemia indicates a pathogenic role of integrin receptors and the proapoptotic death ligand TRAIL. <i>Haematologica</i> , 2012, 97, 1304-1311.	1.7	13
67	Integrative Analyses for Omics Data: A Bayesian Mixture Model to Assess the Concordance of ChIP-chip and ChIP-seq Measurements. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2012, 75, 461-470.	1.1	15
68	Genome-wide analysis of histone H3 acetylation patterns in AML identifies PRDX2 as an epigenetically silenced tumor suppressor gene. <i>Blood</i> , 2012, 119, 2346-2357.	0.6	72
69	Inhibition of the LSD1 (KDM1A) demethylase reactivates the all-trans-retinoic acid differentiation pathway in acute myeloid leukemia. <i>Nature Medicine</i> , 2012, 18, 605-611.	15.2	584
70	<i>EZH2</i> mutations and their association with <i>PICALM</i> and <i>MLL10</i> positive acute leukaemia. <i>British Journal of Haematology</i> , 2012, 157, 387-390.	1.2	19
71	Leukemia Gene Atlas – A Public Platform for Integrative Exploration of Genome-Wide Molecular Data. <i>PLoS ONE</i> , 2012, 7, e39148.	1.1	47
72	Strategy for Robust Detection of Insertions, Deletions, and Point Mutations in CEBPA, a GC-Rich Content Gene, Using 454 Next-Generation Deep-Sequencing Technology. <i>Journal of Molecular Diagnostics</i> , 2011, 13, 129-136.	1.2	38

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73	Targeted next-generation sequencing detects point mutations, insertions, deletions and balanced chromosomal rearrangements as well as identifies novel leukemia-specific fusion genes in a single procedure. <i>Leukemia</i> , 2011, 25, 671-680.	3.3	40
74	Prognosis in patients with MDS or AML and bone marrow blasts between 10% and 30% is not associated with blast counts but depends on cytogenetic and molecular genetic characteristics. <i>Leukemia</i> , 2011, 25, 1361-1364.	3.3	11
75	Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. <i>Blood</i> , 2011, 118, 6153-6163.	0.6	227
76	Increased HDAC1 deposition at hematopoietic promoters in AML and its association with patient survival. <i>Leukemia Research</i> , 2011, 35, 620-625.	0.4	28
77	The Interlaboratory RObustness of Next-generation sequencing (IRON) study: a deep sequencing investigation of TET2, CBL and KRAS mutations by an international consortium involving 10 laboratories. <i>Leukemia</i> , 2011, 25, 1840-1848.	3.3	96
78	R453Plus1Toolbox: an R/Bioconductor package for analyzing Roche 454 Sequencing data. <i>Bioinformatics</i> , 2011, 27, 1162-1163.	1.8	20
79	EZH2 Mutations Can Be Detected in 23% of t(10;11)(p13;q14)/PICALM-MLLT10 Positive Acute Leukemias. <i>Blood</i> , 2011, 118, 3440-3440.	0.6	0
80	Whole Genome Amplification with Subsequent High Throughput Sequencing Allows Comprehensive Genome-Wide Analysis of Single Leukemic Cells. <i>Blood</i> , 2011, 118, 1437-1437.	0.6	0
81	Histone H3 Methylation Mediates All-Trans-Retinoic Acid Responsiveness in Acute Myeloid Leukemia. <i>Blood</i> , 2011, 118, 224-224.	0.6	0
82	Identification of the PML-RAR α Associated DNA Methylome Using Reduced Representation Bisulfite Sequencing in Primary Patient Samples. <i>Blood</i> , 2011, 118, 2436-2436.	0.6	0
83	Multilineage dysplasia has no impact on biologic, clinicopathologic, and prognostic features of AML with mutated nucleophosmin (NPM1). <i>Blood</i> , 2010, 115, 3776-3786.	0.6	109
84	Profiling of histone H3 lysine 9 trimethylation levels predicts transcription factor activity and survival in acute myeloid leukemia. <i>Blood</i> , 2010, 116, 3564-3571.	0.6	90
85	Multilineage dysplasia (MLD) in acute myeloid leukemia (AML) correlates with MDS-related cytogenetic abnormalities and a prior history of MDS or MDS/MPN but has no independent prognostic relevance: a comparison of 408 cases classified as "AML not otherwise specified" (AML-NOS) or "AML with myelodysplasia-related changes" (AML-MRC). <i>Blood</i> , 2010, 116, 2742-2751.	0.6	111
86	Comparative study of unsupervised dimension reduction techniques for the visualization of microarray gene expression data. <i>BMC Bioinformatics</i> , 2010, 11, 567.	1.2	66
87	Gene expression profiling in AML with normal karyotype can predict mutations for molecular markers and allows novel insights into perturbed biological pathways. <i>Leukemia</i> , 2010, 24, 1216-1220.	3.3	57
88	Next-Generation Sequencing Technology Reveals a Characteristic Pattern of Molecular Mutations in 72.8% of Chronic Myelomonocytic Leukemia by Detecting Frequent Alterations in <i>TET2</i> , <i>CBL</i> , <i>RAS</i> , and <i>RUNX1</i> . <i>Journal of Clinical Oncology</i> , 2010, 28, 3858-3865.	0.8	283
89	Robust and Sensitive Detection of Insertions, Deletions and Point Mutations In CEBPA, a GC-Rich Content Gene, Using 454 Next-Generation Deep-Sequencing (NGS).. <i>Blood</i> , 2010, 116, 1657-1657.	0.6	1
90	Global Identification of Genomic Structural Variants In Childhood ETV6/RUNX1 (TEL/AML1) Acute Lymphoblastic Leukemias by Mate-Pair Massively Parallel Sequencing.. <i>Blood</i> , 2010, 116, 3364-3364.	0.6	0

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91	The Interlaboratory RObustness of Next-Generation Sequencing (IRON) Study: Deep-Sequencing Investigating TET2, CBL, and KRAS Mutations In 4464 Amplicons by An International Group Involving 8 Laboratories.. Blood, 2010, 116, 1665-1665.	0.6	0
92	Targeted Next-Generation Sequencing (NGS) Enables a Broad Screening of 95 Molecular Mutations In a One-Step Approach and Detects Recurrent Mutations In AML with a Normal Karyotype In MYH11 and NOTCH1. Blood, 2010, 116, 175-175.	0.6	0
93	Targeted Next-Generation Sequencing and Genome-Wide High-Resolution Copy Number DNA Arrays Allow the Identification of Five Novel RUNX1 Fusions In Hematological Malignancies.. Blood, 2010, 116, 1193-1193.	0.6	1
94	Quantitative comparison of microarray experiments with published leukemia related gene expression signatures. BMC Bioinformatics, 2009, 10, 422.	1.2	40
95	AML with translocation t(8;16)(p11;p13) demonstrates unique cytomorphological, cytogenetic, molecular and prognostic features. Leukemia, 2009, 23, 934-943.	3.3	90