Hans-Ulrich Klein

List of Publications by Year
in descending order

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95	7,576	94433	60623
papers	citations	37 h-index	81 g-index

105	105	105	13519
all docs	docs citations	times ranked	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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2023, 78, 494-503.	3.6	4
2	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimer's disease risk in humans. Alzheimer's and Dementia, 2022, 18, 688-699.	0.8	9
3	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults. Neurology, 2022, 98, .	1.1	22
4	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies DCDC2 gene as predictor of episodic memory maintenance. Alzheimer's and Dementia, 2022, 18, 1797-1811.	0.8	5
5	Mitochondrial respiratory chain protein co-regulation in the human brain. Heliyon, 2022, 8, e09353.	3.2	4
6	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	9.0	144
7	Cortical proteins may provide motor resilience in older adults. Scientific Reports, 2021, 11, 11311.	3.3	14
8	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. Neurobiology of Disease, 2021, 157, 105428.	4.4	36
9	A cortical immune network map identifies distinct microglial transcriptional programs associated with Î²-amyloid and Tau pathologies. Translational Psychiatry, 2021, 11, 50.	4.8	19
10	Characterization of mitochondrial DNA quantity and quality in the human aged and Alzheimerâ€™s disease brain. Molecular Neurodegeneration, 2021, 16, 75.	10.8	44
11	Atlas of RNA editing events affecting protein expression in aged and Alzheimerâ€™s disease human brain tissue. Nature Communications, 2021, 12, 7035.	12.8	19
12	Proximal and distal effects of genetic susceptibility to multiple sclerosis on the T cell epigenome. Nature Communications, 2021, 12, 7078.	12.8	15
13	Multiâ€region brain transcriptomes uncover two subtypes of aging individuals with differences in the impact of APOEe4. Alzheimer's and Dementia, 2021, 17, e057240.	0.8	1
14	Cell type-specific Alzheimer's disease polygenic risk scores are associated with distinct disease processes in preclinical Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055304.	0.8	0
15	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	5.3	75
16	Considerations for integrative multiâ€omic approaches to explore Alzheimer's disease mechanisms. Brain Pathology, 2020, 30, 984-991.	4.1	11
17	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	6.4	199
18	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. Molecular Neurodegeneration, 2020, 15, 44.	10.8	32

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19	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimerâ€™s disease risk in humans. Alzheimer's and Dementia, 2020, 16, e043533.	0.8	2
20	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. Neuron, 2020, 107, 496-508.e6.	8.1	29
21	Bayesian integrative analysis of epigenomic and transcriptomic data identifies Alzheimer's disease candidate genes and networks. PLoS Computational Biology, 2020, 16, e1007771.	3.2	10
22	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimerâ€™s human brains. Nature Neuroscience, 2019, 22, 37-46.	14.8	188
23	How do we measure the epigenome(s)?. Multiple Sclerosis Journal, 2018, 24, 446-448.	3.0	0
24	MS AHI1 genetic risk promotes IFNÎ³ ⁺ CD4 ⁺ T cells. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e414.	6.0	6
25	P3â€136: MODULE QUANTITATIVE TRAIT LOCI ANALYSIS IMPLICATES TMEM106B AND RBFOX1 AS KEY BRAIN TRANSCRIPTOME REGULATORS IN OLDER ADULTS. Alzheimer's and Dementia, 2018, 14, P1120.	0.8	0
26	A multi-omic atlas of the human frontal cortex for aging and Alzheimerâ€™s disease research. Scientific Data, 2018, 5, 180142.	5.3	357
27	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimerâ€™s disease. Nature Neuroscience, 2018, 21, 811-819.	14.8	422
28	Tau Activates Transposable Elements in Alzheimerâ€™s Disease. Cell Reports, 2018, 23, 2874-2880.	6.4	216
29	Integrative analysis of multiple genomic variables using a hierarchical Bayesian model. Bioinformatics, 2017, 33, 3220-3227.	4.1	5
30	Diurnal and seasonal molecular rhythms in human neocortex and their relation to Alzheimerâ€™s disease. Nature Communications, 2017, 8, 14931.	12.8	51
31	Loss of the histone methyltransferase EZH2 induces resistance to multiple drugs in acute myeloid leukemia. Nature Medicine, 2017, 23, 69-78.	30.7	192
32	UNC5C variants are associated with cerebral amyloid angiopathy. Neurology: Genetics, 2017, 3, e176.	1.9	8
33	AML1-ETO requires enhanced C/D box snoRNA/RNP formation to induce self-renewal and leukaemia. Nature Cell Biology, 2017, 19, 844-855.	10.3	132
34	Identification of genes associated with dissociation of cognitive performance and neuropathological burden: Multistep analysis of genetic, epigenetic, and transcriptional data. PLoS Medicine, 2017, 14, e1002287.	8.4	88
35	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. Nature Neuroscience, 2017, 20, 1418-1426.	14.8	377
36	The epigenome in Alzheimerâ€™s disease: current state and approaches for a new path to gene discovery and understanding disease mechanism. Acta Neuropathologica, 2016, 132, 503-514.	7.7	44

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37	Uncovering the Role of the Methylome in Dementia and Neurodegeneration. Trends in Molecular Medicine, 2016, 22, 687-700.	6.7	25
38	Integrative Analysis of Histone ChIPâ€seq and RNAâ€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.	2.9	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.	6.5	40
41	Epigenetic dysregulation of K_{Ca}3.1 channels induces poor prognosis in lung cancer. International Journal of Cancer, 2015, 137, 1306-1317.	5.1	75
42	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	3.5	20
43	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	16.8	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.	7.0	68
45	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	1.4	1
46	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	1.8	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.	7.2	1,291
50	A New Workflow for Whole-Genome Sequencing of Single Human Cells. Human Mutation, 2014, 35, 1260-1270.	2.5	19
51	DNA Methyltransferase Inhibition Reverses Epigenetically Embedded Phenotypes in Lung Cancer Preferentially Affecting Polycomb Target Genes. Clinical Cancer Research, 2014, 20, 814-826.	7.0	45
52	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. Bioinformatics, 2014, 30, 1154-1162.	4.1	31
53	DDX41 Is a Tumor Suppressor Gene Associated with Inherited and Acquired Mutations. Blood, 2014, 124, 125-125.	1.4	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.	1.4	14

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55	Detection of significantly differentially methylated regions in targeted bisulfite sequencing data. Bioinformatics, 2013, 29, 1647-1653.	4.1	230
56	Genomic instability may originate from imatinib-refractory chronic myeloid leukemia stem cells. Blood, 2013, 121, 4175-4183.	1.4	105
57	DNA methylation changes are a late event in acute promyelocytic leukemia and coincide with loss of transcription factor binding. Blood, 2013, 121, 178-187.	1.4	61
58	Robustness of Amplicon Deep Sequencing Underlines Its Utility in Clinical Applications. Journal of Molecular Diagnostics, 2013, 15, 473-484.	2.8	48
59	Cancer gene prioritization by integrative analysis of mRNA expression and DNA copy number data: a comparative review. Briefings in Bioinformatics, 2013, 14, 27-35.	6.5	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. Blood Cancer Journal, 2013, 3, e100-e100.	6.2	28
61	Multiple myeloma is affected by multiple and heterogeneous somatic mutations in adhesion- and receptor tyrosine kinase signaling molecules. Blood Cancer Journal, 2013, 3, e102-e102.	6.2	51
62	Characterization of ZC3H15 as a potential TRAF-2-interacting protein implicated in the NFÎºB pathway and overexpressed in AML. International Journal of Oncology, 2013, 43, 246-254.	3.3	12
63	Endoplasmic reticulum protein GliPR1 regulates G protein signaling and the cell cycle and is overexpressed in AML. Oncology Reports, 2013, 30, 2254-2262.	2.6	13
64	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	1.4	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. Blood, 2013, 122, 2818-2818.	1.4	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. Haematologica, 2012, 97, 1304-1311.	3.5	13
67	Integrative Analyses for Omics Data: A Bayesian Mixture Model to Assess the Concordance of ChIP-chip and ChIP-seq Measurements. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2012, 75, 461-470.	2.3	15
68	Genome-wide analysis of histone H3 acetylation patterns in AML identifies PRDX2 as an epigenetically silenced tumor suppressor gene. Blood, 2012, 119, 2346-2357.	1.4	72
69	Inhibition of the LSD1 (KDM1A) demethylase reactivates the all-trans-retinoic acid differentiation pathway in acute myeloid leukemia. Nature Medicine, 2012, 18, 605-611.	30.7	584
70	EZH2 mutations and their association with PICALMâ€MLLT10 positive acute leukaemia. British Journal of Haematology, 2012, 157, 387-390.	2.5	19
71	Leukemia Gene Atlas â€“ A Public Platform for Integrative Exploration of Genome-Wide Molecular Data. PLoS ONE, 2012, 7, e39148.	2.5	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. Journal of Molecular Diagnostics, 2011, 13, 129-136.	2.8	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. Leukemia, 2011, 25, 671-680.	7.2	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. Leukemia, 2011, 25, 1361-1364.	7.2	11
75	Whole-exome sequencing identifies somatic mutations of BCOR in acute myeloid leukemia with normal karyotype. Blood, 2011, 118, 6153-6163.	1.4	227
76	Increased HDAC1 deposition at hematopoietic promoters in AML and its association with patient survival. Leukemia Research, 2011, 35, 620-625.	0.8	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. Leukemia, 2011, 25, 1840-1848.	7.2	96
78	R453Plus1Toolbox: an R/Bioconductor package for analyzing Roche 454 Sequencing data. Bioinformatics, 2011, 27, 1162-1163.	4.1	20
79	EZH2 Mutations Can Be Detected in 23% of t(10;11)(p13;q14)/PICALM-MLLT10 Positive Acute Leukemias,. Blood, 2011, 118, 3440-3440.	1.4	0
80	Whole Genome Amplification with Subsequent High Throughput Sequencing Allows Comprehensive Genome-Wide Analysis of Single Leukemic Cells. Blood, 2011, 118, 1437-1437.	1.4	0
81	Histone H3 Methylation Mediates All-Trans-Retinoic Acid Responsiveness in Acute Myeloid Leukemia. Blood, 2011, 118, 224-224.	1.4	0
82	Identification of the PML-RARÎ± Associated DNA Methylome Using Reduced Representation Bisulfite Sequencing in Primary Patient Samples. Blood, 2011, 118, 2436-2436.	1.4	0
83	Multilineage dysplasia has no impact on biologic, clinicopathologic, and prognostic features of AML with mutated nucleophosmin (NPM1). Blood, 2010, 115, 3776-3786.	1.4	109
84	Profiling of histone H3 lysine 9 trimethylation levels predicts transcription factor activity and survival in acute myeloid leukemia. Blood, 2010, 116, 3564-3571.	1.4	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 â€œAML not otherwise specifiedâ€•(AML-NOS) or â€œAML with myelodysplasia-related changesâ€•(AML-MRC). Blood, 2010, 116, 2742-2751.	1.4	111
86	Comparative study of unsupervised dimension reduction techniques for the visualization of microarray gene expression data. BMC Bioinformatics, 2010, 11, 567.	2.6	66
87	Gene expression profiling in AML with normal karyotype can predict mutations for molecular markers and allows novel insights into perturbed biological pathways. Leukemia, 2010, 24, 1216-1220.	7.2	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 TET2, CBL, RAS, and RUNX1. Journal of Clinical Oncology, 2010, 28, 3858-3865.	1.6	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).. Blood, 2010, 116, 1657-1657.	1.4	1
90	Global Identification of Genomic Structural Variants In Childhood ETV6/RUNX1 (TEL/AML1) Acute Lymphoblastic Leukemias by Mate-Pair Massively Parallel Sequencing.. Blood, 2010, 116, 3364-3364.	1.4	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.	1.4	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.	1.4	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.	1.4	1
94	Quantitative comparison of microarray experiments with published leukemia related gene expression signatures. BMC Bioinformatics, 2009, 10, 422.	2.6	40
95	AML with translocation t(8;16)(p11;p13) demonstrates unique cytomorphological, cytogenetic, molecular and prognostic features. Leukemia, 2009, 23, 934-943.	7.2	90