

Erik Ben van den Akker

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,760
citations

218381

26
h-index

205818

48
g-index

69
all docs

69
docs citations

69
times ranked

5797
citing authors

#	ARTICLE	IF	CITATIONS
1	The trans-ancestral genomic architecture of glyceic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
2	Genome-wide association study identifies a single major locus contributing to survival into old age; the <i>APOE</i> locus revisited. <i>Aging Cell</i> , 2011, 10, 686-698.	3.0	249
3	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. <i>Human Molecular Genetics</i> , 2014, 23, 4420-4432.	1.4	227
4	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013, 6, 26.	1.8	192
5	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , 2019, 10, 3346.	5.8	188
6	Genome-wide linkage analysis for human longevity: Genetics of Healthy Aging Study. <i>Aging Cell</i> , 2013, 12, 184-193.	3.0	170
7	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. <i>Age</i> , 2013, 35, 235-249.	3.0	105
8	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	5.8	89
9	A nonsynonymous mutation in <i>PLCG2</i> reduces the risk of Alzheimer's disease, dementia with Lewy bodies and frontotemporal dementia, and increases the likelihood of longevity. <i>Acta Neuropathologica</i> , 2019, 138, 237-250.	3.9	87
10	Underlying molecular mechanisms of <i>DIO2</i> susceptibility in symptomatic osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1571-1579.	0.5	75
11	Fibroblast growth factor 21 reflects liver fat accumulation and dysregulation of signalling pathways in the liver of C57BL/6J mice. <i>Scientific Reports</i> , 2016, 6, 30484.	1.6	72
12	Genome-Wide Association Study on Immunoglobulin G Glycosylation Patterns. <i>Frontiers in Immunology</i> , 2018, 9, 277.	2.2	66
13	Human Plasma N-glycosylation as Analyzed by Matrix-Assisted Laser Desorption/Ionization-Fourier Transform Ion Cyclotron Resonance-MS Associates with Markers of Inflammation and Metabolic Health. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 228-242.	2.5	58
14	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug-metabolite atlas. <i>Nature Medicine</i> , 2020, 26, 110-117.	15.2	54
15	Metabolic Age Based on the BBMRI-NL ¹ H-NMR Metabolomics Repository as Biomarker of Age-related Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 541-547.	1.6	50
16	Broad phenotype of cysteine-altering <i>NOTCH3</i> variants in UK Biobank. <i>Neurology</i> , 2020, 95, e1835-e1843.	1.5	49
17	Comprehensive diagnostics of acute myeloid leukemia by whole transcriptome RNA sequencing. <i>Leukemia</i> , 2021, 35, 47-61.	3.3	47
18	Integrating Metabolomics, Genomics, and Disease Pathways in Age-Related Macular Degeneration. <i>Ophthalmology</i> , 2020, 127, 1693-1709.	2.5	43

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19	Meta-analysis on blood transcriptomic studies identifies consistently coexpressed protein-protein interaction modules as robust markers of human aging. <i>Aging Cell</i> , 2014, 13, 216-225.	3.0	42
20	Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. <i>Twin Research and Human Genetics</i> , 2013, 16, 1026-1032.	0.3	40
21	Association of common genetic variants with brain microbleeds. <i>Neurology</i> , 2020, 95, e3331-e3343.	1.5	40
22	IL7R gene expression network associates with human healthy ageing. <i>Immunity and Ageing</i> , 2015, 12, 21.	1.8	39
23	Transcriptional Profiling of Human Familial Longevity Indicates a Role for ASF1A and IL7R. <i>PLoS ONE</i> , 2012, 7, e27759.	1.1	39
24	Uncompromised 10-year survival of oldest old carrying somatic mutations in DNMT3A and TET2. <i>Blood</i> , 2016, 127, 1512-1515.	0.6	38
25	Patients with Concurrent Tuberculosis and Diabetes Have a Pro-Atherogenic Plasma Lipid Profile. <i>EBioMedicine</i> , 2018, 32, 192-200.	2.7	36
26	Machine Learning Electronic Health Record Identification of Patients with Rheumatoid Arthritis: Algorithm Pipeline Development and Validation Study. <i>JMIR Medical Informatics</i> , 2020, 8, e23930.	1.3	29
27	Metabolic effects of a 13-weeks lifestyle intervention in older adults: The Growing Old Together Study. <i>Aging</i> , 2016, 8, 111-124.	1.4	28
28	Employing biomarkers of healthy ageing for leveraging genetic studies into human longevity. <i>Experimental Gerontology</i> , 2016, 82, 166-174.	1.2	27
29	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. <i>Communications Biology</i> , 2019, 2, 285.	2.0	27
30	A Comprehensive Workflow for Applying Single-Cell Clustering and Pseudotime Analysis to Flow Cytometry Data. <i>Journal of Immunology</i> , 2020, 205, 864-871.	0.4	25
31	Integrating protein-protein interaction networks with gene-gene co-expression networks improves gene signatures for classifying breast cancer metastasis. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 188.	1.0	20
32	1H-NMR metabolomics-based surrogates to impute common clinical risk factors and endpoints. <i>EBioMedicine</i> , 2022, 75, 103764.	2.7	15
33	Population matched (pm) germline allelic variants of immunoglobulin (IG) loci: Relevance in infectious diseases and vaccination studies in human populations. <i>Genes and Immunity</i> , 2021, 22, 172-186.	2.2	14
34	A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention. <i>Human Molecular Genetics</i> , 2011, 20, 4748-4757.	1.4	13
35	The effect of standardized food intake on the association between BMI and 1H-NMR metabolites. <i>Scientific Reports</i> , 2016, 6, 38980.	1.6	12
36	Gene expression identifies patients who develop inflammatory arthritis in a clinically suspect arthralgia cohort. <i>Arthritis Research and Therapy</i> , 2020, 22, 266.	1.6	10

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37	Integrating Protein-Protein Interaction Networks with Gene- Gene Co-Expression Networks improves Gene Signatures for Classifying Breast Cancer Metastasis. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 222-238.	1.0	9
38	Dynamic clonal hematopoiesis and functional T-cell immunity in a supercentenarian. <i>Leukemia</i> , 2021, 35, 2125-2129.	3.3	9
39	A data-driven methodology reveals novel myofiber clusters in older human muscles. <i>FASEB Journal</i> , 2020, 34, 5525-5537.	0.2	7
40	The Role of Age-Related Clonal Hematopoiesis in Genetic Sequencing Studies. <i>American Journal of Human Genetics</i> , 2020, 107, 575-576.	2.6	6
41	Lifestyle-Intervention-Induced Reduction of Abdominal Fat Is Reflected by a Decreased Circulating Glycerol Level and an Increased HDL Diameter. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e1900818.	1.5	6
42	A framework for employing longitudinally collected multicenter electronic health records to stratify heterogeneous patient populations on disease history. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2022, 29, 761-769.	2.2	6
43	Exome and Whole Genome Sequencing in Aging and Longevity. <i>Advances in Experimental Medicine and Biology</i> , 2015, 847, 127-139.	0.8	5
44	Discovering fiber type architecture over the entire muscle using data-driven analysis. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021, 99, 1240-1249.	1.1	5
45	ImSpectR: R package to quantify immune repertoire diversity in spectratype and repertoire sequencing data. <i>Bioinformatics</i> , 2020, 36, 1930-1932.	1.8	3
46	Clonal Hematopoiesis Analyses in Clinical, Epidemiologic, and Genetic Aging Studies to Unravel Underlying Mechanisms of Age-Related Dysfunction in Humans. <i>Frontiers in Aging</i> , 2022, 3, .	1.2	3
47	Commentary to: Masoli et al. Clinical Outcomes of CADASIL-Associated NOTCH3 mutations in 451,424 European Ancestry Community Volunteers. (<i>Translational Stroke Research</i> Oct 2018). <i>Translational Stroke Research</i> , 2019, 10, 458-459.	2.3	2
48	High-throughput data-driven analysis of myofiber composition reveals muscle-specific disease and age-associated patterns. <i>FASEB Journal</i> , 2019, 33, 4046-4053.	0.2	2
49	Longitudinal Dynamics of Human B-Cell Response at the Single-Cell Level in Response to Tdap Vaccination. <i>Vaccines</i> , 2021, 9, 1352.	2.1	2
50	T and NK Cells in IL2RG-Deficient Patient 50 Years After Hematopoietic Stem Cell Transplantation. <i>Journal of Clinical Immunology</i> , 2022, 42, 1205-1222.	2.0	2
51	Gene coexpression network analysis for family studies based on a meta-analytic approach. <i>BMC Proceedings</i> , 2016, 10, 119-123.	1.8	1
52	The Transcriptome in Transition: Global Gene Expression Profiles of Young Adult Fruit Flies Depend More Strongly on Developmental Than Adult Diet. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	1
53	Whole Transcriptome RNA Sequencing As a Comprehensive Diagnostic Tool for Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 2762-2762.	0.6	0
54	A Data-Driven Methodology Reveals Novel Myofiber Clusters in Older Human Muscles. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

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55	Reply to the Commentary on population matched (pm) germline allelic variants of immunoglobulin (IG) loci: relevance in infectious diseases and vaccination studies in human populations. <i>Genes and Immunity</i> , 2021, 22, 339-342.	2.2	0