

# Ruud Van Der Breggen

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

2,936  
citations

236925

25  
h-index

434195

31  
g-index

31  
all docs

31  
docs citations

31  
times ranked

6610  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation in peripheral tissues and left-handedness. <i>Scientific Reports</i> , 2022, 12, 5606.	3.3	12
2	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021, 26, 2148-2162.	7.9	21
3	High-dimensional cytometric analysis of colorectal cancer reveals novel mediators of antitumour immunity. <i>Gut</i> , 2020, 69, 691-703.	12.1	92
4	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , 2020, 21, 220.	8.8	27
5	A 40-Marker Panel for High Dimensional Characterization of Cancer Immune Microenvironments by Imaging Mass Cytometry. <i>Frontiers in Immunology</i> , 2019, 10, 2534.	4.8	101
6	Revisiting immune escape in colorectal cancer in the era of immunotherapy. <i>British Journal of Cancer</i> , 2019, 120, 815-818.	6.4	30
7	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019, 86, 599-607.	1.3	47
8	Neoantigen-specific immunity in low mutation burden colorectal cancers of the consensus molecular subtype 4. <i>Genome Medicine</i> , 2019, 11, 87.	8.2	44
9	Annotating Transcriptional Effects of Genetic Variants in Disease-Relevant Tissue: Transcriptome-Wide Allelic Imbalance in Osteoarthritic Cartilage. <i>Arthritis and Rheumatology</i> , 2019, 71, 561-570.	5.6	27
10	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017, 49, 131-138.	21.4	390
11	Aberrant Calreticulin Expression in Articular Cartilage of <i>Dio2</i> Deficient Mice. <i>PLoS ONE</i> , 2016, 11, e0154999.	2.5	2
12	The effect of forced exercise on knee joints in <i>Dio2</i> <sup>+/+</sup> mice: type II iodothyronine deiodinase-deficient mice are less prone to develop OA-like cartilage damage upon excessive mechanical stress. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 571-577.	0.9	31
13	Transcriptional Associations of Osteoarthritis-Mediated Loss of Epigenetic Control in Articular Cartilage. <i>Arthritis and Rheumatology</i> , 2015, 67, 2108-2116.	5.6	47
14	IL7R gene expression network associates with human healthy ageing. <i>Immunity and Ageing</i> , 2015, 12, 21.	4.2	39
15	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	6.2	116
16	Underlying molecular mechanisms of <i>DIO2</i> susceptibility in symptomatic osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1571-1579.	0.9	75
17	A gain of function mutation in <i>TNFRSF11B</i> encoding osteoprotegerin causes osteoarthritis with chondrocalcinosis. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1756-1762.	0.9	44
18	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. <i>PLoS ONE</i> , 2014, 9, e103056.	2.5	142

#	ARTICLE	IF	CITATIONS
19	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.	2.9	227
20	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013, 6, 26.	3.9	192
21	Gene expression analysis of mTOR pathway: association with human longevity. <i>Aging Cell</i> , 2013, 12, 24-31.	6.7	104
22	Increased type II deiodinase protein in OA-affected cartilage and allelic imbalance of OA risk polymorphism rs225014 at DIO2 in human OA joint tissues. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 1254-1258.	0.9	53
23	Transcriptional Profiling of Human Familial Longevity Indicates a Role for ASF1A and IL7R. <i>PLoS ONE</i> , 2012, 7, e27759.	2.5	39
24	Meta-analyses of genes modulating intracellular T3 bio-availability reveal a possible role for the DIO3 gene in osteoarthritis susceptibility. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 164-167.	0.9	50
25	Genome-wide association study identifies a single major locus contributing to survival into old age; the APOE locus revisited. <i>Aging Cell</i> , 2011, 10, 686-698.	6.7	249
26	A genome-wide association study identifies an osteoarthritis susceptibility locus on chromosome 7q22. <i>Arthritis and Rheumatism</i> , 2010, 62, 499-510.	6.7	178
27	A genome-wide linkage scan reveals CD53 as an important regulator of innate TNF- $\alpha$ levels. <i>European Journal of Human Genetics</i> , 2010, 18, 953-959.	2.8	23
28	Genome-wide association study (GWAS)-identified disease risk alleles do not compromise human longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18046-18049.	7.1	138
29	Large replication study and meta-analyses of DVWA as an osteoarthritis susceptibility locus in European and Asian populations. <i>Human Molecular Genetics</i> , 2009, 18, 1518-1523.	2.9	50
30	Identification of DIO2 as a new susceptibility locus for symptomatic osteoarthritis. <i>Human Molecular Genetics</i> , 2008, 17, 1867-1875.	2.9	190
31	A meta-analysis of European and Asian cohorts reveals a global role of a functional SNP in the 5' UTR of GDF5 with osteoarthritis susceptibility. <i>Human Molecular Genetics</i> , 2008, 17, 1497-1504.	2.9	156