

Steffan D Bos

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

3,557
citations

218677

26
h-index

223800

46
g-index

50
all docs

50
docs citations

50
times ranked

6532
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	12.6	710
2	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. <i>Lancet</i> , The, 2012, 380, 815-823.	13.7	373
3	Incidence of gastrointestinal stromal tumours is underestimated: Results of a nation-wide study. <i>European Journal of Cancer</i> , 2005, 41, 2868-2872.	2.8	266
4	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. <i>PLoS Genetics</i> , 2013, 9, e1003266.	3.5	194
5	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
6	Identification of DIO2 as a new susceptibility locus for symptomatic osteoarthritis. <i>Human Molecular Genetics</i> , 2008, 17, 1867-1875.	2.9	190
7	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
8	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 349-355.	0.9	126
9	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2130-2136.	0.9	108
10	Knee and hip articular cartilage have distinct epigenomic landscapes: implications for future cartilage regeneration approaches. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2208-2212.	0.9	96
11	Genome-Wide DNA Methylation Profiles Indicate CD8+ T Cell Hypermethylation in Multiple Sclerosis. <i>PLoS ONE</i> , 2015, 10, e0117403.	2.5	88
12	Multiple sclerosis risk loci and disease severity in 7,125 individuals from 10 studies. <i>Neurology: Genetics</i> , 2016, 2, e87.	1.9	76
13	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
14	GREM1, FRZB and DKK1 mRNA levels correlate with osteoarthritis and are regulated by osteoarthritis-associated factors. <i>Arthritis Research and Therapy</i> , 2013, 15, R126.	3.5	74
15	Large-scale meta-analysis of interleukin-1 beta and interleukin-1 receptor antagonist polymorphisms on risk of radiographic hip and knee osteoarthritis and severity of knee osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2011, 19, 265-271.	1.3	72
16	New insights into osteoarthritis: early developmental features of an ageing-related disease. <i>Current Opinion in Rheumatology</i> , 2008, 20, 553-559.	4.3	66
17	Genes expressed in blood link osteoarthritis with apoptotic pathways. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 1844-1853.	0.9	61
18	Genetic variants are major determinants of CSF antibody levels in multiple sclerosis. <i>Brain</i> , 2015, 138, 632-643.	7.6	54

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19	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
20	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
21	Transcriptional Associations of Osteoarthritis-Mediated Loss of Epigenetic Control in Articular Cartilage. <i>Arthritis and Rheumatology</i> , 2015, 67, 2108-2116.	5.6	47
22	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
23	Oligoclonal bands and age at onset correlate with genetic risk score in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2014, 20, 660-668.	3.0	42
24	Increased DNA methylation of SLFN12 in CD4+ and CD8+ T cells from multiple sclerosis patients. <i>PLoS ONE</i> , 2018, 13, e0206511.	2.5	37
25	The multiple sclerosis susceptibility genes TAGAP and IL2RA are regulated by vitamin D in CD4+ T cells. <i>Genes and Immunity</i> , 2016, 17, 118-127.	4.1	35
26	Allelic variation at the C-reactive protein gene associates to both hand osteoarthritis severity and serum high sensitive C-reactive protein levels in the GARP study. <i>Annals of the Rheumatic Diseases</i> , 2008, 67, 877-879.	0.9	31
27	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. <i>Genes and Immunity</i> , 2014, 15, 126-132.	4.1	26
28	Genetic overlap between multiple sclerosis and several cardiovascular disease risk factors. <i>Multiple Sclerosis Journal</i> , 2016, 22, 1783-1793.	3.0	25
29	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. <i>Neuron</i> , 2016, 92, 333-335.	8.1	24
30	A genome-wide linkage scan reveals CD53 as an important regulator of innate TNF- α levels. <i>European Journal of Human Genetics</i> , 2010, 18, 953-959.	2.8	23
31	The role of plasma cytokine levels, CRP and Selenoprotein S gene variation in OA. <i>Osteoarthritis and Cartilage</i> , 2009, 17, 621-626.	1.3	18
32	Retinoic acid enhances the levels of IL-10 in TLR-stimulated B cells from patients with relapsing-remitting multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2015, 278, 11-18.	2.3	18
33	Multiple Sclerosis Risk Allele in CLEC16A Acts as an Expression Quantitative Trait Locus for CLEC16A and SOCS1 in CD4+ T Cells. <i>PLoS ONE</i> , 2015, 10, e0132957.	2.5	16
34	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. <i>Npj Genomic Medicine</i> , 2017, 2, 24.	3.8	16
35	Allelic imbalance of multiple sclerosis susceptibility genes IKZF3 and IQGAP1 in human peripheral blood. <i>BMC Genetics</i> , 2016, 17, 59.	2.7	14
36	Serum neurofilament light chain concentration predicts disease worsening in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2022, 28, 1859-1870.	3.0	14

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37	Metabolic health in families enriched for longevity is associated with low prevalence of hand osteoarthritis and influences OA biomarker profiles. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 1669-1674.	0.9	13
38	Interleukin-1 gene cluster variants with innate cytokine production profiles and osteoarthritis in subjects from the Genetics, Osteoarthritis and Progression Study. <i>Arthritis and Rheumatism</i> , 2010, 62, 1119-1126.	6.7	10
39	No differential gene expression for CD4+ T cells of MS patients and healthy controls. <i>Multiple Sclerosis Journal - Experimental, Translational and Clinical</i> , 2019, 5, 205521731985690.	1.0	9
40	From genetic associations to functional studies in multiple sclerosis. <i>European Journal of Neurology</i> , 2016, 23, 847-853.	3.3	8
41	Quantitative proteomics reveals protein dysregulation during T cell activation in multiple sclerosis patients compared to healthy controls. <i>Clinical Proteomics</i> , 2022, 19, .	2.1	5
42	Exploring the role of the multiple sclerosis susceptibility gene <i>CLEC16A</i> in T cells. <i>Scandinavian Journal of Immunology</i> , 2021, 94, e13050.	2.7	4
43	83 ANALYSIS OF CANDIDATE OSTEOARTHRITIS GENES IN A META-ANALYSIS OF 8 GENOME-WIDE ASSOCIATION STUDIES. <i>Osteoarthritis and Cartilage</i> , 2011, 19, S42-S43.	1.3	2
44	Pregnancy does not modify the risk of MS in genetically susceptible women. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2020, 7, .	6.0	2
45	CD8+ T cell gene expression analysis identifies differentially expressed genes between multiple sclerosis patients and healthy controls. <i>Multiple Sclerosis Journal - Experimental, Translational and Clinical</i> , 2020, 6, 205521732097851.	1.0	2
46	353 GENOME WIDE EXPRESSION ANALYSIS OF OSTEOARTHRITIS AFFECTED AND PRESERVED CARTILAGE FROM JOINT REPLACEMENT SURGERY MATERIAL IN THE RAAK STUDY. <i>Osteoarthritis and Cartilage</i> , 2011, 19, S159-S160.	1.3	0
47	Genes associated with osteoarthritis identified by microarray-analysis of whole blood samples link oa to apoptotic pathways. <i>Osteoarthritis and Cartilage</i> , 2012, 20, S77-S78.	1.3	0
48	Probing the articular cartilage transcriptome for genetic osteoarthritis susceptibility. <i>Osteoarthritis and Cartilage</i> , 2015, 23, A190-A191.	1.3	0