Steffan D Bos

List of Publications by Year in descending order

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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	Serum neurofilament light chain concentration predicts disease worsening in multiple sclerosis. Multiple Sclerosis Journal, 2022, 28, 1859-1870.	3.0	14
2	Quantitative proteomics reveals protein dysregulation during T cell activation in multiple sclerosis patients compared to healthy controls. Clinical Proteomics, 2022, 19, .	2.1	5
3	Exploring the role of the multiple sclerosis susceptibility gene CLEC16A in T cells. Scandinavian Journal of Immunology, 2021, 94, e13050.	2.7	4
4	Pregnancy does not modify the risk of MS in genetically susceptible women. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, .	6.0	2
5	CD8+ T cell gene expression analysis identifies differentially expressed genes between multiple sclerosis patients and healthy controls. Multiple Sclerosis Journal - Experimental, Translational and Clinical, 2020, 6, 205521732097851.	1.0	2
6	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. Science, 2019, 365, .	12.6	710
7	No differential gene expression for CD4+ T cells of MS patients and healthy controls. Multiple Sclerosis Journal - Experimental, Translational and Clinical, 2019, 5, 205521731985690.	1.0	9
8	Increased DNA methylation of SLFN12 in CD4+ and CD8+ T cells from multiple sclerosis patients. PLoS ONE, 2018, 13, e0206511.	2.5	37
9	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. Npj Genomic Medicine, 2017, 2, 24.	3.8	16
10	From genetic associations to functional studies in multiple sclerosis. European Journal of Neurology, 2016, 23, 847-853.	3.3	8
11	Multiple sclerosis risk loci and disease severity in 7,125 individuals from 10 studies. Neurology: Genetics, 2016, 2, e87.	1.9	76
12	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. Neuron, 2016, 92, 333-335.	8.1	24
13	Allelic imbalance of multiple sclerosis susceptibility genes IKZF3 and IQGAP1 in human peripheral blood. BMC Genetics, 2016, 17, 59.	2.7	14
14	The multiple sclerosis susceptibility genes TAGAP and IL2RA are regulated by vitamin D in CD4+ T cells. Genes and Immunity, 2016, 17, 118-127.	4.1	35
15	Genetic overlap between multiple sclerosis and several cardiovascular disease risk factors. Multiple Sclerosis Journal, 2016, 22, 1783-1793.	3.0	25
16	Transcriptional Associations of Osteoarthritisâ€Mediated Loss of Epigenetic Control in Articular Cartilage. Arthritis and Rheumatology, 2015, 67, 2108-2116.	5.6	47
17	Genome-Wide DNA Methylation Profiles Indicate CD8+ T Cell Hypermethylation in Multiple Sclerosis. PLoS ONE, 2015, 10, e0117403.	2.5	88
18	Multiple Sclerosis Risk Allele in CLEC16A Acts as an Expression Quantitative Trait Locus for CLEC16A and SOCS1 in CD4+ T Cells. PLoS ONE, 2015, 10, e0132957.	2.5	16

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19	Genetic variants are major determinants of CSF antibody levels in multiple sclerosis. Brain, 2015, 138, 632-643.	7.6	54
20	Underlying molecular mechanisms ofDIO2susceptibility in symptomatic osteoarthritis. Annals of the Rheumatic Diseases, 2015, 74, 1571-1579.	0.9	75
21	Probing the articular cartilage transcriptome for genetic osteoarthritis susceptiblity. Osteoarthritis and Cartilage, 2015, 23, A190-A191.	1.3	0
22	A gain of function mutation inTNFRSF11Bencoding osteoprotegerin causes osteoarthritis with chondrocalcinosis. Annals of the Rheumatic Diseases, 2015, 74, 1756-1762.	0.9	44
23	Retinoic acid enhances the levels of IL-10 in TLR-stimulated B cells from patients with relapsingâ€“remitting multiple sclerosis. Journal of Neuroimmunology, 2015, 278, 11-18.	2.3	18
24	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. PLoS ONE, 2014, 9, e103056.	2.5	142
25	Knee and hip articular cartilage have distinct epigenomic landscapes: implications for future cartilage regeneration approaches. Annals of the Rheumatic Diseases, 2014, 73, 2208-2212.	0.9	96
26	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.9	108
27	Genes expressed in blood link osteoarthritis with apoptotic pathways. Annals of the Rheumatic Diseases, 2014, 73, 1844-1853.	0.9	61
28	Oligoclonal bands and age at onset correlate with genetic risk score in multiple sclerosis. Multiple Sclerosis Journal, 2014, 20, 660-668.	3.0	42
29	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. Genes and Immunity, 2014, 15, 126-132.	4.1	26
30	GREM1, FRZB and DKK1 mRNA levels correlate with osteoarthritis and are regulated by osteoarthritis-associated factors. Arthritis Research and Therapy, 2013, 15, R126.	3.5	74
31	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. Epigenetics and Chromatin, 2013, 6, 26.	3.9	192
32	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. PLoS Genetics, 2013, 9, e1003266.	3.5	194
33	Metabolic health in families enriched for longevity is associated with low prevalence of hand osteoarthritis and influences OA biomarker profiles. Annals of the Rheumatic Diseases, 2013, 72, 1669-1674.	0.9	13
34	Increased type II deiodinase protein in OA-affected cartilage and allelic imbalance of OA risk polymorphism rs225014 at DIO2 in human OA joint tissues. Annals of the Rheumatic Diseases, 2012, 71, 1254-1258.	0.9	53
35	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
36	Genes associated with osteoarthritis identified by microarray-analysis of whole blood samples link oa to apoptotic pathways. Osteoarthritis and Cartilage, 2012, 20, S77-S78.	1.3	0

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37	Meta-analyses of genes modulating intracellular T3 bio-availability reveal a possible role for the DIO3 gene in osteoarthritis susceptibility. Annals of the Rheumatic Diseases, 2011, 70, 164-167.	0.9	50
38	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. Annals of the Rheumatic Diseases, 2011, 70, 349-355.	0.9	126
39	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. Osteoarthritis and Cartilage, 2011, 19, 265-271.	1.3	72
40	83 ANALYSIS OF CANDIDATE OSTEOARTHRITIS GENES IN A META-ANALYSIS OF 8 GENOME-WIDE ASSOCIATION STUDIES. Osteoarthritis and Cartilage, 2011, 19, S42-S43.	1.3	2
41	353 GENOME WIDE EXPRESSION ANALYSIS OF OSTEOARTHRITIS AFFECTED AND PRESERVED CARTILAGE FROM JOINT REPLACEMENT SURGERY MATERIAL IN THE RAAK STUDY. Osteoarthritis and Cartilage, 2011, 19, S159-S160.	1.3	0
42	Interleukinâ€1 gene cluster variants with innate cytokine production profiles and osteoarthritis in subjects from the Genetics, Osteoarthritis and Progression Study. Arthritis and Rheumatism, 2010, 62, 1119-1126.	6.7	10
43	A genome-wide linkage scan reveals CD53 as an important regulator of innate TNF-Î± levels. European Journal of Human Genetics, 2010, 18, 953-959.	2.8	23
44	The role of plasma cytokine levels, CRP and Selenoprotein S gene variation in OA. Osteoarthritis and Cartilage, 2009, 17, 621-626.	1.3	18
45	Identification of DIO2 as a new susceptibility locus for symptomatic osteoarthritis. Human Molecular Genetics, 2008, 17, 1867-1875.	2.9	190
46	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. Annals of the Rheumatic Diseases, 2008, 67, 877-879.	0.9	31
47	New insights into osteoarthritis: early developmental features of an ageing-related disease. Current Opinion in Rheumatology, 2008, 20, 553-559.	4.3	66
48	Incidence of gastrointestinal stromal tumours is underestimated: Results of a nation-wide study. European Journal of Cancer, 2005, 41, 2868-2872.	2.8	266