

Shad B Smith

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

5,484
citations

117571

34
h-index

149623

56
g-index

61
all docs

61
docs citations

61
times ranked

7642
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling Secondary Phenotypes Conditional on Genotypes in Case-Control Studies. <i>Stats</i> , 2022, 5, 203-214.	0.5	0
2	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. <i>Sleep</i> , 2021, 44, .	0.6	5
3	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021, 108, 564-582.	2.6	18
4	Phenotypic profile clustering pragmatically identifies diagnostically and mechanistically informative subgroups of chronic pain patients. <i>Pain</i> , 2021, 162, 1528-1538.	2.0	19
5	A genetic polymorphism that is associated with mitochondrial energy metabolism increases risk of fibromyalgia. <i>Pain</i> , 2020, 161, 2860-2871.	2.0	17
6	Reversion mutation of cDNA CA8-204 minigene construct produces a truncated functional peptide that regulates calcium release in vitro and produces profound analgesia in vivo. <i>Mammalian Genome</i> , 2020, 31, 287-294.	1.0	1
7	Clinical Pain Phenotyping for Omics Studies. , 2020, , 49-71.		0
8	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	2.2	38
9	A functional substitution in the aromatic amino acid decarboxylase enzyme worsens somatic symptoms via a serotonergic pathway. <i>Annals of Neurology</i> , 2019, 86, 168-180.	2.8	9
10	Profound analgesia is associated with a truncated peptide resulting from tissue specific alternative splicing of DRG CA8-204 regulated by an exon-level cis-eQTL. <i>PLoS Genetics</i> , 2019, 15, e1008226.	1.5	4
11	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019, 160, 579-591.	2.0	37
12	Discovery of Novel Mechanisms for Idiopathic Pain Disorders Through Genome Wide Approaches. <i>FASEB Journal</i> , 2019, 33, 206.1.	0.2	0
13	Genomics of Cardiovascular Measures of Autonomic Tone. <i>Journal of Cardiovascular Pharmacology</i> , 2018, 71, 180-191.	0.8	6
14	Human carbonic anhydrase-8 AAV8 gene therapy inhibits nerve growth factor signaling producing prolonged analgesia and anti-hyperalgesia in mice. <i>Gene Therapy</i> , 2018, 25, 297-311.	2.3	6
15	Car8 dorsal root ganglion expression and genetic regulation of analgesic responses are associated with a cis-eQTL in mice. <i>Mammalian Genome</i> , 2017, 28, 407-415.	1.0	7
16	Impact of human CA8 on thermal antinociception in relation to morphine equivalence in mice. <i>NeuroReport</i> , 2017, 28, 1215-1220.	0.6	6
17	Evidence that dry eye represents a chronic overlapping pain condition. <i>Molecular Pain</i> , 2017, 13, 174480691772930.	1.0	34
18	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	5.8	147

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19	Effect of Human Genetic Variability on Gene Expression in Dorsal Root Ganglia and Association with Pain Phenotypes. <i>Cell Reports</i> , 2017, 19, 1940-1952.	2.9	83
20	Epiregulin and EGFR interactions are involved in pain processing. <i>Journal of Clinical Investigation</i> , 2017, 127, 3353-3366.	3.9	85
21	Modification of COMT-dependent pain sensitivity by psychological stress and sex. <i>Pain</i> , 2016, 157, 858-867.	2.0	49
22	Overlapping Chronic Pain Conditions: Implications for Diagnosis and Classification. <i>Journal of Pain</i> , 2016, 17, T93-T107.	0.7	329
23	Identification of clusters of individuals relevant to temporomandibular disorders and other chronic pain conditions. <i>Pain</i> , 2016, 157, 1266-1278.	2.0	104
24	COMT gene locus. <i>Pain</i> , 2015, 156, 2072-2083.	2.0	28
25	Carbonic Anhydrase-8 Regulates Inflammatory Pain by Inhibiting the ITPR1-Cytosolic Free Calcium Pathway. <i>PLoS ONE</i> , 2015, 10, e0118273.	1.1	30
26	Genome-wide association meta-analyses to identify common genetic variants associated with hallux valgus in Caucasian and African Americans. <i>Journal of Medical Genetics</i> , 2015, 52, 762-769.	1.5	18
27	MicroRNA expression profiles differentiate chronic pain condition subtypes. <i>Translational Research</i> , 2015, 166, 706-720.e11.	2.2	32
28	The nicotinic $\alpha 6$ subunit gene determines variability in chronic pain sensitivity via cross-inhibition of P2X2/3 receptors. <i>Science Translational Medicine</i> , 2015, 7, 287ra72.	5.8	59
29	Epistasis between polymorphisms in COMT, ESR1, and GCH1 influences COMT enzyme activity and pain. <i>Pain</i> , 2014, 155, 2390-2399.	2.0	59
30	Facial pain with localized and widespread manifestations: Separate pathways of vulnerability. <i>Pain</i> , 2013, 154, 2335-2343.	2.0	31
31	Pain modality- and sex-specific effects of COMT genetic functional variants. <i>Pain</i> , 2013, 154, 1368-1376.	2.0	81
32	Clinical Orofacial Characteristics Associated With Risk of First-Onset TMD: The OPPERA Prospective Cohort Study. <i>Journal of Pain</i> , 2013, 14, T33-T50.	0.7	142
33	Study Protocol, Sample Characteristics, and Loss to Follow-Up: The OPPERA Prospective Cohort Study. <i>Journal of Pain</i> , 2013, 14, T2-T19.	0.7	59
34	Genetic Variants Associated With Development of TMD and Its Intermediate Phenotypes: The Genetic Architecture of TMD in the OPPERA Prospective Cohort Study. <i>Journal of Pain</i> , 2013, 14, T91-T101.e3.	0.7	76
35	Preclinical episodes of orofacial pain symptoms and their association with health care behaviors in the OPPERA prospective cohort study. <i>Pain</i> , 2013, 154, 750-760.	2.0	37
36	Summary of Findings From the OPPERA Prospective Cohort Study of Incidence of First-Onset Temporomandibular Disorder: Implications and Future Directions. <i>Journal of Pain</i> , 2013, 14, T116-T124.	0.7	189

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37	The phenotypic and genetic signatures of common musculoskeletal pain conditions. <i>Nature Reviews Rheumatology</i> , 2013, 9, 340-350.	3.5	215
38	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013, 45, 690-696.	9.4	232
39	Construction of a Global Pain Systems Network Highlights Phospholipid Signaling as a Regulator of Heat Nociception. <i>PLoS Genetics</i> , 2012, 8, e1003071.	1.5	23
40	Genetically determined P2X7 receptor pore formation regulates variability in chronic pain sensitivity. <i>Nature Medicine</i> , 2012, 18, 595-599.	15.2	335
41	Large candidate gene association study reveals genetic risk factors and therapeutic targets for fibromyalgia. <i>Arthritis and Rheumatism</i> , 2012, 64, 584-593.	6.7	78
42	Potential Genetic Risk Factors for Chronic TMD: Genetic Associations from the OPPERA Case Control Study. <i>Journal of Pain</i> , 2011, 12, T92-T101.	0.7	157
43	Cytokine biomarkers and chronic pain: Association of genes, transcription, and circulating proteins with temporomandibular disorders and widespread palpation tenderness. <i>Pain</i> , 2011, 152, 2802-2812.	2.0	108
44	Pain sensitivity and vasopressin analgesia are mediated by a gene-sex-environment interaction. <i>Nature Neuroscience</i> , 2011, 14, 1569-1573.	7.1	110
45	Development of Temporomandibular Disorders Is Associated With Greater Bodily Pain Experience. <i>Clinical Journal of Pain</i> , 2010, 26, 116-120.	0.8	89
46	Effect of catechol-O-methyltransferase polymorphism on response to propranolol therapy in chronic musculoskeletal pain: a randomized, double-blind, placebo-controlled, crossover pilot study. <i>Pharmacogenetics and Genomics</i> , 2010, 20, 239-248.	0.7	120
47	Pain perception is altered by a nucleotide polymorphism in <i>SCN9A</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5148-5153.	3.3	279
48	Multiple chronic pain states are associated with a common amino acid-changing allele in <i>KCNS1</i> . <i>Brain</i> , 2010, 133, 2519-2527.	3.7	224
49	A Genome-wide <i>Drosophila</i> Screen for Heat Nociception Identifies β as an Evolutionarily Conserved Pain Gene. <i>Cell</i> , 2010, 143, 628-638.	13.5	283
50	The β subunit of the Na ⁺ ,K ⁺ -ATPase mediates variable nociceptive sensitivity in the formalin test. <i>Pain</i> , 2009, 144, 294-302.	2.0	43
51	Quantitative trait locus and computational mapping identifies <i>Kcnj9</i> (<i>GIRK3</i>) as a candidate gene affecting analgesia from multiple drug classes. <i>Pharmacogenetics and Genomics</i> , 2008, 18, 231-241.	0.7	51
52	Social Modulation of Pain as Evidence for Empathy in Mice. <i>Science</i> , 2006, 312, 1967-1970.	6.0	710
53	Influence of genotype, dose and sex on pruritogen-induced scratching behavior in the mouse. <i>Pain</i> , 2006, 124, 50-58.	2.0	96
54	Screening for pain phenotypes: Analysis of three congenic mouse strains on a battery of nine nociceptive assays. <i>Pain</i> , 2006, 126, 24-34.	2.0	70

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55	Influence of Nociception and Stress-induced Antinociception on Genetic Variation in Isoflurane Anesthetic Potency among Mouse Strains. <i>Anesthesiology</i> , 2005, 103, 751-758.	1.3	40
56	Variable sensitivity to noxious heat is mediated by differential expression of the CGRP gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12938-12943.	3.3	151
57	Paclitaxel-induced neuropathic hypersensitivity in mice: Responses in 10 inbred mouse strains. <i>Life Sciences</i> , 2004, 74, 2593-2604.	2.0	123
58	The Heritability of Antinociception: Common Pharmacogenetic Mediation of Five Neurochemically Distinct Analgesics. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2003, 304, 547-559.	1.3	95
59	Tactile system and nociception. , 0, , 55-64.		0