Richard Sherva

List of Publications by Year
in descending order

56 papers	3,966 citations	159585 30 h-index	182427 51 g-index
58 all docs	58 docs citations	58 times ranked	7422 citing authors

#	Article	IF	Citations
1	P90. A Genetically Informed Examination of Posttraumatic Stress Disorder and Traumatic Brain Injuryâ€™s Impact on Dementia Risk in US Veterans. Biological Psychiatry, 2022, 91, S123-S124.	1.3	0
2	Shared genetic risk between eating disorderâ€•and substanceâ€•useâ€•related phenotypes: Evidence from genomeâ€•wide association studies. Addiction Biology, 2021, 26, e12880.	2.6	28
3	Genome-wide association study of phenotypes measuring progression from first cocaine or opioid use to dependence reveals novel risk genes. Exploration of Medicine, 2021, 2, 60-73.	1.5	6
4	Genome-wide association study of stimulant dependence. Translational Psychiatry, 2021, 11, 363.	4.8	4
5	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. Nicotine and Tobacco Research, 2020, 22, 900-909.	2.6	17
6	Post-GWAS analysis of six substance use traits improves the identification and functional interpretation of genetic risk loci. Drug and Alcohol Dependence, 2020, 206, 107703.	3.2	19
7	A large-scale genome-wide association study meta-analysis of cannabis use disorder. Lancet Psychiatry,the, 2020, 7, 1032-1045.	7.4	200
8	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. Nature Communications, 2020, 11, 5562.	12.8	80
9	Genomeâ€•wide association study of rate of cognitive decline in Alzheimer's disease patients identifies novel genes and pathways. Alzheimer's and Dementia, 2020, 16, 1134-1145.	0.8	28
10	EXPLORING THE ROLE OF GENETIC REGULATION OF GENE EXPRESSION IN SUBSTANCE USE AND DEPENDENCE. European Neuropsychopharmacology, 2019, 29, S803-S804.	0.7	0
11	GENOME-WIDE ASSOCIATION STUDY OF COMORBID ALCOHOL DEPENDENCE AND MAJOR DEPRESSION. European Neuropsychopharmacology, 2019, 29, S971.	0.7	0
12	POLYGENIC RISK BURDEN AND CANNABIS USE COMORBIDITY IN PATIENTS WITH SCHIZOPHRENIA AND BIPOLAR DISORDER. European Neuropsychopharmacology, 2019, 29, S951.	0.7	1
13	Genome-wide Association Study Identifies a Regulatory Variant of RGMA Associated With Opioid Dependence in European Americans. Biological Psychiatry, 2018, 84, 762-770.	1.3	64
14	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	14.8	490
15	Genomeâ€•wide association metaâ€•analysis of age at first cannabis use. Addiction, 2018, 113, 2073-2086.	3.3	24
16	Association of maternal and infant variants inPNOCandCOMTgenes with neonatal abstinence syndrome severity. American Journal on Addictions, 2017, 26, 42-49.	1.4	39
17	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanolâ€Response Behaviors in Model Organisms. Alcoholism: Clinical and Experimental Research, 2017, 41, 911-928.	2.4	43
18	Genetic Risk Variants Associated With Comorbid Alcohol Dependence and Major Depression. JAMA Psychiatry, 2017, 74, 1234.	11.0	74

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19	Oxytocin receptor gene polymorphisms, attachment, and PTSD: Results from the National Health and Resilience in Veterans Study. Journal of Psychiatric Research, 2017, 94, 139-147.	3.1	46
20	Two novel loci, COBL and SLC10A2, for Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2017, 13, 119-129.	0.8	87
21	S100A10 identified in a genome-wide gene Ã— cannabis dependence interaction analysis of risky sexual behaviours. Journal of Psychiatry and Neuroscience, 2017, 42, 252-261.	2.4	9
22	Genome-wide Association Study of Cannabis Dependence Severity, Novel Risk Variants, and Shared Genetic Risks. JAMA Psychiatry, 2016, 73, 472.	11.0	148
23	The executive prominent/memory prominent spectrum in Alzheimer's disease is highly heritable. Neurobiology of Aging, 2016, 41, 115-121.	3.1	11
24	The genetics of alcohol dependence: Twin and SNPâ€based heritability, and genomeâ€wide association study based on AUDIT scores. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 739-748.	1.7	56
25	Genomewide Association Study for Maximum Number of Alcoholic Drinks in European Americans and African Americans. Alcoholism: Clinical and Experimental Research, 2015, 39, 1137-1147.	2.4	58
26	Variations in opioid receptor genes in neonatal abstinence syndrome. Drug and Alcohol Dependence, 2015, 155, 253-259.	3.2	55
27	P2-016: Identification of genetic variants associated with Alzheimer's disease: Progression rate. , 2015, 11, P487-P487.		0
28	Genome-Wide Association Study of Nicotine Dependence in American Populations: Identification of Novel Risk Loci in Both African-Americans and European-Americans. Biological Psychiatry, 2015, 77, 493-503.	1.3	78
29	Nf1 Regulates Alcohol Dependence-Associated Excessive Drinking and Gamma-Aminobutyric Acid Release in the Central Amygdala in Mice and Is Associated with Alcohol Dependence in Humans. Biological Psychiatry, 2015, 77, 870-879.	1.3	14
30	Genomeâ€wide association study of the rate of cognitive decline in Alzheimer's disease. Alzheimer's and Dementia, 2014, 10, 45-52.	0.8	147
31	Genome-Wide Association Study of Opioid Dependence: Multiple Associations Mapped to Calcium and Potassium Pathways. Biological Psychiatry, 2014, 76, 66-74.	1.3	192
32	Calibrating Longitudinal Cognition in Alzheimer's Disease Across Diverse Test Batteries and Datasets. Neuroepidemiology, 2014, 43, 194-205.	2.3	43
33	Association of Granulomatosis With Polyangiitis (Wegener's) With HLAâ€“DPB1*04 and SEMA6A Gene Variants: Evidence From Genomeâ€Wide Analysis. Arthritis and Rheumatism, 2013, 65, 2457-2468.	6.7	138
34	Metaâ€analysis of genetic polymorphisms in granulomatosis with polyangiitis (Wegener's) reveals shared susceptibility loci with rheumatoid arthritis. Arthritis and Rheumatism, 2012, 64, 3463-3471.	6.7	33
35	Identification of Novel Candidate Genes for Alzheimer's Disease by Autozygosity Mapping using Genome Wide SNP Data. Journal of Alzheimer's Disease, 2011, 23, 349-359.	2.6	46
36	A 3-bp deletion in the HBS1L-MYB intergenic region on chromosome 6q23 is associated with HbF expression. Blood, 2011, 117, 4935-4945.	1.4	116

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37	ACSL6 Is Associated with the Number of Cigarettes Smoked and Its Expression Is Altered by Chronic Nicotine Exposure. PLoS ONE, 2011, 6, e28790.	2.5	11
38	Power and Pitfalls of the Genome-Wide Association Study Approach to Identify Genes for Alzheimerâ€™s Disease. Current Psychiatry Reports, 2011, 13, 138-146.	4.5	27
39	Common CD36 SNPs reduce protein expression and may contribute to a protective atherogenic profile. Human Molecular Genetics, 2011, 20, 193-201.	2.9	126
40	Pharmacogenetic Effect of the Stromelysin (MMP3) Polymorphism on Stroke Risk in Relation to Antihypertensive Treatment. Stroke, 2011, 42, 330-335.	2.0	26
41	Fetal hemoglobin in sickle cell anemia: genome-wide association studies suggest a regulatory region in the 5â€² olfactory receptor gene cluster. Blood, 2010, 115, 1815-1822.	1.4	146
42	Genetic modifiers of Hb E/Î²0 thalassemia identified by a two-stage genome-wide association study. BMC Medical Genetics, 2010, 11, 51.	2.1	25
43	Multiple Independent Loci at Chromosome 15q25.1 Affect Smoking Quantity: a Meta-Analysis and Comparison with Lung Cancer and COPD. PLoS Genetics, 2010, 6, e1001053.	3.5	332
44	Variation in Nicotinic Acetylcholine Receptor Genes is Associated with Multiple Substance Dependence Phenotypes. Neuropsychopharmacology, 2010, 35, 1921-1931.	5.4	103
45	Associations and Interactions Between SNPs in the Alcohol Metabolizing Genes and Alcoholism Phenotypes in European Americans. Alcoholism: Clinical and Experimental Research, 2009, 33, 848-857.	2.4	46
46	Genome-Wide Studies in Sickle Cell Anemia Show Associations Between SNPs in the Olfactory Receptor Gene Cluster and Fetal Hemoglobin Concentration.. Blood, 2009, 114, 821-821.	1.4	2
47	Association of a single nucleotide polymorphism in neuronal acetylcholine receptor subunit alpha 5 (CHRNA5) with smoking status and with â€˜pleasurable buzzâ€™ during early experimentation with smoking. Addiction, 2008, 103, 1544-1552.	3.3	129
48	A Whole-Genome Scan for Stroke or Myocardial Infarction in Family Blood Pressure Program Families. Stroke, 2008, 39, 1115-1120.	2.0	9
49	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. Diabetes, 2008, 57, 3161-3165.	0.6	37
50	Variants in the CD36 gene associate with the metabolic syndrome and high-density lipoprotein cholesterol. Human Molecular Genetics, 2008, 17, 1695-1704.	2.9	164
51	Evidence for a quantitative trait locus affecting low levels of apolipoprotein B and low density lipoprotein on chromosome 10 in Caucasian families. Journal of Lipid Research, 2007, 48, 2632-2639.	4.2	9
52	A Whole Genome Scan for Pulse Pressure/Stroke Volume Ratio in African Americans: The HyperGEN Study. American Journal of Hypertension, 2007, 20, 398-402.	2.0	25
53	No evidence for multiple loci affecting rheumatoid arthritis risk on chromosome 6p21. BMC Proceedings, 2007, 1, S42.	1.6	1
54	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. Genetic Epidemiology, 2007, 31, S34-S42.	1.3	3

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55	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	21.4	333
56	Genome-wide association study of phenotypes measuring progression from first cocaine or opioid use to dependence reveals novel risk genes. Exploration of Medicine, 0, , .	1.5	0