# Shiva M Singh

List of Publications by Year
in descending order

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|---|---|---|---|
| 77 papers | 2,204 citations | 201674 27 h-index | 254184 43 g-index |
| 78 all docs | 78 docs citations | 78 times ranked | 2757 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Long-lasting alterations to DNA methylation and ncRNAs could underlie the effects of fetal alcohol exposure in mice. DMM Disease Models and Mechanisms, 2013, 6, 977-92. | 2.4 | 113 |
| 2 | Epigenetic contributors to the discordance of monozygotic twins. Clinical Genetics, 2002, 62, 97-103. | 2.0 | 108 |
| 3 | Associative DNA methylation changes in children with prenatal alcohol exposure. Epigenomics, 2015, 7, 1259-1274. | 2.1 | 93 |
| 4 | Site-specific cytosine methylation in S-COMT promoter in 31 brain regions with implications for studies involving schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 133B, 37-42. | 1.7 | 90 |
| 5 | Involvement of gene-diet/drug interaction in DNA methylation and its contribution to complex diseases: from cancer to schizophrenia. Clinical Genetics, 2003, 64, 451-460. | 2.0 | 86 |
| 6 | Microarray Analysis of Mouse Brain Gene Expression Following Acute Ethanol Treatment. Neurochemical Research, 2004, 29, 357-369. | 3.3 | 85 |
| 7 | Maternal voluntary drinking in C57BL/6J mice: Advancing a model for fetal alcohol spectrum disorders. Behavioural Brain Research, 2011, 223, 376-387. | 2.2 | 75 |
| 8 | Temporal expression of genes encoding free radicalâ€“metabolizing enzymes is associated with higher mRNA levels during in utero development in mice. Genesis, 1990, 11, 149-159. | 2.1 | 67 |
| 9 | Ontogenetic De Novo Copy Number Variations (CNVs) as a Source of Genetic Individuality: Studies on Two Families with MZD Twins for Schizophrenia. PLoS ONE, 2011, 6, e17125. | 2.5 | 67 |
| 10 | Neurodevelopmental alcohol exposure elicits long-term changes to gene expression that alter distinct molecular pathways dependent on timing of exposure. Journal of Neurodevelopmental Disorders, 2013, 5, 6. | 3.1 | 66 |
| 11 | The effects of olanzapine on genome-wide DNA methylation in the hippocampus and cerebellum. Clinical Epigenetics, 2014, 6, 1. | 4.1 | 62 |
| 12 | Molecular Characterization of a MSRV-like Sequence Identified by RDA from Monozygotic Twin Pairs Discordant for Schizophrenia. Genomics, 1999, 61, 133-144. | 2.9 | 61 |
| 13 | Long-term genomic and epigenomic dysregulation as a consequence of prenatal alcohol exposure: a model for fetal alcohol spectrum disorders. Frontiers in Genetics, 2014, 5, 161. | 2.3 | 57 |
| 14 | Long-term alterations to the brain transcriptome in a maternal voluntary consumption model of fetal alcohol spectrum disorders. Brain Research, 2012, 1458, 18-33. | 2.2 | 52 |
| 15 | Alteration of Gene Expression, DNA Methylation, and Histone Methylation in Free Radical Scavenging Networks in Adult Mouse Hippocampus following Fetal Alcohol Exposure. PLoS ONE, 2016, 11, e0154836. | 2.5 | 51 |
| 16 | Incidental neurodevelopmental episodes in the etiology of schizophrenia: An expanded model involving epigenetics and development. Clinical Genetics, 2004, 65, 435-440. | 2.0 | 50 |
| 17 | Strategies for precision modulation of gene expression by epigenome editing: an overview. Epigenetics and Chromatin, 2015, 8, 34. | 3.9 | 50 |
| 18 | DNA methylation differences in monozygotic twin pairs discordant for schizophrenia identifies psychosis related genes and networks. BMC Medical Genomics, 2015, 8, 17. | 1.5 | 47 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Long-term alterations to DNA methylation as a biomarker of prenatal alcohol exposure: From mouse models to human children with fetal alcohol spectrum disorders. Alcohol, 2017, 60, 67-75. | 1.7 | 44 |
| 20 | Changes to histone modifications following prenatal alcohol exposure: An emerging picture. Alcohol, 2017, 60, 41-52. | 1.7 | 41 |
| 21 | Olanzapine induced DNA methylation changes support the dopamine hypothesis of psychosis. Journal of Molecular Psychiatry, 2013, 1, 19. | 2.0 | 40 |
| 22 | Retroviruses and schizophrenia revisited. , 1996, 67, 19-24. | | 36 |
| 23 | Exploring the Complexity of Intellectual Disability in Fetal Alcohol Spectrum Disorders. Frontiers in Pediatrics, 2014, 2, 90. | 1.9 | 36 |
| 24 | Links between white matter microstructure and cortisol reactivity to stress in early childhood: Evidence for moderation by parenting. NeuroImage: Clinical, 2014, 6, 77-85. | 2.7 | 35 |
| 25 | Copy Number Variation Distribution in Six Monozygotic Twin Pairs Discordant for Schizophrenia. Twin Research and Human Genetics, 2014, 17, 108-120. | 0.6 | 34 |
| 26 | Site and sequence specific DNA methylation in the neurofibromatosis (NF1) gene includes C5839T: the site of the recurrent substitution mutation in exon 31. Human Molecular Genetics, 1996, 5, 503-507. | 2.9 | 33 |
| 27 | Reduced expression of brain cannabinoid receptor 1 (Cnr1) is coupled with an increased complementary micro-RNA (miR-26b) in a mouse model of fetal alcohol spectrum disorders. Clinical Epigenetics, 2013, 5, 14. | 4.1 | 32 |
| 28 | Molecular Changes during Neurodevelopment following Second-Trimester Binge Ethanol Exposure in a Mouse Model of Fetal Alcohol Spectrum Disorder: From Immediate Effects to Long-Term Adaptation. Developmental Neuroscience, 2014, 36, 29-43. | 2.0 | 32 |
| 29 | Examination of ethanol responsive liver and brain specific gene expression, in the mouse strains with variable ethanol preferences, using cDNA expression arrays. Biochemical Genetics, 2002, 40, 395-410. | 1.7 | 26 |
| 30 | Biological relevance of CNV calling methods using familial relatedness including monozygotic twins. BMC Bioinformatics, 2014, 15, 114. | 2.6 | 25 |
| 31 | Genetic Segregation of Brain Gene Expression Identifies Retinaldehyde Binding Protein 1 and Syntaxin 12 as Potential Contributors to Ethanol Preference in Mice. Behavior Genetics, 2004, 34, 425-439. | 2.1 | 24 |
| 32 | Developmental and behavioral consequences of early life maternal separation stress in a mouse model of fetal alcohol spectrum disorder. Behavioural Brain Research, 2016, 308, 94-103. | 2.2 | 24 |
| 33 | Olanzapine-induced methylation alters cadherin gene families and associated pathways implicated in psychosis. BMC Neuroscience, 2014, 15, 112. | 1.9 | 23 |
| 34 | Neurodevelopmental Timing of Ethanol Exposure May Contribute to Observed Heterogeneity of Behavioral Deficits in a Mouse Model of Fetal Alcohol Spectrum Disorder (FASD). Journal of Behavioral and Brain Science, 2013, 03, 85-99. | 0.5 | 23 |
| 35 | Analysis of behavior using genetical genomics in mice as a model: from alcohol preferences to gene expression differences. Genome, 2007, 50, 877-897. | 2.0 | 21 |
| 36 | (Epi)genomics and neurodevelopment in schizophrenia: monozygotic twins discordant for schizophrenia augment the search for disease-related (epi)genomic alterationsBased on a lecture during the joint meeting of the Genetics Society of Canada and the Society of Developmental Biology, 1 March 2008, at Banff Centre, Banff, Alberta, Canada, in recognition of the William F. Grant and Peter B. Moens Award of Excellence (2008) of the Genetics Society of Canada to Professor Shiva M. Singh.. Genome, 2009, 52, 8-19. | 2.0 | 21 |

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|---|---|---|---|
| 37 | Autism meets schizophrenia via cadherin pathway. Schizophrenia Research, 2010, 116, 293-294. | 2.0 | 21 |
| 38 | Hippocampal Gene Expression Meta-Analysis Identifies Aging and Age-Associated Spatial Learning Impairment (ASLI) Genes and Pathways. PLoS ONE, 2013, 8, e69768. | 2.5 | 20 |
| 39 | Molecular characterization of a 2.7-kb, 12q13-specific, retroviral-related sequence isolated by RDA from monozygotic twin pairs discordant for schizophrenia. Genome, 2002, 45, 381-390. | 2.0 | 19 |
| 40 | DNA methylation and mRNA expression of SYN III, a candidate gene for schizophrenia. BMC Medical Genetics, 2008, 9, 115. | 2.1 | 19 |
| 41 | Third Trimester-Equivalent Ethanol Exposure Is Characterized by an Acute Cellular Stress Response and an Ontogenetic Disruption of Genes Critical for Synaptic Establishment and Function in Mice. Developmental Neuroscience, 2014, 36, 499-519. | 2.0 | 19 |
| 42 | DNA methylation in psychosis: insights into etiology and treatment. Epigenomics, 2015, 7, 67-74. | 2.1 | 17 |
| 43 | Strain-Specific Brain Metallothionein II (MT-II) Gene Expression, Its Ethanol Responsiveness, and Association With Ethanol Preference in Mice. Alcoholism: Clinical and Experimental Research, 2003, 27, 388-395. | 2.4 | 15 |
| 44 | Copy number variation showers in schizophrenia: an emerging hypothesis. Molecular Psychiatry, 2009, 14, 356-358. | 7.9 | 15 |
| 45 | Ethanolâ€Responsive Genes (Crtam, Zbtb16, and Mobp) Located in the Alcoholâ€QTL Region of Chromosome 9 Are Associated With Alcohol Preference in Mice. Alcoholism: Clinical and Experimental Research, 2009, 33, 1409-1416. | 2.4 | 13 |
| 46 | Divergence of the vertebrate sp1A/ryanodine receptor domain and SOCS box-containing (Spsb) gene family and its expression and regulation within the mouse brain. Genomics, 2009, 93, 358-366. | 2.9 | 13 |
| 47 | Gene Network Construction from Microarray Data Identifies a Key Network Module and Several Candidate Hub Genes in Age-Associated Spatial Learning Impairment. Frontiers in Systems Neuroscience, 2017, 11, 75. | 2.5 | 13 |
| 48 | Hippocampal DNA Methylation in a Mouse Model of Fetal Alcohol Spectrum Disorder That Includes Maternal Separation Stress Only Partially Explains Changes in Gene Expression. Frontiers in Genetics, 2020, 11, 70. | 2.3 | 12 |
| 49 | Studies on Syntaxin 12 and Alcohol Preference Involving C57BL/6J and DBA/2J Strains of Mice. Behavior Genetics, 2009, 39, 183-191. | 2.1 | 11 |
| 50 | Delineation of the Role of Nicotinic Acetylcholine Receptor Genes in Alcohol Preference in Mice. Behavior Genetics, 2010, 40, 660-671. | 2.1 | 10 |
| 51 | A Macro Role for Imprinted Clusters of MicroRNAs in the Brain. MicroRNA (Shariqah, United Arab) Tj ETQq1 1 0.784314 rgBT /Overloc | 1.2 | 10 |
| 52 | Human COL5A1 polymorphisms and quadriceps muscleâ€“tendon mechanical stiffness in vivo. Experimental Physiology, 2016, 101, 1581-1592. | 2.0 | 10 |
| 53 | Regulation of catalase-specific mRNA and its processing during development in mice. Genesis, 1989, 10, 339-344. | 2.1 | 9 |
| 54 | Olanzapine-induced DNA methylation in the hippocampus and cerebellum in genes mapped to human 22q11 and implicated in schizophrenia. Psychiatric Genetics, 2015, 25, 88-94. | 1.1 | 9 |

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|---|---|---|---|
| 55 | Insights into the origin of DNA methylation differences between monozygotic twins discordant for schizophrenia. Journal of Molecular Psychiatry, 2015, 3, 7. | 2.0 | 9 |
| 56 | Postzygotic Somatic Mutations in the Human Brain Expand the Threshold-Liability Model of Schizophrenia. Frontiers in Psychiatry, 2020, 11, 587162. | 2.6 | 9 |
| 57 | Child sex moderates the relationship between cortisol stress reactivity and symptoms over time. Comprehensive Psychiatry, 2018, 87, 161-170. | 3.1 | 8 |
| 58 | Hippocampal transcriptome analysis following maternal separation implicates altered RNA processing in a mouse model of fetal alcohol spectrum disorder. Journal of Neurodevelopmental Disorders, 2020, 12, 15. | 3.1 | 8 |
| 59 | Towards Unraveling Ethanol-specific Neuro-metabolomics Based on Ethanol Responsive Genes In vivo. Neurochemical Research, 2005, 30, 1179-1190. | 3.3 | 7 |
| 60 | cis-Regulatory sequences of the genes involved in apoptosis, cell growth, and proliferation may provide a target for some of the effects of acute ethanol exposure. Brain Research, 2006, 1088, 31-44. | 2.2 | 7 |
| 61 | Role of Potassium Channel Gene Kcnj10 in Ethanol Preference in C57bl/6J and DBA/2J Mice. Alcoholism: Clinical and Experimental Research, 2009, 33, 394-399. | 2.4 | 7 |
| 62 | Neurodevelopmental epigenetic etiologies: insights from studies on mouse models of fetal alcohol spectrum disorders. Epigenomics, 2013, 5, 465-468. | 2.1 | 7 |
| 63 | Epigenetic Impacts of Early Life Stress in Fetal Alcohol Spectrum Disorders Shape the Neurodevelopmental Continuum. Frontiers in Molecular Neuroscience, 2021, 14, 671891. | 2.9 | 7 |
| 64 | Genetic regulation of gene-specific mRNA by ethanolin vivo and its possible role in ethanol preference in a cross with RI lines in mice. Biochemical Genetics, 1996, 34, 219-238. | 1.7 | 6 |
| 65 | Analysis of Metallothionein Brain Gene Expression in Relation to Ethanol Preference in Mice Using Cosegregation and Gene Knockouts. Alcoholism: Clinical and Experimental Research, 2006, 30, 15-25. | 2.4 | 6 |
| 66 | Origin of Sex-Biased Mental Disorders: An Evolutionary Perspective. Journal of Molecular Evolution, 2021, 89, 195-213. | 1.8 | 6 |
| 67 | Genetics and differential expression of NADH:ubiquinone oxidoreductase B8 subunit in brains of genetic strains of mice differing in voluntary alcohol consumption. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1579, 164-172. | 2.4 | 5 |
| 68 | Monozygotic twins with early-onset schizophrenia and late-onset bipolar disorder: a case report. Journal of Medical Case Reports, 2013, 7, 134. | 0.8 | 5 |
| 69 | Coordinated Tcf7l2 regulation in a mouse model implicates Wnt signaling in fetal alcohol spectrum disorders. Biochemistry and Cell Biology, 2019, 97, 375-379. | 2.0 | 5 |
| 70 | Fetal alcohol and the right to be born healthyÃ¢â‚¬Â¦. Frontiers in Genetics, 2014, 5, 356. | 2.3 | 4 |
| 71 | Genetic regulation of gene-specific mRNA by ethanolin vivo and its possible role in ethanol preference in a cross with RI lines in mice. Biochemical Genetics, 1996, 34, 219-238. | 1.7 | 3 |
| 72 | Associations Between Childrenâ€™s Telomere Length, Parental Intrusiveness, and the Development of Early Externalizing Behaviors. Child Psychiatry and Human Development, 2023, 54, 672-682. | 1.9 | 3 |

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|---|---|---|---|
| 73 | Search for missing schizophrenia genes will require a new developmental neurogenomic perspective. Journal of Genetics, 2013, 92, 335-340. | 0.7 | 1 |
| 74 | A novel deletion cluster at 13q14.2-q21.33 in an 80-year man with late onset leukemia: Clinical and molecular findings. Indian Journal of Human Genetics, 2013, 19, 96. | 0.7 | 1 |
| 75 | ATP2A2 rs3026468 does not associate with quadriceps contractile properties and acute muscle potentiation in humans. Physiological Genomics, 2019, 51, 10-11. | 2.3 | 1 |
| 76 | Maternal Separation Stress in Fetal Alcohol Spectrum Disorders: A Case of Double Whammy. , 2019, , 325-333. | | 0 |
| 77 | Metabolomics in Drug Response and Addiction. , 2010, , 237-253. | | 0 |