

Valerie W Hu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

41
papers

1,969
citations

24
h-index

44
g-index

44
ext. papers

2,340
ext. citations

4.2
avg, IF

5
L-index

#	Paper	IF	Citations
41	Altered DNA methylation in a severe subtype of idiopathic autism: Evidence for sex differences in affected metabolic pathways. <i>Autism</i> , 2021 , 25, 887-910	6.6	3
40	Sex differences in the effects of prenatal bisphenol A exposure on autism-related genes and their relationships with the hippocampus functions. <i>Scientific Reports</i> , 2021 , 11, 1241	4.9	5
39	Autism-Related Transcription Factors Underlying the Sex-Specific Effects of Prenatal Bisphenol A Exposure on Transcriptome-Interactome Profiles in the Offspring Prefrontal Cortex.. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
38	Prenatal exposure to bisphenol A alters the transcriptome-interactome profiles of genes associated with Alzheimer's disease in the offspring hippocampus. <i>Scientific Reports</i> , 2020 , 10, 9487	4.9	13
37	Phenotypic Subtyping and Re-Analysis of Existing Methylation Data from Autistic Probands in Simplex Families Reveal ASD Subtype-Associated Differentially Methylated Genes and Biological Functions. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	4
36	Phenotypic Subtyping and Re-analyses of Existing Transcriptomic Data from Autistic Probands in Simplex Families Reveal Differentially Expressed and ASD Trait-Associated Genes. <i>Frontiers in Neurology</i> , 2020 , 11, 578972	4.1	3
35	Sex Differences in the Effects of Prenatal Bisphenol A Exposure on Genes Associated with Autism Spectrum Disorder in the Hippocampus. <i>Scientific Reports</i> , 2019 , 9, 3038	4.9	32
34	ASD Phenotype-Genotype Associations in Concordant and Discordant Monozygotic and Dizygotic Twins Stratified by Severity of Autistic Traits. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	8
33	Integrated genome-wide Alu methylation and transcriptome profiling analyses reveal novel epigenetic regulatory networks associated with autism spectrum disorder. <i>Molecular Autism</i> , 2018 , 9, 27	6.5	26
32	Are endocrine disrupting compounds environmental risk factors for autism spectrum disorder?. <i>Hormones and Behavior</i> , 2018 , 101, 13-21	3.7	42
31	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". <i>Current Behavioral Neuroscience Reports</i> , 2016 , 3, 264-274	1.7	70
30	Investigation of sex differences in the expression of RORA and its transcriptional targets in the brain as a potential contributor to the sex bias in autism. <i>Molecular Autism</i> , 2015 , 6, 7	6.5	50
29	Phenotype Definition: A Cornerstone of Autism Research, Diagnosis and Therapy 2014 , 3-22		
28	Searching in the Dark Non-coding RNA as a New Avenue of Autism Research 2014 , 175-202		
27	Genome-wide identification of transcriptional targets of RORA reveals direct regulation of multiple genes associated with autism spectrum disorder. <i>Molecular Autism</i> , 2013 , 4, 14	6.5	79
26	The expanding genomic landscape of autism: discovering the 'forest' beyond the 'trees'. <i>Future Neurology</i> , 2013 , 8, 29-42	1.5	15
25	Differential recruitment of coregulators to the RORA promoter adds another layer of complexity to gene (dys) regulation by sex hormones in autism. <i>Molecular Autism</i> , 2013 , 4, 39	6.5	36

24	From genes to environment: using integrative genomics to build a "systems-level" understanding of autism spectrum disorders. <i>Child Development</i> , 2013 , 84, 89-103	4.9	31
23	A Novel Stratification Method in Linkage Studies to Address Inter- and Intra-Family Heterogeneity in Autism. <i>PLoS ONE</i> , 2013 , 8, e67569	3.7	14
22	Developing a Predictive Gene Classifier for Autism Spectrum Disorders Based upon Differential Gene Expression Profiles of Phenotypic Subgroups. <i>North American Journal of Medicine & Science</i> , 2013 , 6,		18
21	Is retinoic acid-related orphan receptor-alpha (RORA) a target for gene-environment interactions contributing to autism?. <i>NeuroToxicology</i> , 2012 , 33, 1434-1435	4.4	19
20	Subphenotype-Dependent Disease Markers for Diagnosis and Personalized Treatment of Autism Spectrum Disorders. <i>Disease Markers</i> , 2012 , 33, 277-288	3.2	12
19	Subphenotype-dependent disease markers for diagnosis and personalized treatment of autism spectrum disorders. <i>Disease Markers</i> , 2012 , 33, 277-88	3.2	8
18	Sex hormones in autism: androgens and estrogens differentially and reciprocally regulate RORA, a novel candidate gene for autism. <i>PLoS ONE</i> , 2011 , 6, e17116	3.7	136
17	Novel autism subtype-dependent genetic variants are revealed by quantitative trait and subphenotype association analyses of published GWAS data. <i>PLoS ONE</i> , 2011 , 6, e19067	3.7	52
16	Global methylation profiling of lymphoblastoid cell lines reveals epigenetic contributions to autism spectrum disorders and a novel autism candidate gene, RORA, whose protein product is reduced in autistic brain. <i>FASEB Journal</i> , 2010 , 24, 3036-51	0.9	265
15	Investigation of post-transcriptional gene regulatory networks associated with autism spectrum disorders by microRNA expression profiling of lymphoblastoid cell lines. <i>Genome Medicine</i> , 2010 , 2, 23	14.4	164
14	Gene expression profiling of lymphoblasts from autistic and nonaffected sib pairs: altered pathways in neuronal development and steroid biosynthesis. <i>PLoS ONE</i> , 2009 , 4, e5775	3.7	111
13	Novel clustering of items from the Autism Diagnostic Interview-Revised to define phenotypes within autism spectrum disorders. <i>Autism Research</i> , 2009 , 2, 67-77	5.1	75
12	Gene expression profiling differentiates autism case-controls and phenotypic variants of autism spectrum disorders: evidence for circadian rhythm dysfunction in severe autism. <i>Autism Research</i> , 2009 , 2, 78-97	5.1	143
11	Gene expression profiling of lymphoblastoid cell lines from monozygotic twins discordant in severity of autism reveals differential regulation of neurologically relevant genes. <i>BMC Genomics</i> , 2006 , 7, 118	4.5	160
10	Does metabolic radiolabeling stimulate the stress response? Gene expression profiling reveals differential cellular responses to internal beta vs. external gamma radiation. <i>FASEB Journal</i> , 2003 , 17, 1470-86	0.9	30
9	³ H-thymidine is a defective tool with which to measure rates of DNA synthesis. <i>FASEB Journal</i> , 2002 , 16, 1456-7	0.9	42
8	Metabolic radiolabeling: experimental tool or Trojan horse? (³⁵ S)-Methionine induces DNA fragmentation and p53-dependent ROS production. <i>FASEB Journal</i> , 2001 , 15, 1562-8	0.9	38
7	Radiolabeling revisited: metabolic labeling with (³⁵ S)-methionine inhibits cell cycle progression, proliferation, and survival. <i>FASEB Journal</i> , 2000 , 14, 448-54	0.9	29

6	Chelation of iron within the erythrocytic Plasmodium falciparum parasite by iron chelators. <i>Molecular and Biochemical Parasitology</i> , 1999 , 101, 43-59	1.9	41
5	A mitosis-specific phosphorylation of the gap junction protein connexin43 in human vascular cells: biochemical characterization and localization. <i>Journal of Cell Biology</i> , 1997 , 137, 203-10	7.3	79
4	Interleukin-1 alpha suppresses gap junction-mediated intercellular communication in human endothelial cells. <i>Experimental Cell Research</i> , 1994 , 213, 218-23	4.2	28
3	Modulation of gap junctions in senescent endothelial cells. <i>Experimental Cell Research</i> , 1994 , 214, 172-6	4.2	60
2	X-ray absorption edge studies on cyanide-bound cytochrome C oxidase. <i>FEBS Letters</i> , 1977 , 84, 287-90	3.8	19
1	Role of microRNAs in Autism Spectrum Disorder	215-235	