

# Valerie W Hu

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

2,579  
citations

201385

27  
h-index

301761

39  
g-index

44  
all docs

44  
docs citations

44  
times ranked

3127  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.4	14
2	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.	1.6	29
3	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, 13201.	1.8	17
4	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, 6877.	1.8	18
5	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.	1.1	4
6	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.	1.6	33
7	ASD Phenotype's 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, 3804.	1.8	24
8	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.	1.6	46
9	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.	2.6	32
10	Are endocrine disrupting compounds environmental risk factors for autism spectrum disorder?. <i>Hormones and Behavior</i> , 2018, 101, 13-21.	1.0	61
11	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". <i>Current Behavioral Neuroscience Reports</i> , 2016, 3, 264-274.	0.6	113
12	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.	2.6	68
13	Phenotype Definition: A Cornerstone of Autism Research, Diagnosis and Therapy. , 2014, , 3-22.		0
14	Searching in the "Dark": Non-coding RNA as a New Avenue of Autism Research. , 2014, , 175-202.		0
15	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.	2.6	99
16	The expanding genomic landscape of autism: discovering the "forest" beyond the "trees". <i>Future Neurology</i> , 2013, 8, 29-42.	0.9	29
17	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.	2.6	51
18	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.	1.7	39

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19	A Novel Stratification Method in Linkage Studies to Address Inter- and Intra-Family Heterogeneity in Autism. <i>PLoS ONE</i> , 2013, 8, e67569.	1.1	18
20	Developing a Predictive Gene Classifier for Autism Spectrum Disorders Based upon Differential Gene Expression Profiles of Phenotypic Subgroups. <i>North American Journal of Medicine &amp; Science</i> , 2013, 6, .	3.8	32
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.	1.4	22
22	Subphenotype-Dependent Disease Markers for Diagnosis and Personalized Treatment of Autism Spectrum Disorders. <i>Disease Markers</i> , 2012, 33, 277-288.	0.6	17
23	Subphenotype-dependent disease markers for diagnosis and personalized treatment of autism spectrum disorders. <i>Disease Markers</i> , 2012, 33, 277-88.	0.6	8
24	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.	1.1	178
25	A systems approach towards an understanding, diagnosis and personalized treatment of autism spectrum disorders. <i>Pharmacogenomics</i> , 2011, 12, 1235-1238.	0.6	8
26	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.	1.1	82
27	Global methylation profiling of lymphoblastoid cell lines reveals epigenetic contributions to autism spectrum disorders and a novel autism candidate gene, <i>RORA</i> , whose protein product is reduced in autistic brain. <i>FASEB Journal</i> , 2010, 24, 3036-3051.	0.2	320
28	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.	3.6	196
29	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.	1.1	134
30	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.	2.1	108
31	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.	2.1	184
32	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.	1.2	200
33	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, 1470-1486.	0.2	30
34	<sup>3</sup> H-thymidine is a defective tool with which to measure rates of DNA synthesis. <i>FASEB Journal</i> , 2002, 16, 1456-1457.	0.2	49
35	Metabolic radiolabeling: experimental tool or Trojan horse? <sup>35</sup> S-methionine induces DNA fragmentation and p53-dependent ROS production. <i>FASEB Journal</i> , 2001, 15, 1562-1568.	0.2	41
36	Radiolabeling revisited: metabolic labeling with <sup>35</sup> S-methionine inhibits cell cycle progression, proliferation, and survival. <i>FASEB Journal</i> , 2000, 14, 448-454.	0.2	32

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37	Chelation of iron within the erythrocytic Plasmodium falciparum parasite by iron chelators. Molecular and Biochemical Parasitology, 1999, 101, 43-59.	0.5	44
38	A Mitosis-specific Phosphorylation of the Gap Junction Protein Connexin43 in Human Vascular Cells: Biochemical Characterization and Localization. Journal of Cell Biology, 1997, 137, 203-210.	2.3	84
39	Interleukin-1 $\beta$ Suppresses Gap Junction-Mediated Intercellular Communication in Human Endothelial Cells. Experimental Cell Research, 1994, 213, 218-223.	1.2	30
40	Modulation of Gap Junctions in Senescent Endothelial Cells. Experimental Cell Research, 1994, 214, 172-176.	1.2	63
41	X-ray absorption edge studies on cyanide-bound cytochromecoxidase. FEBS Letters, 1977, 84, 287-290.	1.3	21