

# Sheng Chih Jin

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

5,286  
citations

218677

26  
h-index

98798

67  
g-index

83  
all docs

83  
docs citations

83  
times ranked

9536  
citing authors

#	ARTICLE	IF	CITATIONS
1	De novo mutations in congenital heart disease with neurodevelopmental and other congenital anomalies. <i>Science</i> , 2015, 350, 1262-1266.	12.6	646
2	Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. <i>Nature Genetics</i> , 2017, 49, 1593-1601.	21.4	624
3	A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. <i>Nature Genetics</i> , 2010, 42, 525-529.	21.4	518
4	Rare coding variants in the phospholipase D3 gene confer risk for Alzheimer's disease. <i>Nature</i> , 2014, 505, 550-554.	27.8	425
5	CWAS of Cerebrospinal Fluid Tau Levels Identifies Risk Variants for Alzheimer's Disease. <i>Neuron</i> , 2013, 78, 256-268.	8.1	344
6	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1052-1061.	14.8	330
7	Coding variants in TREM2 increase risk for Alzheimer's disease. <i>Human Molecular Genetics</i> , 2014, 23, 5838-5846.	2.9	263
8	Alzheimer's disease-associated TREM2 variants exhibit either decreased or increased ligand-dependent activation. <i>Alzheimer's and Dementia</i> , 2017, 13, 381-387.	0.8	192
9	CLCN2 chloride channel mutations in familial hyperaldosteronism type II. <i>Nature Genetics</i> , 2018, 50, 349-354.	21.4	188
10	Evidence for gene-environment interaction in a genome wide study of nonsyndromic cleft palate. <i>Genetic Epidemiology</i> , 2011, 35, n/a-n/a.	1.3	145
11	TREM2 is associated with increased risk for Alzheimer's disease in African Americans. <i>Molecular Neurodegeneration</i> , 2015, 10, 19.	10.8	130
12	De Novo Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. <i>Neuron</i> , 2018, 99, 302-314.e4.	8.1	112
13	Missense variant in TREML2 protects against Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014, 35, 1510.e19-1510.e26.	3.1	110
14	Pooled-DNA sequencing identifies novel causative variants in PSEN1, GRN and MAPT in a clinical early-onset and familial Alzheimer's disease Ibero-American cohort. <i>Alzheimer's Research and Therapy</i> , 2012, 4, 34.	6.2	103
15	Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. <i>Nature Genetics</i> , 2020, 52, 1046-1056.	21.4	96
16	De Novo Pathogenic Variants in CACNA1E Cause Developmental and Epileptic Encephalopathy with Contractures, Macrocephaly, and Dyskinesias. <i>American Journal of Human Genetics</i> , 2018, 103, 666-678.	6.2	87
17	Exome sequencing implicates genetic disruption of prenatal neuro-gliogenesis in sporadic congenital hydrocephalus. <i>Nature Medicine</i> , 2020, 26, 1754-1765.	30.7	84
18	Resequencing analysis of five Mendelian genes and the top genes from genome-wide association studies in Parkinson's Disease. <i>Molecular Neurodegeneration</i> , 2016, 11, 29.	10.8	70

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19	Mutations in Chromatin Modifier and Ephrin Signaling Genes in Vein of Galen Malformation. <i>Neuron</i> , 2019, 101, 429-443.e4.	8.1	56
20	The PSEN1, p.E318G Variant Increases the Risk of Alzheimer's Disease in APOE- $\epsilon$ 4 Carriers. <i>PLoS Genetics</i> , 2013, 9, e1003685.	3.5	55
21	Molecular Genetics and Complex Inheritance of Congenital Heart Disease. <i>Genes</i> , 2021, 12, 1020.	2.4	46
22	Impaired neurogenesis alters brain biomechanics in a neuroprogenitor-based genetic subtype of congenital hydrocephalus. <i>Nature Neuroscience</i> , 2022, 25, 458-473.	14.8	46
23	The FGF and FGFR Gene Family and Risk of Cleft Lip with or Without Cleft Palate. <i>Cleft Palate-Craniofacial Journal</i> , 2013, 50, 96-103.	0.9	39
24	EphrinB2-EphB4-RASA1 Signaling in Human Cerebrovascular Development and Disease. <i>Trends in Molecular Medicine</i> , 2019, 25, 265-286.	6.7	39
25	Association of Damaging Variants in Genes With Increased Cancer Risk Among Patients With Congenital Heart Disease. <i>JAMA Cardiology</i> , 2021, 6, 457.	6.1	34
26	Unique features in the intracellular transport of typhoid toxin revealed by a genome-wide screen. <i>PLoS Pathogens</i> , 2019, 15, e1007704.	4.7	33
27	<i>DIAPH1</i> Variants in Non-East Asian Patients With Sporadic Moyamoya Disease. <i>JAMA Neurology</i> , 2021, 78, 993.	9.0	33
28	Exome Sequencing Implicates Impaired GABA Signaling and Neuronal Ion Transport in Trigeminal Neuralgia. <i>IScience</i> , 2020, 23, 101552.	4.1	32
29	Histone H2B monoubiquitination regulates heart development via epigenetic control of cilia motility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14049-14054.	7.1	30
30	Mutations in <i>TFAP2B</i> and previously unimplicated genes of the BMP, Wnt, and Hedgehog pathways in syndromic craniosynostosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15116-15121.	7.1	24
31	Brain ventricles as windows into brain development and disease. <i>Neuron</i> , 2022, 110, 12-15.	8.1	23
32	PPIL4 is essential for brain angiogenesis and implicated in intracranial aneurysms in humans. <i>Nature Medicine</i> , 2021, 27, 2165-2175.	30.7	23
33	<i>SLC12A</i> ion transporter mutations in sporadic and familial human congenital hydrocephalus. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e892.	1.2	22
34	Biallelic variants in <i>HPDL</i> cause pure and complicated hereditary spastic paraplegia. <i>Brain</i> , 2021, 144, 1422-1434.	7.6	22
35	PTEN mutations in autism spectrum disorder and congenital hydrocephalus: developmental pleiotropy and therapeutic targets. <i>Trends in Neurosciences</i> , 2021, 44, 961-976.	8.6	19
36	Insights From Genetic Studies of Cerebral Palsy. <i>Frontiers in Neurology</i> , 2020, 11, 625428.	2.4	18

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37	Recessive Inheritance of Congenital Hydrocephalus With Other Structural Brain Abnormalities Caused by Compound Heterozygous Mutations in ATP1A3. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 425.	3.7	14
38	Loss of TNR causes a nonprogressive neurodevelopmental disorder with spasticity and transient opisthotonus. <i>Genetics in Medicine</i> , 2020, 22, 1061-1068.	2.4	14
39	Biallelic <i>AOPEP</i> Loss-of-Function Variants Cause Progressive Dystonia with Prominent Limb Involvement. <i>Movement Disorders</i> , 2022, 37, 137-147.	3.9	14
40	Human Genetics and Molecular Mechanisms of Congenital Hydrocephalus. <i>World Neurosurgery</i> , 2018, 119, 441-443.	1.3	12
41	Genomics of human congenital hydrocephalus. <i>Child's Nervous System</i> , 2021, 37, 3325-3340.	1.1	12
42	Variants in Mitochondrial <i>ATP</i> Synthase Cause Variable Neurologic Phenotypes. <i>Annals of Neurology</i> , 2022, 91, 225-237.	5.3	12
43	X-linked markers in the <i>Duchenne</i> muscular dystrophy gene associated with oral clefts. <i>European Journal of Oral Sciences</i> , 2013, 121, 63-68.	1.5	11
44	Bi-allelic variants in <i>SPATA5L1</i> lead to intellectual disability, spastic-dystonic cerebral palsy, epilepsy, and hearing loss. <i>American Journal of Human Genetics</i> , 2021, 108, 2006-2016.	6.2	11
45	Exome Sequencing as a Potential Diagnostic Adjunct in Sporadic Congenital Hydrocephalus. <i>JAMA Pediatrics</i> , 2021, 175, 310.	6.2	10
46	De novo <i>MYH9</i> mutation in congenital scalp hemangioma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002998.	1.2	9
47	Biallelic loss-of-function variants in the splicing regulator <i>NSRP1</i> cause a severe neurodevelopmental disorder with spastic cerebral palsy and epilepsy. <i>Genetics in Medicine</i> , 2021, 23, 2455-2460.	2.4	9
48	Sequencing of a Chinese tetralogy of Fallot cohort reveals clustering mutations in myogenic heart progenitors. <i>JCI Insight</i> , 2022, 7, .	5.0	9
49	Digenic mutations of human <i>OCRL</i> paralogs in Dent's disease type 2 associated with Chiari I malformation. <i>Human Genome Variation</i> , 2016, 3, 16042.	0.7	8
50	A novel association of campomelic dysplasia and hydrocephalus with an unbalanced chromosomal translocation upstream of <i>SOX9</i> . <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002766.	1.2	8
51	Analysis workflow to assess de novo genetic variants from human whole-exome sequencing. <i>STAR Protocols</i> , 2021, 2, 100383.	1.2	7
52	Mutation in <i>ZDHHC15</i> Leads to Hypotonic Cerebral Palsy, Autism, Epilepsy, and Intellectual Disability. <i>Neurology: Genetics</i> , 2021, 7, e602.	1.9	7
53	Variant recurrence confirms the existence of a <i>FBXO31</i> -related spastic-dystonic cerebral palsy syndrome. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 951-955.	3.7	6
54	Genomic approaches to improve the clinical diagnosis and management of patients with congenital hydrocephalus. <i>Journal of Neurosurgery: Pediatrics</i> , 2022, 29, 168-177.	1.3	6

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55	Familial and syndromic forms of arachnoid cyst implicate genetic factors in disease pathogenesis. <i>Cerebral Cortex</i> , 2023, 33, 3012-3025.	2.9	6
56	Integrative modeling of transmitted and <i>de novo</i> variants identifies novel risk genes for congenital heart disease. <i>Quantitative Biology</i> , 2021, 9, 216-227.	0.5	4
57	The phenotypic spectrum of PCDH12 associated disorders - Five new cases and review of the literature. <i>European Journal of Paediatric Neurology</i> , 2022, 36, 7-13.	1.6	4
58	Computational Genomics in the Era of Precision Medicine: Applications to Variant Analysis and Gene Therapy. <i>Journal of Personalized Medicine</i> , 2022, 12, 175.	2.5	4
59	Mutation spectrum of congenital heart disease in a consanguineous Turkish population. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2022, 10, e1944.	1.2	4
60	Pooled-DNA Sequencing for Elucidating New Genomic Risk Factors, Rare Variants Underlying Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 299-314.	0.9	3
61	Recessive <i>COL4A2</i> Mutation Leads to Intellectual Disability, Epilepsy, and Spastic Cerebral Palsy. <i>Neurology: Genetics</i> , 2021, 7, e583.	1.9	3
62	Quantifying concordant genetic effects of <i>de novo</i> mutations on multiple disorders. <i>ELife</i> , 0, 11, .	6.0	3
63	Network assisted analysis of <i>de novo</i> variants using protein-protein interaction information identified 46 candidate genes for congenital heart disease. <i>PLoS Genetics</i> , 2022, 18, e1010252.	3.5	3
64	Whole-exome sequencing reveals damaging gene variants associated with hypoalphalipoproteinemia. <i>Journal of Lipid Research</i> , 2022, 63, 100209.	4.2	2
65	Biallelic Variants in the Ectonucleotidase <i>ENTPD1</i> Cause a Complex Neurodevelopmental Disorder with Intellectual Disability, Distinct White Matter Abnormalities, and Spastic Paraplegia. <i>Annals of Neurology</i> , 2022, 92, 304-321.	5.3	2
66	Exome Sequencing Defines the Molecular Pathogenesis of Vein of Galen Malformation. <i>Neurosurgery</i> , 2019, 66, 310-341.	1.1	1
67	Protein kinase <i>D1</i> variant associated with human epilepsy and peripheral nerve hypermyelination. <i>Clinical Genetics</i> , 2021, 100, 176-186.	2.0	1
68	<i>Q2A10A06</i> : A Common Allele in <i>SPI1</i> Lowers Risk and Delays Age at Onset for Alzheimer's Disease. <i>Alzheimer's and Dementia</i> , 2016, 12, P253.	0.8	0
69	Exome Sequencing Implicates SWI/SNF Chromatin Remodeling Genes in Human Congenital Hydrocephalus. <i>Neurosurgery</i> , 2019, 66, 310-133.	1.1	0
70	The Phenotypic Spectrum of PCDH12-Associated Disorders: Five New Cases and Review of the Literature. , 2021, 52, .		0