Pu Dai

List of Publications by Year
in descending order

85 papers	1,664 citations	331670 21 h-index	330143 37 g-index
95 all docs	95 docs citations	95 times ranked	1795 citing authors

#	Article	IF	Citations
1	GJB2 mutation spectrum in 2063 Chinese patients with nonsyndromic hearing impairment. Journal of Translational Medicine, 2009, 7, 26.	4.4	157
2	Loss-of-Function Mutations in the PRPS1 Gene Cause a Type of Nonsyndromic X-linked Sensorineural Deafness, DFN2. American Journal of Human Genetics, 2010, 86, 65-71.	6.2	88
3	Identification of Adeno-Associated Viral Vectors That Target Neonatal and Adult Mammalian Inner Ear Cell Subtypes. Human Gene Therapy, 2016, 27, 687-699.	2.7	79
4	Unilateral Cochlear Implants for Severe, Profound, or Moderate Sloping to Profound Bilateral Sensorineural Hearing Loss. JAMA Otolaryngology - Head and Neck Surgery, 2020, 146, 942.	2.2	69
5	The prevalence of the 235delC GJB2 mutation in a Chinese deaf population. Genetics in Medicine, 2007, 9, 283-289.	2.4	68
6	Concurrent Hearing and Genetic Screening of 180,469 Neonates with Follow-up in Beijing, China. American Journal of Human Genetics, 2019, 105, 803-812.	6.2	66
7	Distinct and novel SLC26A4/Pendrin mutations in Chinese and U.S. patients with nonsyndromic hearing loss. Physiological Genomics, 2009, 38, 281-290.	2.3	61
8	SLC26A4 c.919-2A>G varies among Chinese ethnic groups as a cause of hearing loss. Genetics in Medicine, 2008, 10, 586-592.	2.4	57
9	Extremely low penetrance of deafness associated with the mitochondrial 12S rRNA mutation in 16 Chinese families: Implication for early detection and prevention of deafness. Biochemical and Biophysical Research Communications, 2006, 340, 194-199.	2.1	52
10	De novo mutation in ATP6V1B2 impairs lysosome acidification and causes dominant deafness-onychodystrophy syndrome. Cell Research, 2014, 24, 1370-1373.	12.0	52
11	Correlation of Cochlear Blood Supply with Mitochondrial DNA Common Deletion in Presbyacusis. Acta Oto-Laryngologica, 2004, 124, 130-136.	0.9	50
12	Noninvasive prenatal testing for autosomal recessive conditions by maternal plasma sequencing in a case of congenital deafness. Genetics in Medicine, 2014, 16, 972-976.	2.4	47
13	Molecular Etiology of Hearing Impairment in Inner Mongolia: mutations in SLC26A4 gene and relevant phenotype analysis. Journal of Translational Medicine, 2008, 6, 74.	4.4	46
14	Genetic mutations in nonsyndromic deafness patients of Chinese minority and han ethnicities in Yunnan, China. Journal of Translational Medicine, 2013, 11, 312.	4.4	42
15	Coexistence of mitochondrial 12S rRNA C1494T and CO1/tRNASer(UCN) G7444A mutations in two Han Chinese pedigrees with aminoglycoside-induced and non-syndromic hearing loss. Biochemical and Biophysical Research Communications, 2007, 362, 94-100.	2.1	39
16	A quantitative cSMART assay for noninvasive prenatal screening of autosomal recessive nonsyndromic hearing loss caused by GJB2 and SLC26A4 mutations. Genetics in Medicine, 2017, 19, 1309-1316.	2.4	33
17	Comprehensive genetic testing of Chinese SNHL patients and variants interpretation using ACMG guidelines and ethnically matched normal controls. European Journal of Human Genetics, 2020, 28, 231-243.	2.8	29
18	Mutation Spectrum of Common Deafness-Causing Genes in Patients with Non-Syndromic Deafness in the Xiamen Area, China. PLoS ONE, 2015, 10, e0135088.	2.5	29

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19	A subunit of V-ATPases, ATP6V1B2, underlies the pathology of intellectual disability. EBioMedicine, 2019, 45, 408-421.	6.1	28
20	Novel compound heterozygous mutations in the MYO15A gene in autosomal recessive hearing loss identified by whole-exome sequencing. Journal of Translational Medicine, 2013, 11, 284.	4.4	26
21	Correlation analysis of phenotype and genotype of GJB2 in patients with non-syndromic hearing loss in China. Gene, 2015, 570, 272-276.	2.2	23
22	Myc and Fgf Are Required for Zebrafish Neuromast Hair Cell Regeneration. PLoS ONE, 2016, 11, e0157768.	2.5	22
23	Identification of a novel mutation in POU3F4 for prenatal diagnosis in a Chinese family with X-linked nonsyndromic hearing loss. Journal of Genetics and Genomics, 2010, 37, 787-793.	3.9	21
24	The Relationship between the p.V37I Mutation in GJB2 and Hearing Phenotypes in Chinese Individuals. PLoS ONE, 2015, 10, e0129662.	2.5	21
25	A de novo GJB2 (connexin 26) mutation, R75W, in a Chinese pedigree with hearing loss and palmoplantar keratoderma. American Journal of Medical Genetics, Part A, 2009, 149A, 689-692.	1.2	20
26	Congenital Middle Ear Abnormalities With Absence of the Oval Window. Otology and Neurotology, 2014, 35, 1191-1195.	1.3	20
27	KCNJ10 May Not Be a Contributor to Nonsyndromic Enlargement of Vestibular Aqueduct (NSEVA) in Chinese Subjects. PLoS ONE, 2014, 9, e108134.	2.5	20
28	Phenotypic Heterogeneity in a DFNA20/26 family segregating a novel ACTG1 mutation. BMC Genetics, 2016, 17, 33.	2.7	19
29	Mutation of IFNLR1, an interferon lambda receptor 1, is associated with autosomal-dominant non-syndromic hearing loss. Journal of Medical Genetics, 2018, 55, 298-306.	3.2	16
30	Intraoperative CT-guided cochlear implantation in congenital ear deformity. Acta Oto-Laryngologica, 2012, 132, 951-958.	0.9	15
31	Targeted gene capture and massively parallel sequencing identify TMC1 as the causative gene in a sixâ€generation Chinese family with autosomal dominant hearing loss. American Journal of Medical Genetics, Part A, 2015, 167, 2357-2365.	1.2	15
32	Identification ofTMPRSS3as a Significant Contributor to Autosomal Recessive Hearing Loss in the Chinese Population. Neural Plasticity, 2017, 2017, 1-8.	2.2	15
33	Computer-Aided Three-Dimensional Reconstruction and Measurement of the Optic Canal and Intracanalicular Structures. Laryngoscope, 1999, 109, 1499-1502.	2.0	14
34	A novel EYA4 mutation causing hearing loss in a Chinese DFNA family and genotype-phenotype review of EYA4 in deafness. Journal of Translational Medicine, 2015, 13, 154.	4.4	14
35	The relationship between the GJB3 c.538C>T variant and hearing phenotype in the Chinese population. International Journal of Pediatric Otorhinolaryngology, 2017, 102, 67-70.	1.0	14
36	Analysis of genotypeâ€“phenotype relationships in 90 Chinese probands with Waardenburg syndrome. Human Genetics, 2022, 141, 839-852.	3.8	13

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37	Impact of next-generation sequencing on molecular diagnosis of inherited non-syndromic hearing loss. Journal of Otology, 2014, 9, 122-125.	1.0	12
38	Extremely low penetrance of deafness associated with the mitochondrial 12S rRNA T1095C mutation in three Chinese families. Biochemical and Biophysical Research Communications, 2006, 348, 200-205.	2.1	11
39	Identification of Two Novel Compound Heterozygous PTPRQ Mutations Associated with Autosomal Recessive Hearing Loss in a Chinese Family. PLoS ONE, 2015, 10, e0124757.	2.5	11
40	Novel Mutations and Mutation Combinations ofTMPRSS3Cause Various Phenotypes in One Chinese Family with Autosomal Recessive Hearing Impairment. BioMed Research International, 2017, 2017, 1-8.	1.9	11
41	A novel pore-region mutation, c.887Gâ€‰›â€‰A (p.G296D) in KCNQ4, causing hearing loss in a Chinese family with autosomal dominant non-syndromic deafness 2. BMC Medical Genetics, 2017, 18, 36.	2.1	10
42	Clinical and molecular characterization of POU3F4 mutations in multiple DFNX2 Chinese families. BMC Medical Genetics, 2018, 19, 157.	2.1	10
43	Congenital sensorineural hearing loss as the initial presentation ofPTPN11-associated Noonan syndrome with multiple lentigines or Noonan syndrome: clinical features and underlying mechanisms. Journal of Medical Genetics, 2021, 58, 465-474.	3.2	10
44	A Missense Mutation in POU4F3 Causes Midfrequency Hearing Loss in a Chinese ADNSHL Family. BioMed Research International, 2018, 2018, 1-7.	1.9	9
45	Genetic mutations in non-syndromic deafness patients in Hainan Province have a different mutational spectrum compared to patients from Mainland China. International Journal of Pediatric Otorhinolaryngology, 2018, 108, 49-54.	1.0	8
46	Skewed X-chromosome inactivation and next-generation sequencing to identify a novel SMPX variants associated with X-linked hearing loss in a Chinese family. International Journal of Pediatric Otorhinolaryngology, 2018, 113, 88-93.	1.0	8
47	Genotype-phenotype variability in Chinese cases of Treacher Collins syndrome. Acta Oto-Laryngologica, 2019, 139, 567-575.	0.9	8
48	Retrospective study of Langerhans cell histiocytosis in ear, nose and neck. American Journal of Otolaryngology - Head and Neck Medicine and Surgery, 2020, 41, 102369.	1.3	8
49	Novel Compound Heterozygous Mutations in MYO7A Associated with Usher Syndrome 1 in a Chinese Family. PLoS ONE, 2014, 9, e103415.	2.5	7
50	The natural history of OTOF-related auditory neuropathy spectrum disorders: a multicenter study. Human Genetics, 2022, 141, 853-863.	3.8	7
51	Sheathless acoustic based flow cell sorter for enrichment of rare cells. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2022, 101, 311-324.	1.5	7
52	A novel PIK3CD C896T mutation detected in bilateral sudden sensorineural hearing loss using next generation sequencing: An indication of primary immunodeficiency. Journal of Otology, 2016, 11, 78-83.	1.0	6
53	Mutation spectra and founder effect of TMC1 in patients with nonâ€‰syndromic deafness in Xiamen area, China. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 301-307.	1.7	6
54	Hearing Phenotypes of Patients with Hearing Loss Homozygous for the GJB2 c.235delc Mutation. Neural Plasticity, 2020, 2020, 1-11.	2.2	6

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55	Multiple synostoses syndrome: Clinical report and retrospective analysis. American Journal of Medical Genetics, Part A, 2020, 182, 1438-1448.	1.2	6
56	Variant analysis of 92 Chinese Han families with hearing loss. BMC Medical Genomics, 2022, 15, 12.	1.5	6
57	De novo dominant mutation of GJB2 in two Chinese families with nonsyndromic hearing loss. International Journal of Pediatric Otorhinolaryngology, 2011, 75, 1333-1336.	1.0	5
58	A novel mutation in POU3F4 in a Chinese family with X-linked non-syndromic hearing loss. Journal of Otology, 2015, 10, 78-82.	1.0	5
59	Treatment of venous pulsatile tinnitus by compression reconstruction of sigmoid sinus. Acta Oto-Laryngologica, 2021, 141, 242-249.	0.9	5
60	A Novel Mutation in the TECTA Gene in a Chinese Family with Autosomal Dominant Nonsyndromic Hearing Loss. PLoS ONE, 2014, 9, e89240.	2.5	5
61	Identification of a p.R143Q dominant mutation in the gap junction beta-2 gene in three Chinese patients with different hearing phenotypes. Acta Oto-Laryngologica, 2012, 133, 55-58.	0.9	4
62	Hearing loss associated with an unusual mutation combination in the gap junction beta 2 (GJB2) gene in a Chinese family. International Journal of Pediatric Otorhinolaryngology, 2014, 78, 599-603.	1.0	4
63	Rapid identification of aminoglycoside-induced deafness gene mutations using multiplex real-time polymerase chain reaction. International Journal of Pediatric Otorhinolaryngology, 2015, 79, 1067-1072.	1.0	4
64	Effects of cochlear implant surgical technique on post-operative electrode impedance. Acta Oto-Laryngologica, 2016, 136, 677-681.	0.9	4
65	Detecting novel mutations and combined Klinefelter syndrome in Usher syndrome cases. Acta Oto-Laryngologica, 2019, 139, 479-486.	0.9	4
66	Clinical characteristics of petrosal cholesteatoma and value of MRI-DWI in the diagnosis. Acta Oto-Laryngologica, 2020, 140, 281-285.	0.9	4
67	Prelingual Sensorineural Hearing Loss Caused by a Novel GJB2 Dominant Mutation in a Chinese Family. BioMed Research International, 2020, 2020, 1-6.	1.9	4
68	Cochlear implantation in patients with canal wall down mastoidectomy cavities. Acta Oto-Laryngologica, 2018, 138, 993-997.	0.9	3
69	Application of multiplanar reconstruction of spiral CT in the diagnosis and treatment of enlarged vestibular aqueducts. Acta Oto-Laryngologica, 2019, 139, 665-670.	0.9	3
70	Establishment of human induced pluripotent stem cell line (CPGHi002-A) from a 10-month-old female patient with DDOD syndrome carrying a heterozygous c.1516 CÂ›ÂT mutation in ATP6V1B2. Stem Cell Research, 2020, 48, 101986.	0.7	3
71	Study of complex structural variations of X-linked deafness-2 based on single-molecule sequencing. Bioscience Reports, 2021, 41, .	2.4	3
72	Gene4HL: An Integrated Genetic Database for Hearing Loss. Frontiers in Genetics, 2021, 12, 773009.	2.3	3

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73	Novel CRISPR/Cas12a-based genetic diagnostic approach for SLC26A4 mutation-related hereditary hearing loss. European Journal of Medical Genetics, 2022, 65, 104406.	1.3	3
74	Stereo morphology of temporal bone and ear. Chinese Medical Journal, 2004, 117, 733-7.	2.3	3
75	Evolutionary origin of pathogenic <scp>GJB2</scp> alleles in China. Clinical Genetics, 2022, 102, 305-313.	2.0	3
76	Syndromic Deafness Gene ATP6V1B2 Controls Degeneration of Spiral Ganglion Neurons Through Modulating Proton Flux. Frontiers in Cell and Developmental Biology, 2021, 9, 742714.	3.7	2
77	Analysis of revision and reimplantation of cochlear implantations in 45 cases. Clinical Otolaryngology, 2019, 44, 1109-1114.	1.2	1
78	Generation of a gene corrected human isogenic iPSC line (CPGHi002-A-1) from a DDOD patient with heterozygous c.1516 C>T mutation in the ATP6V1B2 gene. Stem Cell Research, 2021, 53, 102271.	0.7	1
79	Correspondence on â€œDOORS syndrome and a recurrent truncating ATP6V1B2 variantâ€•by Beauregard-Lacroix et al.. Genetics in Medicine, 2021, 23, 1578-1579.	2.4	1
80	Genetic architecture and phenotypic landscape of deafness and onychodystrophy syndromes. Human Genetics, 2022, 141, 821-838.	3.8	1
81	Petrous bone cholesteatoma: our experience of 20Âyears and management of two giant cases affecting rhinopharynx. European Archives of Oto-Rhino-Laryngology, 2022, 279, 2791-2801.	1.6	1
82	A novel missense variant in CEACAM16 gene causes autosomal dominant nonsyndromic hearing loss. Annals of Human Genetics, 2022, , .	0.8	1
83	Modified Friedman stage in predicting glossopharyngeal obstruction in obstructive sleep apnea. Acta Oto-Laryngologica, 2017, 137, 78-81.	0.9	0
84	Sequential Bilateral Cochlear Implantation in a Child with Severe External, Middle, and Inner Ear Malformations: Surgical Considerations and Practical Aspects. Orl, 2021, 83, 1-7.	1.1	0
85	Transcriptome analysis of the early stage ifnlr1-mutant zebrafish indicates the immune response to auditory dysfunction. Gene Expression Patterns, 2022, 43, 119229.	0.8	0