Shin-Ichi Usami

List of Publications by Year
in descending order

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175	5,253	81839	114418
papers	citations	39 h-index	63 g-index

181	181	181	4581
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Congenital hearing loss. Nature Reviews Disease Primers, 2017, 3, 16094.	18.1	328
2	Distribution and frequencies of PDS (SLC26A4) mutations in Pendred syndrome and nonsyndromic hearing loss associated with enlarged vestibular aqueduct: a unique spectrum of mutations in Japanese. European Journal of Human Genetics, 2003, 11, 916-922.	1.4	220
3	Expression of the P2X₂Receptor Subunit of the ATP-Gated Ion Channel in the Cochlea: Implications for Sound Transduction and Auditory Neurotransmission. Journal of Neuroscience, 1999, 19, 8377-8388.	1.7	164
4	A New Autosomal Recessive Form of Stickler Syndrome Is Caused by a Mutation in the COL9A1 Gene. American Journal of Human Genetics, 2006, 79, 449-457.	2.6	145
5	GJB2 deafness gene shows a specific spectrum of mutations in Japan, including a frequent founder mutation. Human Genetics, 2003, 112, 329-333.	1.8	144
6	Genetic and Clinical Features of Sensorineural Hearing Loss Associated With the 1555 Mitochondrial Mutation. Laryngoscope, 1997, 107, 483-490.	1.1	137
7	Utilizing Ethnic-Specific Differences in Minor Allele Frequency to Recategorize Reported Pathogenic Deafness Variants. American Journal of Human Genetics, 2014, 95, 445-453.	2.6	137
8	Identification of CRYM as a Candidate Responsible for Nonsyndromic Deafness, through cDNA Microarray Analysis of Human Cochlear and Vestibular Tissues**Nucleotide sequence data reported herein are available in the DDBJ/EMBL/GenBank databases; for details, see the Electronic-Database Information section of this article.. American Journal of Human Genetics, 2003, 72, 73-82.	2.6	122
9	Mutation spectrum and genotypeâ€“phenotype correlation of hearing loss patients caused by SLC26A4 mutations in the Japanese: a large cohort study. Journal of Human Genetics, 2014, 59, 262-268.	1.1	113
10	IgG4-related chronic rhinosinusitis: A new clinical entity of nasal disease. Acta Oto-Laryngologica, 2011, 131, 518-526.	0.3	91
11	Ethnic-Specific Spectrum of GJB2 and SLC26A4 Mutations. Annals of Otology, Rhinology and Laryngology, 2015, 124, 61S-76S.	0.6	91
12	Targeted Exon Sequencing Successfully Discovers Rare Causative Genes and Clarifies the Molecular Epidemiology of Japanese Deafness Patients. PLoS ONE, 2013, 8, e71381.	1.1	88
13	Mutations in the COCH gene are a frequent cause of autosomal dominant progressive cochleo-vestibular dysfunction, but not of Meniere's disease. European Journal of Human Genetics, 2003, 11, 744-748.	1.4	85
14	Massively Parallel DNA Sequencing Successfully Identifies New Causative Mutations in Deafness Genes in Patients with Cochlear Implantation and EAS. PLoS ONE, 2013, 8, e75793.	1.1	83
15	Clinical features of patients with GJB2 (connexin 26) mutations: severity of hearing loss is correlated with genotypes and protein expression patterns. Journal of Human Genetics, 2005, 50, 76-83.	1.1	79
16	Achievement of hearing preservation in the presence of an electrode covering the residual hearing region. Acta Oto-Laryngologica, 2011, 131, 405-412.	0.3	70
17	Etiology of single-sided deafness and asymmetrical hearing loss. Acta Oto-Laryngologica, 2017, 137, S2-S7.	0.3	70
18	Deafness Gene Variations in a 1120 Nonsyndromic Hearing Loss Cohort. Annals of Otology, Rhinology and Laryngology, 2015, 124, 49S-60S.	0.6	68

#	Article	IF	Citations
19	Simultaneous Screening of Multiple Mutations by Invader Assay Improves Molecular Diagnosis of Hereditary Hearing Loss: A Multicenter Study. PLoS ONE, 2012, 7, e31276.	1.1	65
20	Comparison of the diagnostic value of 3 T MRI after intratympanic injection of GBCA, electrocochleography, and the glycerol test in patients with Meniere's disease. Acta Oto-Laryngologica, 2012, 132, 141-145.	0.3	62
21	Prevalence and Clinical Features of Hearing Loss Patients with CDH23 Mutations: A Large Cohort Study. PLoS ONE, 2012, 7, e40366.	1.1	61
22	A Comprehensive Study on the Etiology of Patients Receiving Cochlear Implantation With Special Emphasis on Genetic Epidemiology. Otology and Neurotology, 2016, 37, e126-e134.	0.7	61
23	Mutations in the WFS1 gene are a frequent cause of autosomal dominant nonsyndromic low-frequency hearing loss in Japanese. Journal of Human Genetics, 2007, 52, 510-515.	1.1	56
24	Hearing preservation and clinical outcome of 32 consecutive electric acoustic stimulation (EAS) surgeries. Acta Oto-Laryngologica, 2014, 134, 717-727.	0.3	56
25	Frequency and clinical features of hearing loss caused by STRC deletions. Scientific Reports, 2019, 9, 4408.	1.6	56
26	Clinical characteristics and genotypeâ€“phenotype correlation of hearing loss patients withSLC26A4mutations. Acta Oto-Laryngologica, 2007, 127, 1292-1297.	0.3	54
27	Effect of single-drug treatment on idiopathic sudden sensorineural hearing loss. Auris Nasus Larynx, 2003, 30, 123-127.	0.5	53
28	Nationwide epidemiological survey of idiopathic sudden sensorineural hearing loss in Japan. Acta Oto-Laryngologica, 2017, 137, S8-S16.	0.3	52
29	Constitutive activation of <scp>DIA</scp> 1 (<scp>DIAPH</scp> 1) via Câ€terminal truncation causes human sensorineural hearing loss. EMBO Molecular Medicine, 2016, 8, 1310-1324.	3.3	51
30	A mutational hot spot in theKCNQ4 gene responsible for autosomal dominant hearing impairment. Human Mutation, 2002, 20, 15-19.	1.1	48
31	Deafness Gene Expression Patterns in the Mouse Cochlea Found by Microarray Analysis. PLoS ONE, 2014, 9, e92547.	1.1	48
32	Sensorineural hearing loss caused by mitochondrial dna mutations. Journal of Communication Disorders, 1998, 31, 423-435.	0.8	47
33	Comprehensive Genetic Screening of KCNQ4 in a Large Autosomal Dominant Nonsyndromic Hearing Loss Cohort: Genotype-Phenotype Correlations and a Founder Mutation. PLoS ONE, 2013, 8, e63231.	1.1	47
34	The responsible genes in Japanese deafness patients and clinical application using Invader assay. Acta Oto-Laryngologica, 2008, 128, 446-454.	0.3	44
35	Gene Expression Profiles of the Cochlea and Vestibular Endorgans. Annals of Otology, Rhinology and Laryngology, 2015, 124, 6S-48S.	0.6	44
36	Hearing preservation cochlear implantation in children: The HEARRING Group consensus and practice guide. Cochlear Implants International, 2018, 19, 1-13.	0.5	43

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37	Mutations in the MYO15A Gene Are a Significant Cause of Nonsyndromic Hearing Loss. Annals of Otology, Rhinology and Laryngology, 2015, 124, 158S-168S.	0.6	42
38	Three Familial Cases of Hearing Loss Associated with Enlargement of the Vestibular Aqueduct. Annals of Otology, Rhinology and Laryngology, 1997, 106, 1063-1069.	0.6	41
39	Application of Deafness Diagnostic Screening Panel Based on Deafness Mutation/Gene Database Using Invader Assay. Genetic Testing and Molecular Biomarkers, 2007, 11, 333-340.	1.7	41
40	Clinical profile of hearing loss in children with congenital cytomegalovirus (CMV) infection: CMV DNA diagnosis using preserved umbilical cord. Acta Oto-Laryngologica, 2011, 131, 976-982.	0.3	41
41	Long-term results of hearing preservation cochlear implant surgery in patients with residual low frequency hearing. Acta Oto-Laryngologica, 2017, 137, 516-521.	0.3	40
42	Patients withCDH23mutations and the 1555A>G mitochondrial mutation are good candidates for electric acoustic stimulation (EAS). Acta Oto-Laryngologica, 2012, 132, 377-384.	0.3	39
43	Semi-quantitative evaluation of endolymphatic hydrops by bilateral intratympanic gadolinium-based contrast agent (GBCA) administration with MRI for Meniere's disease. Acta Oto-Laryngologica, 2010, 130, 10-16.	0.3	38
44	Clinical Application of a Custom AmpliSeq Library and Ion Torrent PGM Sequencing to Comprehensive Mutation Screening for Deafness Genes. Genetic Testing and Molecular Biomarkers, 2015, 19, 209-217.	0.3	37
45	Hearing Handicap in Adults With Unilateral Deafness and Bilateral Hearing Loss. Otology and Neurotology, 2013, 34, 644-649.	0.7	36
46	Massively Parallel DNA Sequencing Facilitates Diagnosis of Patients with Usher Syndrome Type 1. PLoS ONE, 2014, 9, e90688.	1.1	36
47	Outcomes of cochlear implantation for the patients with specific genetic etiologies: a systematic literature review. Acta Oto-Laryngologica, 2017, 137, 730-742.	0.3	35
48	OTOF mutation screening in Japanese severe to profound recessive hearing loss patients. BMC Medical Genetics, 2013, 14, 95.	2.1	34
49	WFS1 mutation screening in a large series of Japanese hearing loss patients: Massively parallel DNA sequencing-based analysis. PLoS ONE, 2018, 13, e0193359.	1.1	33
50	Endolymphatic hydrops and therapeutic effects are visualized in â€˜atypicalâ€™ Meniere's disease. Acta Oto-Laryngologica, 2009, 129, 1326-1329.	0.3	32
51	The Patients Associated With TMPRSS3 Mutations Are Good Candidates for Electric Acoustic Stimulation. Annals of Otology, Rhinology and Laryngology, 2015, 124, 193S-204S.	0.6	32
52	OTOF mutation analysis with massively parallel DNA sequencing in 2,265 Japanese sensorineural hearing loss patients. PLoS ONE, 2019, 14, e0215932.	1.1	31
53	POU4F3 mutation screening in Japanese hearing loss patients: Massively parallel DNA sequencing-based analysis identified novel variants associated with autosomal dominant hearing loss. PLoS ONE, 2017, 12, e0177636.	1.1	31
54	Idiopathic sudden sensorineural hearing loss and acute low-tone sensorineural hearing loss: a comparison of the results of a nationwide epidemiological survey in Japan. Acta Oto-Laryngologica, 2017, 137, S38-S43.	0.3	30

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55	TECTA mutations in Japanese with mid-frequency hearing loss affected by zona pellucida domain protein secretion. Journal of Human Genetics, 2012, 57, 587-592.	1.1	29
56	An effective screening strategy for deafness in combination with a next-generation sequencing platform: a consecutive analysis. Journal of Human Genetics, 2016, 61, 253-261.	1.1	29
57	Detection and Confirmation of Deafness-Causing Copy Number Variations in the STRC Gene by Massively Parallel Sequencing and Comparative Genomic Hybridization. Annals of Otology, Rhinology and Laryngology, 2016, 125, 918-923.	0.6	28
58	Massively Parallel DNA Sequencing Successfully Identified Seven Families With Deafness-Associated MYO6 Mutations. Annals of Otology, Rhinology and Laryngology, 2015, 124, 148S-157S.	0.6	27
59	Cochlear Implantation From the Perspective of Genetic Background. Anatomical Record, 2020, 303, 563-593.	0.8	27
60	The effects of cochlear implantation in Japanese single-sided deafness patients: five case reports. Acta Oto-Laryngologica, 2016, 136, 460-464.	0.3	26
61	Connexin 26 distribution in gap junctions between melanocytes in the human vestibular dark cell area. The Anatomical Record, 2001, 262, 137-146.	2.3	25
62	Effects of EAS cochlear implantation surgery on vestibular function. Acta Oto-Laryngologica, 2013, 133, 1128-1132.	0.3	25
63	Detailed Hearing and Vestibular Profiles in the Patients with COCH Mutations. Annals of Otology, Rhinology and Laryngology, 2015, 124, 100S-110S.	0.6	25
64	The clinical features and prognosis of mumps-associated hearing loss: a retrospective, multi-institutional investigation in Japan. Acta Oto-Laryngologica, 2017, 137, S44-S47.	0.3	25
65	The effect of initial treatment on hearing prognosis in idiopathic sudden sensorineural hearing loss: a nationwide survey in Japan. Acta Oto-Laryngologica, 2017, 137, S30-S33.	0.3	25
66	Simple and efficient germline copy number variant visualization method for the Ion AmpliSeqâ„¢ custom panel. Molecular Genetics & Genomic Medicine, 2018, 6, 678-686.	0.6	25
67	The genetic etiology of hearing loss in Japan revealed by the social health insurance-based genetic testing of 10K patients. Human Genetics, 2022, 141, 665-681.	1.8	25
68	Mutations in LOXHD1 Gene Cause Various Types and Severities of Hearing Loss. Annals of Otology, Rhinology and Laryngology, 2015, 124, 135S-141S.	0.6	24
69	Language development in Japanese children who receive cochlear implant and/or hearing aid. International Journal of Pediatric Otorhinolaryngology, 2012, 76, 433-438.	0.4	23
70	Mutational Spectrum and Clinical Features of Patients With ACTG1 Mutations Identified by Massively Parallel DNA Sequencing. Annals of Otology, Rhinology and Laryngology, 2015, 124, 84S-93S.	0.6	23
71	Epidemiological survey of acute low-tone sensorineural hearing loss. Acta Oto-Laryngologica, 2017, 137, S34-S37.	0.3	22
72	Digenic inheritance of mutations in EPHA2 and SLC26A4 in Pendred syndrome. Nature Communications, 2020, 11, 1343.	5.8	22

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73	Social Health Insurance-Based Simultaneous Screening for 154 Mutations in 19 Deafness Genes Efficiently Identified Causative Mutations in Japanese Hearing Loss Patients. PLoS ONE, 2016, 11, e0162230.	1.1	22
74	The diagnostic performance of a novel ELISA for human CTP (Cochlin-tomoprotein) to detect perilymph leakage. PLoS ONE, 2018, 13, e0191498.	1.1	22
75	Mutation analysis of COL9A3, a gene highly expressed in the cochlea, in hearing loss patients. Auris Nasus Larynx, 2005, 32, 113-117.	0.5	21
76	Gene Expression Pattern after Insertion of Dexamethasone-Eluting Electrode into the Guinea Pig Cochlea. PLoS ONE, 2014, 9, e110238.	1.1	21
77	Frequency of mitochondrial mutations in non-syndromic hearing loss as well as possibly responsible variants found by whole mitochondrial genome screening. Journal of Human Genetics, 2014, 59, 100-106.	1.1	21
78	Novel ABHD12 Mutations in PHARC Patients. Annals of Otology, Rhinology and Laryngology, 2015, 124, 77S-83S.	0.6	21
79	Genetic testing has the potential to impact hearing preservation following cochlear implantation. Acta Oto-Laryngologica, 2020, 140, 438-444.	0.3	21
80	Experience with the Vibrant Soundbridge RW-Coupler for round window Vibroplasty with tympanosclerosis. Acta Oto-Laryngologica, 2012, 132, 676-682.	0.3	20
81	The use of a MITO-Porter to deliver exogenous therapeutic RNA to a mitochondrial diseaseâ€™s cell with a A1555G mutation in the mitochondrial 12S rRNA gene results in an increase in mitochondrial respiratory activity. Mitochondrion, 2020, 55, 134-144.	1.6	20
82	Electric-acoustic stimulation with longer electrodes for potential deterioration in low-frequency hearing. Acta Oto-Laryngologica, 2020, 140, 624-630.	0.3	20
83	Prevalence and clinical features of hearing loss caused by EYA4 variants. Scientific Reports, 2020, 10, 3662.	1.6	20
84	Carrier frequency of the GJB2 mutations that cause hereditary hearing loss in the Japanese population. Journal of Human Genetics, 2015, 60, 613-617.	1.1	19
85	De Novo Mutation in X-Linked Hearing Lossâ€“Associated POU3F4 in a Sporadic Case of Congenital Hearing Loss. Annals of Otology, Rhinology and Laryngology, 2015, 124, 169S-176S.	0.6	19
86	Novel PTPRQ Mutations Identified in Three Congenital Hearing Loss Patients With Various Types of Hearing Loss. Annals of Otology, Rhinology and Laryngology, 2015, 124, 184S-192S.	0.6	19
87	Frequency of Usher syndrome type 1 in deaf children by massively parallel DNA sequencing. Journal of Human Genetics, 2016, 61, 419-422.	1.1	19
88	Laser-capture micro dissection combined with next-generation sequencing analysis of cell type-specific deafness gene expression in the mouse cochlea. Hearing Research, 2017, 348, 87-97.	0.9	19
89	Comprehensive analysis of syndromic hearing loss patients in Japan. Scientific Reports, 2019, 9, 11976.	1.6	19
90	Haplotype Analysis of GJB2 Mutations: Founder Effect or Mutational Hot Spot?. Genes, 2020, 11, 250.	1.0	19

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91	Genetic background of candidates for EAS (Electric-Acoustic Stimulation). Audiological Medicine, 2010, 8, 28-32.	0.4	18
92	Long term speech perception after cochlear implant in pediatric patients with GJB2 mutations. Auris Nasus Larynx, 2013, 40, 435-439.	0.5	18
93	Correlation Between White Matter Lesions and Intelligence Quotient in Patients With Congenital Cytomegalovirus Infection. Pediatric Neurology, 2016, 55, 52-57.	1.0	18
94	Feasibility of hearing preservation for residual hearing with longer cochlear implant electrodes. Acta Oto-Laryngologica, 2018, 138, 1080-1085.	0.3	18
95	Hearing Loss Caused by a P2RX2 Mutation Identified in a MELAS Family With a Coexisting Mitochondrial 3243AG Mutation. Annals of Otology, Rhinology and Laryngology, 2015, 124, 177S-183S.	0.6	17
96	Cochlear volume as a predictive factor for residual-hearing preservation after conventional cochlear implantation. Acta Oto-Laryngologica, 2018, 138, 345-350.	0.3	17
97	The Prevalence and Clinical Characteristics of TECTA-Associated Autosomal Dominant Hearing Loss. Genes, 2019, 10, 744.	1.0	17
98	Comprehensive Genetic Analysis of Japanese Autosomal Dominant Sensorineural Hearing Loss Patients. PLoS ONE, 2016, 11, e0166781.	1.1	17
99	A rational approach to identifying newborns with hearing loss caused by congenital cytomegalovirus infection by dried blood spot screening. Acta Oto-Laryngologica, 2018, 138, 708-712.	0.3	16
100	Sensorineural hearing loss and mild cardiac phenotype caused by an EYA4 mutation. Human Genome Variation, 2018, 5, 23.	0.4	15
101	Mid-Frequency Hearing Loss Is Characteristic Clinical Feature of OTOA-Associated Hearing Loss. Genes, 2019, 10, 715.	1.0	15
102	Mutational Spectrum and Clinical Features of Patients with LOXHD1 Variants Identified in an 8074 Hearing Loss Patient Cohort. Genes, 2019, 10, 735.	1.0	15
103	Novel ACTG1 mutations in patients identified by massively parallel DNA sequencing cause progressive hearing loss. Scientific Reports, 2020, 10, 7056.	1.6	15
104	A nationwide multicenter study of the Cochlin tomo-protein detection test: clinical characteristics of perilymphatic fistula cases. Acta Oto-Laryngologica, 2017, 137, S53-S59.	0.3	14
105	Differences between acoustic trauma and other types of acute noise-induced hearing loss in terms of treatment and hearing prognosis. Acta Oto-Laryngologica, 2017, 137, S48-S52.	0.3	14
106	SOD1gene polymorphisms in sudden sensorineural hearing loss. Acta Oto-Laryngologica, 2016, 136, 465-469.	0.3	13
107	Prognostic impact of gene polymorphisms in patients with idiopathic sudden sensorineural hearing loss. Acta Oto-Laryngologica, 2017, 137, S24-S29.	0.3	13
108	The Clinical Next-Generation Sequencing Database: A Tool for the Unified Management of Clinical Information and Genetic Variants to Accelerate Variant Pathogenicity Classification. Human Mutation, 2017, 38, 252-259.	1.1	12

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109	Bilateral delayed endolymphatic hydrops evaluated by bilateral intratympanic injection of gadodiamide with 3T-MRI. PLoS ONE, 2018, 13, e0206891.	1.1	12
110	Prevalence of the mitochondrial 1555 A>G and 1494 C>T mutations in a community-dwelling population in Japan. Human Genome Variation, 2020, 7, 27.	0.4	12
111	A comparative analysis of genetic hearing loss phenotypes in European/American and Japanese populations. Human Genetics, 2020, 139, 1315-1323.	1.8	12
112	Clinical Characteristics and In Vitro Analysis of MYO6 Variants Causing Late-onset Progressive Hearing Loss. Genes, 2020, 11, 273.	1.0	12
113	Human deafness-associated variants alter the dynamics of key molecules in hair cell stereocilia F-actin cores. Human Genetics, 2022, 141, 363-382.	1.8	12
114	An Usher syndrome type 1 patient diagnosed before the appearance of visual symptoms by MYO7A mutation analysis. International Journal of Pediatric Otorhinolaryngology, 2013, 77, 298-302.	0.4	11
115	Relationships among drinking and smoking habits, history of diseases, body mass index and idiopathic sudden sensorineural hearing loss in Japanese patients. Acta Oto-Laryngologica, 2017, 137, S17-S23.	0.3	11
116	Treatment algorithm for idiopathic sudden sensorineural hearing loss based on epidemiologic surveys of a large Japanese cohort. Acta Oto-Laryngologica, 2020, 140, 32-39.	0.3	11
117	Congenital Membranous Stapes Footplate Producing Episodic Pressure-Induced Perilymphatic Fistula Symptoms. Frontiers in Neurology, 2020, 11, 585747.	1.1	11
118	A phase I/IIa double blind single institute trial of low dose sirolimus for Pendred syndrome/DFNB4. Medicine (United States), 2020, 99, e19763.	0.4	11
119	Systematic Literature Review of Hearing Preservation Rates in Cochlear Implantation Associated With Medium- and Longer-Length Flexible Lateral Wall Electrode Arrays. Frontiers in Surgery, 0, 9, .	0.6	10
120	Preâ€Baha Operation Three Dimensional Computed Tomography With Markers for Determining Optimal Implant Site. Laryngoscope, 2008, 118, 1824-1826.	1.1	9
121	The advantages of sound localization and speech perception of bilateral electric acoustic stimulation. Acta Oto-Laryngologica, 2015, 135, 147-153.	0.3	9
122	USH2 Caused by GPR98 Mutation Diagnosed by Massively Parallel Sequencing in Advance of the Occurrence of Visual Symptoms. Annals of Otology, Rhinology and Laryngology, 2015, 124, 123S-128S.	0.6	9
123	Novel Mutations in LRTOMT Associated With Moderate Progressive Hearing Loss in Autosomal Recessive Inheritance. Annals of Otology, Rhinology and Laryngology, 2015, 124, 142S-147S.	0.6	9
124	Genetic background in late-onset sensorineural hearing loss patients. Journal of Human Genetics, 2022, 67, 223-230.	1.1	9
125	Silicone impression material foreign body in the middle ear: Two case reports and literature review. Auris Nasus Larynx, 2015, 42, 419-423.	0.5	8
126	Non-ocular Stickler Syndrome With a Novel Mutation in COL11A2 Diagnosed by Massively Parallel Sequencing in Japanese Hearing Loss Patients. Annals of Otology, Rhinology and Laryngology, 2015, 124, 111S-117S.	0.6	8

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127	Novel Mutations in GRXCR1 at DFNB25 Lead to Progressive Hearing Loss and Dizziness. Annals of Otology, Rhinology and Laryngology, 2015, 124, 129S-134S.	0.6	8
128	Milestones toward cochlear gene therapy for patients with hereditary hearing loss. Laryngoscope Investigative Otolaryngology, 2021, 6, 958-967.	0.6	8
129	Inner hair cells of mice express the glutamine transporter SAT1. Hearing Research, 2012, 292, 59-63.	0.9	7
130	Germinal Mosaicism in a Family With BO Syndrome. Annals of Otology, Rhinology and Laryngology, 2015, 124, 118S-122S.	0.6	7
131	Discrimination of Japanese monosyllables in patients with high-frequency hearing loss. Auris Nasus Larynx, 2016, 43, 269-280.	0.5	6
132	Diagnostic pitfalls for <scp>GJB</scp>2â€related hearing loss: A novel deletion detected by Arrayâ€<scp>CGH</scp> analysis in a Japanese patient with congenital profound hearing loss. Clinical Case Reports (discontinued), 2018, 6, 2111-2116.	0.2	6
133	The availability of an adhesive bone conduction hearing device: a preliminary report of a single-center experience. Acta Oto-Laryngologica, 2020, 140, 319-326.	0.3	6
134	Prevalence and clinical features of autosomal dominant and recessive TMC1-associated hearing loss. Human Genetics, 2022, 141, 929-937.	1.8	6
135	Frequency of the STRC-CATSPER2 deletion in STRC-associated hearing loss patients. Scientific Reports, 2022, 12, 634.	1.6	6
136	Variants in CDH23 cause a broad spectrum of hearing loss: from non-syndromic to syndromic hearing loss as well as from congenital to age-related hearing loss. Human Genetics, 2022, 141, 903-914.	1.8	6
137	Prevalence and Clinical Characteristics of Hearing Loss Caused by MYH14 Variants. Genes, 2021, 12, 1623.	1.0	5
138	Molecular diagnosis of deafness. Audiology Japan, 2011, 54, 44-55.	0.1	5
139	Identification of a Novel CLRN1 Gene Mutation in Usher Syndrome Type 3. Annals of Otology, Rhinology and Laryngology, 2015, 124, 94S-99S.	0.6	4
140	Detailed Clinical Features of Deafness Caused by a Claudin-14 Variant. International Journal of Molecular Sciences, 2019, 20, 4579.	1.8	4
141	Vestibular Preservation After Cochlear Implantation Using the Round Window Approach. Frontiers in Neurology, 2021, 12, 656592.	1.1	4
142	Identification of a Novel Copy Number Variation of EYA4 Causing Autosomal Dominant Non-syndromic Hearing Loss. Otology and Neurotology, 2021, 42, e866-e874.	0.7	4
143	Speech perception in noise in patients with idiopathic sudden hearing loss. Acta Oto-Laryngologica, 2022, 142, 302-307.	0.3	4
144	Etiology of hearing loss affects auditory skill development and vocabulary development in pediatric cochlear implantation cases. Acta Oto-Laryngologica, 2022, 142, 308-315.	0.3	4

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145	Different cortical metabolic activation by visual stimuli possibly due to different time courses of hearing loss in patients withGJB2andSLC26A4mutations. Acta Oto-Laryngologica, 2011, 131, 1232-1236.	0.3	3
146	Phylogeny and biogeography of arcticâ€alpine butterflies of the genus Oeneis (Nymphalidae: Satyrinae). Entomological Science, 2021, 24, 183-195.	0.3	3
147	Vestibular nerve deficiency and vestibular function in children with unilateral hearing loss caused by cochlear nerve deficiency. Acta Oto-Laryngologica, 2021, 141, 835-840.	0.3	3
148	Detailed clinical features and genotypeâ€“phenotype correlation in an OTOF-related hearing loss cohort in Japan. Human Genetics, 2022, 141, 865-875.	1.8	3
149	Evaluation of cortical processing of language by use of positron emission tomography in hearing loss children with congenital cytomegalovirus infection. International Journal of Pediatric Otorhinolaryngology, 2014, 78, 285-289.	0.4	2
150	High-Frequency Involved Hearing Loss Caused by Novel Mitochondrial DNA Mutation in 16S Ribosomal RNA Gene. Otology and Neurotology, 2014, 35, 1087-1090.	0.7	2
151	A plea for systematic literature analysis and conclusive study design, comment on: â€œSystematic review of magnetic resonance imaging for diagnosis of Meniere diseaseâ€. Journal of Vestibular Research: Equilibrium and Orientation, 2019, , 1-7.	0.8	2
152	Cochlear implantation in a patient with a POU4F3 mutation. Clinical Case Reports (discontinued), 2021, 9, 298-303.	0.2	2
153	Improvement of a Rapid and Highly Sensitive Method for the Diagnosis of the Mitochondrial m.1555A>G Mutation Based on a Single-Stranded Tag Hybridization Chromatographic Printed-Array Strip. Genetic Testing and Molecular Biomarkers, 2021, 25, 79-83.	0.3	2
154	Results of electric acoustic stimulation for partial deafness in japan: three case reports. Audiology Japan, 2011, 54, 678-685.	0.1	2
155	Development and validation of an iPad-based Japanese language monosyllable speech perception test (iCI2004 monosyllable). Acta Oto-Laryngologica, 2021, 141, 267-272.	0.3	2
156	Molecular Diagnosis of Deafnessâ€”A Preface. Annals of Otology, Rhinology and Laryngology, 2015, 124, 5S-5S.	0.6	1
157	Acute sensorineural hearing loss. Acta Oto-Laryngologica, 2017, 137, S1-S1.	0.3	1
158	Detailed MR imaging assessment of endolymphatic hydrops in patients with SLC26A4 mutations.. Auris Nasus Larynx, 2020, 47, 958-964.	0.5	1
159	A nationwide epidemiologic, clinical, genetic study of Usher syndrome in Japan. Acta Oto-Laryngologica, 2021, 141, 841-846.	0.3	1
160	Vibrant soundbridge implantation prior to auricular reconstruction with unilateral microtiaâ€atresia. Clinical Case Reports (discontinued), 2021, 9, e04408.	0.2	1
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