Guy Van Camp

List of Publications by Year
in descending order

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376 papers	20,070 citations	9786 73 h-index	18130 120 g-index
382 all docs	382 docs citations	382 times ranked	15193 citing authors

#	Article	IF	Citations
1	Mutations in the Connexin 26 Gene (GJB2) among Ashkenazi Jews with Nonsyndromic Recessive Deafness. New England Journal of Medicine, 1998, 339, 1500-1505.	27.0	513
2	GJB2 Mutations and Degree of Hearing Loss: A Multicenter Study. American Journal of Human Genetics, 2005, 77, 945-957.	6.2	455
3	Nano-targeted induction of dual ferroptotic mechanisms eradicates high-risk neuroblastoma. Journal of Clinical Investigation, 2018, 128, 3341-3355.	8.2	406
4	Forty-six genes causing nonsyndromic hearing impairment: Which ones should be analyzed in DNA diagnostics?. Mutation Research - Reviews in Mutation Research, 2009, 681, 189-196.	5.5	386
5	Congenital hearing loss. Nature Reviews Disease Primers, 2017, 3, 16094.	30.5	328
6	Nonsyndromic hearing impairment is associated with a mutation in DFNA5. Nature Genetics, 1998, 20, 194-197.	21.4	323
7	Mutations in the human Î±-tectorin gene cause autosomal dominant non-syndromic hearing impairment. Nature Genetics, 1998, 19, 60-62.	21.4	323
8	Non-syndromic hearing loss associated with enlarged vestibular aqueduct is caused by PDS mutations. Human Genetics, 1999, 104, 188-192.	3.8	289
9	Mutations in COL11A2 cause non-syndromic hearing loss (DFNA13). Nature Genetics, 1999, 23, 413-419.	21.4	285
10	A novel deletion involving the connexin-30 gene, del(GJB6-d13s1854), found in trans with mutations in the GJB2 gene (connexin-26) in subjects with DFNB1 non-syndromic hearing impairment. Journal of Medical Genetics, 2005, 42, 588-594.	3.2	282
11	Prevalence and Evolutionary Origins of the del(GJB6-D13S1830) Mutation in the DFNB1 Locus in Hearing-Impaired Subjects: a Multicenter Study. American Journal of Human Genetics, 2003, 73, 1452-1458.	6.2	269
12	Mutations in the gene encoding pejvakin, a newly identified protein of the afferent auditory pathway, cause DFNB59 auditory neuropathy. Nature Genetics, 2006, 38, 770-778.	21.4	262
13	Mutations in the novel protocadherin PCDH15 cause Usher syndrome type 1F. Human Molecular Genetics, 2001, 10, 1709-1718.	2.9	257
14	The Complexity of Age-Related Hearing Impairment: Contributing Environmental and Genetic Factors. Audiology and Neuro-Otology, 2007, 12, 345-358.	1.3	244
15	L1 knockout mice show dilated ventricles, vermis hypoplasia and impaired exploration patterns. Human Molecular Genetics, 1998, 7, 999-1009.	2.9	228
16	Identification of mutations in the connexin 26 gene that cause autosomal recessive nonsyndromic hearing loss. Human Mutation, 1998, 11, 387-394.	2.5	216
17	Occupational Noise, Smoking, and a High Body Mass Index are Risk Factors for Age-related Hearing Impairment and Moderate Alcohol Consumption is Protective: A European Population-based Multicenter Study. JARO - Journal of the Association for Research in Otolaryngology, 2008, 9, 264-276.	1.8	214
18	Mutations in the Wolfram syndrome 1 gene (WFS1) are a common cause of low frequency sensorineural hearing loss. Human Molecular Genetics, 2001, 10, 2501-2508.	2.9	213

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19	Mutations in the transcriptional activator EYA4 cause late-onset deafness at the DFNA10 locus. Human Molecular Genetics, 2001, 10, 195-200.	2.9	210
20	CRASH Syndrome: Clinical Spectrum of Corpus Callosum Hypoplasia, Retardation, Adducted Thumbs, Spastic Paraparesis and Hydrocephalus Due to Mutations in One Single Gene, L1. European Journal of Human Genetics, 1995, 3, 273-284.	2.8	201
21	A genotype-phenotype correlation for GJB2 (connexin 26) deafness. Journal of Medical Genetics, 2004, 41, 147-154.	3.2	178
22	Two Frequent Missense Mutations in Pendred Syndrome. Human Molecular Genetics, 1998, 7, 1099-1104.	2.9	174
23	GRM7 variants confer susceptibility to age-related hearing impairment. Human Molecular Genetics, 2009, 18, 785-796.	2.9	174
24	Primary tumor sidedness has an impact on prognosis and treatment outcome in metastatic colorectal cancer: results from two randomized first-line panitumumab studies. Annals of Oncology, 2017, 28, 1862-1868.	1.2	174
25	L1-associated diseases: clinical geneticists divide, molecular geneticists unite. Human Molecular Genetics, 1997, 6, 1625-1632.	2.9	172
26	A common founder for the 35delG GJB2 gene mutation in connexin 26 hearing impairment. Journal of Medical Genetics, 2001, 38, 515-518.	3.2	169
27	MASA syndrome is due to mutations in the neural cell adhesion gene L1CAM. Nature Genetics, 1994, 7, 408-413.	21.4	165
28	Mutational spectrum of theWFS1 gene in Wolfram syndrome, nonsyndromic hearing impairment, diabetes mellitus, and psychiatric disease. Human Mutation, 2003, 22, 275-287.	2.5	160
29	Mutations in the KCNQ4 gene are responsible for autosomal dominant deafness in four DFNA2 families. Human Molecular Genetics, 1999, 8, 1321-1328.	2.9	154
30	A Dominant-NegativeGFI1BMutation in the Gray Platelet Syndrome. New England Journal of Medicine, 2014, 370, 245-253.	27.0	152
31	Function and Expression Pattern of Nonsyndromic Deafness Genes. Current Molecular Medicine, 2009, 9, 546-564.	1.3	151
32	Nonmuscle Myosin Heavy-Chain Gene MYH14 Is Expressed in Cochlea and Mutated in Patients Affected by Autosomal Dominant Hearing Impairment (DFNA4). American Journal of Human Genetics, 2004, 74, 770-776.	6.2	150
33	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.	6.2	145
34	High Prevalence of Symptoms of Meniere's Disease in three Families With a Mutation in the COCH Gene. Human Molecular Genetics, 1999, 8, 1425-1429.	2.9	144
35	GJB2 deafness gene shows a specific spectrum of mutations in Japan, including a frequent founder mutation. Human Genetics, 2003, 112, 329-333.	3.8	144
36	Van Buchem Disease (Hyperostosis Corticalis Generalisata) Maps to Chromosome 17q12-q21. American Journal of Human Genetics, 1998, 62, 391-399.	6.2	141

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37	Linkage of Autosomal Dominant Hearing Loss to the Short Arm of Chromosome 1 in Two Families. New England Journal of Medicine, 1994, 331, 425-431.	27.0	137
38	A deafness mutation isolates a second role for the tectorial membrane in hearing. Nature Neuroscience, 2005, 8, 1035-1042.	14.8	130
39	Apoptosis in acquired and genetic hearing impairment: The programmed death of the hair cell. Hearing Research, 2011, 281, 18-27.	2.0	128
40	Recommendations for the Description of Genetic and Audiological Data for Families with Nonsyndromic Hereditary Hearing Impairment. Audiological Medicine, 2003, 1, 148-150.	0.4	125
41	Heterozygous Loss-of-Function SEC61A1 Mutations Cause Autosomal-Dominant Tubulo-Interstitial and Glomerulocystic Kidney Disease with Anemia. American Journal of Human Genetics, 2016, 99, 174-187.	6.2	124
42	The grainyhead like 2 gene (GRHL2), alias TFCP2L3, is associated with age-related hearing impairment. Human Molecular Genetics, 2008, 17, 159-169.	2.9	121
43	Genetics of microtia and associated syndromes. Journal of Medical Genetics, 2009, 46, 361-369.	3.2	119
44	Discrimination among thermophilic Campylobacter species by polymerase chain reaction amplification of 23S rRNA gene fragments. Journal of Clinical Microbiology, 1993, 31, 3340-3343.	3.9	118
45	Genetic Studies on Noise-Induced Hearing Loss: A Review. Ear and Hearing, 2009, 30, 151-159.	2.1	114
46	Localization of a gene for otosclerosis to chromosome 15q25-q26. Human Molecular Genetics, 1998, 7, 285-290.	2.9	112
47	Connexin-26 mutations in sporadic non-syndromal sensorineural deafness. Lancet, The, 1998, 351, 415.	13.7	109
48	The contribution of genes involved in potassium-recycling in the inner ear to noise-induced hearing loss. Human Mutation, 2006, 27, 786-795.	2.5	109
49	Functional Null Mutations of MSRB3 Encoding Methionine Sulfoxide Reductase Are Associated with Human Deafness DFNB74. American Journal of Human Genetics, 2011, 88, 19-29.	6.2	107
50	Heimler Syndrome Is Caused by Hypomorphic Mutations in the Peroxisome-Biogenesis Genes PEX1 and PEX6. American Journal of Human Genetics, 2015, 97, 535-545.	6.2	103
51	KCNQ4: a gene for age-related hearing impairment?. Human Mutation, 2006, 27, 1007-1016.	2.5	101
52	Genotype-phenotype correlation in L1 associated diseases.. Journal of Medical Genetics, 1998, 35, 399-404.	3.2	99
53	The DFNA5 gene, responsible for hearing loss and involved in cancer, encodes a novel apoptosis-inducing protein. European Journal of Human Genetics, 2011, 19, 965-973.	2.8	99
54	A Mutation in CABP2 , Expressed in Cochlear Hair Cells, Causes Autosomal-Recessive Hearing Impairment. American Journal of Human Genetics, 2012, 91, 636-645.	6.2	96

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55	A duplication in the L1CAM gene associated with Xâ€“linked hydrocephalus. Nature Genetics, 1993, 4, 421-425.	21.4	91
56	A Second Gene for Otosclerosis, OTSC2, Maps to Chromosome 7q34-36. American Journal of Human Genetics, 2001, 68, 495-500.	6.2	91
57	The influence of genetic variation in oxidative stress genes on human noise susceptibility. Hearing Research, 2005, 202, 87-96.	2.0	88
58	A genome-wide association study for age-related hearing impairment in the Saami. European Journal of Human Genetics, 2010, 18, 685-693.	2.8	88
59	Large-scale analysis of DFNA5 methylation reveals its potential as biomarker for breast cancer. Clinical Epigenetics, 2018, 10, 51.	4.1	86
60	Progressive hearing loss, hypoplasia of the cochlea and widened vestibular aqueducts are very common features in Pendredâ€™s syndrome. International Journal of Pediatric Otorhinolaryngology, 1998, 45, 113-123.	1.0	85
61	The WFS1 gene, responsible for low frequency sensorineural hearing loss and Wolfram syndrome, is expressed in a variety of inner ear cells. Histochemistry and Cell Biology, 2003, 119, 247-256.	1.7	85
62	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.	2.8	85
63	Association between variations in CAT and noise-induced hearing loss in two independent noise-exposed populations. Human Molecular Genetics, 2007, 16, 1872-1883.	2.9	85
64	Hearing Disability Measured by the Speech, Spatial, and Qualities of Hearing Scale in Clinically Normal-Hearing and Hearing-Impaired Middle-Aged Persons, and Disability Screening by Means of a Reduced SSQ (the SSQ5). Ear and Hearing, 2012, 33, 615-616.	2.1	85
65	A Mutation in HOXA2 Is Responsible for Autosomal-Recessive Microtia in an Iranian Family. American Journal of Human Genetics, 2008, 82, 982-991.	6.2	84
66	Genome-wide association analysis demonstrates the highly polygenic character of age-related hearing impairment. European Journal of Human Genetics, 2015, 23, 110-115.	2.8	84
67	Determination of the carrier frequency of the common GJB2 (connexin-26) 35delG mutation in the Belgian population using an easy and reliable screening method. Human Mutation, 1999, 14, 263-266.	2.5	83
68	Whole-exome characterization of pancreatic neuroendocrine tumor cell lines BON-1 and QGP-1. Journal of Molecular Endocrinology, 2015, 54, 137-147.	2.5	83
69	Mutations in the WFS1 gene that cause low-frequency sensorineural hearing loss are small non-inactivating mutations. Human Genetics, 2002, 110, 389-394.	3.8	81
70	Hearing impairment and neurological dysfunction associated with a mutation in the mitochondrial tRNASer(UCN) gene. European Journal of Human Genetics, 1999, 7, 45-51.	2.8	80
71	Age-related hearing impairment (ARHI): environmental risk factors and genetic prospects. Experimental Gerontology, 2003, 38, 353-359.	2.8	80
72	Branchio-oto-renal syndrome (BOR): novel mutations in theEYA1gene, and a review of the mutational genetics of BOR. Human Mutation, 2008, 29, 537-544.	2.5	79

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73	Variations in HSP70 genes associated with noise-induced hearing loss in two independent populations. European Journal of Human Genetics, 2009, 17, 329-335.	2.8	78
74	Punching Holes in Cellular Membranes: Biology and Evolution of Gasdermins. Trends in Cell Biology, 2021, 31, 500-513.	7.9	78
75	DNA Diagnostics of Hereditary Hearing Loss: A Targeted Resequencing Approach Combined with a Mutation Classification System. Human Mutation, 2016, 37, 812-819.	2.5	76
76	Maternally inherited hearing impairment. Clinical Genetics, 2000, 57, 409-414.	2.0	75
77	Mutation of COL11A2 causes autosomal recessive non-syndromic hearing loss at the DFNB53 locus. Journal of Medical Genetics, 2005, 42, e61-e61.	3.2	75
78	The coding polymorphism T263I in TGF-Î²1 is associated with otosclerosis in two independent populations. Human Molecular Genetics, 2007, 16, 2021-2030.	2.9	75
79	The etiology of otosclerosis: A combination of genes and environment. Laryngoscope, 2010, 120, 1195-1202.	2.0	75
80	A novel DFNB1 deletion allele supports the existence of a distant cisâ€regulatory region that controls GJB2 and GJB6 expression. Clinical Genetics, 2010, 78, 267-274.	2.0	75
81	The clinical spectrum of mutations in L1, a neuronal cell adhesion molecule. , 1996, 64, 73-77.		74
82	The Genetic Landscape of Malignant Pleural Mesothelioma: Results from Massively Parallel Sequencing. Journal of Thoracic Oncology, 2016, 11, 1615-1626.	1.1	74
83	DFNA8/12 caused by TECTA mutations is the most identified subtype of nonsyndromic autosomal dominant hearing loss. Human Mutation, 2011, 32, 825-834.	2.5	73
84	GJB2: The spectrum of deafness-causing allele variants and their phenotype. Human Mutation, 2004, 24, 305-311.	2.5	72
85	Linkage of otosclerosis to a third locus (OTSC3) on human chromosome 6p21.3-22.3. Journal of Medical Genetics, 2002, 39, 473-477.	3.2	71
86	Pharmacological Levels of Withaferin A (Withania somnifera) Trigger Clinically Relevant Anticancer Effects Specific to Triple Negative Breast Cancer Cells. PLoS ONE, 2014, 9, e87850.	2.5	70
87	Contribution of the N-acetyltransferase 2 polymorphism NAT2*6A to age-related hearing impairment. Journal of Medical Genetics, 2007, 44, 570-578.	3.2	69
88	Long-term acquired everolimus resistance in pancreatic neuroendocrine tumours can be overcome with novel PI3K-AKT-mTOR inhibitors. British Journal of Cancer, 2016, 114, 650-658.	6.4	69
89	Audiometric shape and presbycusis. International Journal of Audiology, 2009, 48, 222-232.	1.7	67
90	Candidate Gene Association Study for Noiseâ€induced Hearing Loss in Two Independent Noiseâ€exposed Populations. Annals of Human Genetics, 2009, 73, 215-224.	0.8	67

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91	Analysis of Gene Polymorphisms Associated with K⁺ Ion Circulation in the Inner Ear of Patients Susceptible and Resistant to Noiseâ€induced Hearing Loss. Annals of Human Genetics, 2009, 73, 411-421.	0.8	67
92	ClinGen expert clinical validity curation of 164 hearing loss geneâ€“disease pairs. Genetics in Medicine, 2019, 21, 2239-2247.	2.4	67
93	A Genome-wide Analysis Identifies Genetic Variants in the RELN Gene Associated with Otosclerosis. American Journal of Human Genetics, 2009, 84, 328-338.	6.2	66
94	Amplification and sequencing of variable regions in bacterial 23S ribosomal RNA genes with conserved primer sequences. Current Microbiology, 1993, 27, 147-151.	2.2	65
95	In vivo model of drug-induced valvular heart disease in rats: pergolide-induced valvular heart disease demonstrated with echocardiography and correlation with pathology. European Heart Journal, 2007, 28, 2156-2162.	2.2	65
96	Mutation analysis of the GJB2 (Connexin 26) gene in Egypt. Human Mutation, 2005, 26, 60-61.	2.5	63
97	A fifth locus for otosclerosis, OTSC5, maps to chromosome 3q22-24. Journal of Medical Genetics, 2004, 41, 450-453.	3.2	62
98	Pendred syndrome and DFNB4â€mutation screening of SLC26A4 by denaturing highâ€performance liquid chromatography and the identification of eleven novel mutations. American Journal of Medical Genetics, Part A, 2004, 124A, 1-9.	1.2	61
99	A sensitive and specific diagnostic test for hearing loss using a microdroplet PCRâ€based approach and next generation sequencing. American Journal of Medical Genetics, Part A, 2013, 161, 145-152.	1.2	61
100	A gene for autosomal dominant late-onset progressive non-syndromic hearing loss, DFNA10, maps to chromosome 6. Human Molecular Genetics, 1996, 5, 853-856.	2.9	60
101	Mutations in the KCNQ4 K+ channel gene, responsible for autosomal dominant hearing loss, cluster in the channel pore region. American Journal of Medical Genetics Part A, 2000, 93, 184-187.	2.4	59
102	Association of Bone Morphogenetic Proteins With Otosclerosis. Journal of Bone and Mineral Research, 2008, 23, 507-516.	2.8	58
103	Mutation analysis of TMC1 identifies four new mutations and suggests an additional deafness gene at loci DFNA36 and DFNB7/11. Clinical Genetics, 2008, 74, 223-232.	2.0	58
104	DFNA5, a Gene Involved in Hearing Loss and Cancer: A Review. Annals of Otology, Rhinology and Laryngology, 2012, 121, 197-207.	1.1	58
105	Thoracic Aortic Aneurysm in Infancy in Aneurysmsâ€“<scp>O</scp>steoarthritis Syndrome Due to a Novel <scp>SMAD</scp>3 Mutation: Further Delineation of the Phenotype. American Journal of Medical Genetics, Part A, 2013, 161, 1028-1035.	1.2	58
106	Methylation analysis of Gasdermin E shows great promise as a biomarker for colorectal cancer. Cancer Medicine, 2019, 8, 2133-2145.	2.8	58
107	Congenital non-syndromal sensorineural hearing impairment due to connexin 26 gene mutations â€” molecular and audiological findings. International Journal of Pediatric Otorhinolaryngology, 1999, 50, 3-13.	1.0	57
108	The Role of Connexins in Human Disease. Ear and Hearing, 2003, 24, 314-323.	2.1	57

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109	A Genotype-Phenotype Correlation with Gender-Effect for Hearing Impairment Caused by <i>TECTA</i> Mutations. Cellular Physiology and Biochemistry, 2004, 14, 369-376.	1.6	56
110	Withaferin A induces heme oxygenase (HO-1) expression in endothelial cells via activation of the Keap1/Nrf2 pathway. Biochemical Pharmacology, 2016, 109, 48-61.	4.4	55
111	A new locus for otosclerosis, OTSC8, maps to the pericentromeric region of chromosome 9. Human Genetics, 2008, 123, 267-272.	3.8	54
112	Genome-wide SNP-Based Linkage Scan Identifies a Locus on 8q24 for an Age-Related Hearing Impairment Trait. American Journal of Human Genetics, 2008, 83, 401-407.	6.2	54
113	<scp>GSDME</scp> and its role in cancer: From behind the scenes to the front of the stage. International Journal of Cancer, 2021, 148, 2872-2883.	5.1	54
114	A seventh locus for otosclerosis, OTSC7, maps to chromosome 6q13â€“16.1. European Journal of Human Genetics, 2007, 15, 362-368.	2.8	53
115	Single-nucleotide polymorphisms in the COL1A1 regulatory regions are associated with otosclerosis. Clinical Genetics, 2007, 71, 406-414.	2.0	53
116	Overcoming cetuximab resistance in HNSCC: The role of AURKB and DUSP proteins. Cancer Letters, 2014, 354, 365-377.	7.2	53
117	Linkage Analysis of Progressive Hearing Loss in Five Extended Families Maps the DFNA2 Gene to a 1.25-Mb Region on Chromosome 1p. Genomics, 1997, 41, 70-74.	2.9	52
118	Consanguineous nuclear families used to identify a new locus for recessive non-syndromic hearing loss on 14q. Human Molecular Genetics, 1995, 4, 1643-1648.	2.9	51
119	Mutation in the zonadhesin-like domain of Î±-tectorin associated with autosomal dominant non-syndromic hearing loss. European Journal of Human Genetics, 1999, 7, 255-258.	2.8	51
120	Alpha-tectorin involvement in hearing disabilities: one gene - two phenotypes. Human Genetics, 1999, 105, 211-216.	3.8	51
121	Nonsyndromic Hearing Loss. Ear and Hearing, 2003, 24, 275-288.	2.1	51
122	Mice lacking Dfna5 show a diverging number of cochlear fourth row outer hair cells. Neurobiology of Disease, 2005, 19, 386-399.	4.4	51
123	A comprehensive catalogue of the coding and non-coding transcripts of the human inner ear. Hearing Research, 2016, 333, 266-274.	2.0	51
124	X-linked hydrocephalus and MASA syndrome present in one family are due to a single missense mutation in exon 28 of the L1CAM gene. Human Molecular Genetics, 1994, 3, 2255-2256.	2.9	50
125	New gene for autosomal recessive non-syndromic hearing loss maps to either chromosome 3q or 19p. American Journal of Medical Genetics Part A, 1997, 71, 467-471.	2.4	50
126	DFNA5: hearing impairment exon instead of hearing impairment gene?. Journal of Medical Genetics, 2004, 41, 401-406.	3.2	50

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127	Cx26 partial loss causes accelerated presbycusis by redox imbalance and dysregulation of Nfr2 pathway. Redox Biology, 2018, 19, 301-317.	9.0	50
128	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. BMC Medical Genomics, 2012, 5, 17.	1.5	49
129	An autosomal recessive nonsyndromic form of sensorineural hearing loss maps to 3p-DFNB6.. Genome Research, 1995, 5, 305-308.	5.5	48
130	A mutational hot spot in theKCNQ4 gene responsible for autosomal dominant hearing impairment. Human Mutation, 2002, 20, 15-19.	2.5	48
131	A locus-specific mutation database for the neural cell adhesion molecule L1CAM (Xq28). Human Mutation, 1996, 8, 391-391.	2.5	47
132	The M34T Allele Variant of Connexin 26. Genetic Testing and Molecular Biomarkers, 2000, 4, 335-344.	1.7	47
133	Longitudinal and Cross-Sectional Phenotype Analysis in a New, Large Dutch DFNA2/KCNQ4 Family. Annals of Otology, Rhinology and Laryngology, 2002, 111, 267-274.	1.1	47
134	Otosclerosis: a genetically heterogeneous disease involving at least three different genes. Bone, 2002, 30, 624-630.	2.9	47
135	Deafness Genes and Their Diagnostic Applications. Audiology and Neuro-Otology, 2004, 9, 2-22.	1.3	47
136	Mutation in the COCH gene is associated with superior semicircular canal dehiscence. American Journal of Medical Genetics, Part A, 2009, 149A, 280-285.	1.2	47
137	The deafness gene DFNA5 induces programmed cell death through mitochondria and MAPK-related pathways. Frontiers in Cellular Neuroscience, 2015, 9, 231.	3.7	47
138	Mutations in Splicing Factor Genes Are a Major Cause of Autosomal Dominant Retinitis Pigmentosa in Belgian Families. PLoS ONE, 2017, 12, e0170038.	2.5	47
139	Branchio-Oto-Renal Syndrome: Identification of Novel Mutations, Molecular Characterization, Mutation Distribution, and Prospects for Genetic Testing. Genetic Testing and Molecular Biomarkers, 1997, 1, 243-251.	1.7	46
140	Phenotypic variability of patients homozygous for the GJB2 mutation 35delG cannot be explained by the influence of one major modifier gene. European Journal of Human Genetics, 2009, 17, 517-524.	2.8	46
141	A Frame-Shift Mutation in CAV1 Is Associated with a Severe Neonatal Progeroid and Lipodystrophy Syndrome. PLoS ONE, 2015, 10, e0131797.	2.5	46
142	A Novel Locus for Autosomal Dominant Nonsyndromic Hearing Loss, DFNA13, Maps to Chromosome 6p. American Journal of Human Genetics, 1997, 61, 924-927.	6.2	45
143	Localization of a novel gene for nonsyndromic hearing loss (DFNB17) to chromosome region 7q31. American Journal of Medical Genetics Part A, 1998, 78, 107-113.	2.4	45
144	The ABCA4 2588G>C Stargardt mutation: single origin and increasing frequency from South-West to North-East Europe. European Journal of Human Genetics, 2002, 10, 197-203.	2.8	45

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145	The predictive value of primary tumor location in patients with metastatic colorectal cancer: A systematic review. Critical Reviews in Oncology/Hematology, 2018, 121, 1-10.	4.4	45
146	Molecular Characterization of WFS1 in Patients with Wolfram Syndrome. Journal of Molecular Diagnostics, 2003, 5, 88-95.	2.8	44
147	Whole-Genome Saliva and Blood DNA Methylation Profiling in Individuals with a Respiratory Allergy. PLoS ONE, 2016, 11, e0151109.	2.5	44
148	Identification of three novelTECTA mutations in Iranian families with autosomal recessive nonsyndromic hearing impairment at the DFNB21 locus. American Journal of Medical Genetics, Part A, 2007, 143A, 1623-1629.	1.2	43
149	A novel TECTA mutation confirms the recognizable phenotype among autosomal recessive hearing impairment families. International Journal of Pediatric Otorhinolaryngology, 2008, 72, 249-255.	1.0	43
150	A common ancestor for COCH related cochleovestibular (DFNA9) patients in Belgium and The Netherlands bearing the P51S mutation. Journal of Medical Genetics, 2001, 38, 61-65.	3.2	43
151	Speech Recognition Scores Related to Age and Degree of Hearing Impairment in DFNA2/KCNQ4 and DFNA9/COCH. JAMA Otolaryngology, 2001, 127, 1045.	1.2	42
152	Ca ²⁺ -binding protein 2 inhibits Ca ²⁺ -channel inactivation in mouse inner hair cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1717-E1726.	7.1	42
153	Genetics of Otosclerosis. Otology and Neurotology, 2009, 30, 1021-1032.	1.3	41
154	High Frequency of the p.R34X Mutation in the TMC1 Gene Associated with Nonsyndromic Hearing Loss Is Due to Founder Effects. Genetic Testing and Molecular Biomarkers, 2010, 14, 307-311.	0.7	41
155	Effect of Primary Tumor Location on Second- or Later-line Treatment Outcomes in Patients With RAS Wild-type Metastatic Colorectal Cancer and All Treatment Lines in Patients With RAS Mutations in Four Randomized Panitumumab Studies. Clinical Colorectal Cancer, 2018, 17, 170-178.e3.	2.3	41
156	Autosomal Recessive Stickler Syndrome in Two Families Is Caused by Mutations in theCOL9A1Gene. , 2011, 52, 4774.		40
157	Identification of Enteropathogenic Campylobacter Species by Oligonucleotide Probes and Polymerase Chain Reaction Based on 16S rRNA Genes. Systematic and Applied Microbiology, 1993, 16, 30-36.	2.8	39
158	A Gene for Fluctuating, Progressive Autosomal Dominant Nonsyndromic Hearing Loss, DFNA16, Maps to Chromosome 2q23-24.3. American Journal of Human Genetics, 1999, 65, 141-150.	6.2	39
159	Mutation and Methylation Analysis of Circulating Tumor DNA Can Be Used for Follow-up of Metastatic Colorectal Cancer Patients. Clinical Colorectal Cancer, 2018, 17, e369-e379.	2.3	39
160	Structure of 16S and 23S Ribosomal RNA Genes in Campylobacter Species: Phylogenetic Analysis of the Genus Campylobacter and Presence of Internal Transcribed Spacers. Systematic and Applied Microbiology, 1993, 16, 361-368.	2.8	38
161	Hereditary Otovestibular Dysfunction and M??ni??re's Disease in a Large Belgian Family Is Caused by a Missense Mutation in the COCH Gene. Otology and Neurotology, 2001, 22, 874-881.	1.3	38
162	A splice-site mutation and overexpression of MYO6 cause a similar phenotype in two families with autosomal dominant hearing loss. European Journal of Human Genetics, 2008, 16, 593-602.	2.8	38

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