Guy Van Camp

List of Publications by Year
in descending order

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374 papers	20,070 citations	11235 73 h-index	21239 119 g-index
382 all docs	382 docs citations	382 times ranked	16331 citing authors

#	Article	IF	Citations
1	A wide range of protective and predisposing variants in aggrecan influence the susceptibility for otosclerosis. Human Genetics, 2022, 141, 951-963.	1.8	6
2	Genetics of otosclerosis: finally catching up with other complex traits?. Human Genetics, 2022, 141, 939-950.	1.8	6
3	Longitudinal Copy-Number Alteration Analysis in Plasma Cell-Free DNA of Neuroendocrine Neoplasms is a Novel Specific Biomarker for Diagnosis, Prognosis, and Follow-up. Clinical Cancer Research, 2022, 28, 338-349.	3.2	16
4	Genomeâ€wide DNA methylation profiling and identification of potential panâ€cancer and tumorâ€specific biomarkers. Molecular Oncology, 2022, 16, 2432-2447.	2.1	9
5	<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.	2.3	54
6	Copy number alterations in plasma cell-free DNA from metastatic gastroenteropancreatic neuroendocrine neoplasms.. Journal of Clinical Oncology, 2021, 39, 372-372.	0.8	0
7	Predictive Sensitivity and Concordance of Machine-learning Tools for Diagnosing DFNA9 in a Large Series of p.Pro51Ser Variant Carriers in the COCH-gene. Otology and Neurotology, 2021, Publish Ahead of Print, 671-677.	0.7	0
8	On the pathophysiology of DFNA9: Effect of pathogenic variants in the COCH gene on inner ear functioning in human and transgenic mice. Hearing Research, 2021, 401, 108162.	0.9	17
9	Resequencing of candidate genes for Keratoconus reveals a role for Ehlersâ€“Danlos Syndrome genes. European Journal of Human Genetics, 2021, 29, 1745-1755.	1.4	8
10	Echinacea purpurea (L.) Moench treatment of monocytes promotes tonic interferon signaling, increased innate immunity gene expression and DNA repeat hypermethylated silencing of endogenous retroviral sequences. BMC Complementary Medicine and Therapies, 2021, 21, 141.	1.2	7
11	Punching Holes in Cellular Membranes: Biology and Evolution of Gasdermins. Trends in Cell Biology, 2021, 31, 500-513.	3.6	78
12	Disease-specific ACMG/AMP guidelines improve sequence variant interpretation for hearing loss. Genetics in Medicine, 2021, 23, 2208-2212.	1.1	18
13	Hearing Function: Identification of New Candidate Genes Further Explaining the Complexity of This Sensory Ability. Genes, 2021, 12, 1228.	1.0	1
14	Genotype-phenotype Correlation Study in a Large Series of Patients Carrying the p.Pro51Ser (p.P51S) Variant in COCH (DFNA9): Part Iâ€”A Cross-sectional Study of Hearing Function in 111 Carriers. Ear and Hearing, 2021, 42, 1508-1524.	1.0	10
15	Genotype-Phenotype Correlation Study in a Large Series of Patients Carrying the p.Pro51Ser (p.P51S) Variant in COCH (DFNA9) Part II: A Prospective Cross-Sectional Study of the Vestibular Phenotype in 111 Carriers. Ear and Hearing, 2021, 42, 1525-1543.	1.0	12
16	Transduction Efficiency and Immunogenicity of Viral Vectors for Cochlear Gene Therapy: A Systematic Review of Preclinical Animal Studies. Frontiers in Cellular Neuroscience, 2021, 15, 728610.	1.8	5
17	DNA Methylation as a Diagnostic Biomarker for Malignant Mesothelioma: A Systematic Review and Meta-Analysis. Journal of Thoracic Oncology, 2021, 16, 1461-1478.	0.5	8
18	Characteristic ERK1/2 signaling dynamics distinguishes necroptosis from apoptosis. IScience, 2021, 24, 103074.	1.9	9

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19	Marine Seagrass Extract of Thalassia testudinum Suppresses Colorectal Tumor Growth, Motility and Angiogenesis by Autophagic Stress and Immunogenic Cell Death Pathways. Marine Drugs, 2021, 19, 52.	2.2	13
20	Cochlin Deficiency Protects Aged Mice from Noise-Induced Hearing Loss. International Journal of Molecular Sciences, 2021, 22, 11549.	1.8	5
21	Attitudes of Potential Participants Towards Potential Gene Therapy Trials in Autosomal Dominant Progressive Sensorineural Hearing Loss. Otology and Neurotology, 2021, 42, 384-389.	0.7	3
22	Antiproliferative, Antiangiogenic, and Antimetastatic Therapy Response by Mangiferin in a Syngeneic Immunocompetent Colorectal Cancer Mouse Model Involves Changes in Mitochondrial Energy Metabolism. Frontiers in Pharmacology, 2021, 12, 670167.	1.6	9
23	Etiological Work-up in Referrals From Neonatal Hearing Screening: 20 Years of Experience. Otology and Neurotology, 2020, 41, 1240-1248.	0.7	8
24	468P PANIB 20139173: Randomized, multicentre phase II trial comparing fluorouracil, leucovorin and oxaliplatin (FOLFOX) plus panitumumab versus FOLFOX plus bevacizumab in patients with previously untreated, RAS wild-type (WT) metastatic colorectal cancer (mCRC). Annals of Oncology, 2020, 31, S440.	0.6	1
25	PDX1 DNA Methylation Distinguishes Two Subtypes of Pancreatic Neuroendocrine Neoplasms with a Different Prognosis. Cancers, 2020, 12, 1461.	1.7	19
26	Autosomal Dominantly Inherited GREB1L Variants in Individuals with Profound Sensorineural Hearing Impairment. Genes, 2020, 11, 687.	1.0	23
27	Aging of Preleukemic Thymocytes Drives CpG Island Hypermethylation in T-cell Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 274-289.	2.6	21
28	Hotspot DAXX, PTCH2 and CYFIP2 mutations in pancreatic neuroendocrine neoplasms. Endocrine-Related Cancer, 2019, 26, 1-12.	1.6	24
29	Clinical applications of (epi)genetics in gastroenteropancreatic neuroendocrine neoplasms: Moving towards liquid biopsies. Reviews in Endocrine and Metabolic Disorders, 2019, 20, 333-351.	2.6	10
30	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. Scientific Reports, 2019, 9, 15192.	1.6	32
31	Determination of the Potential Tumor-Suppressive Effects of Gsdme in a Chemically Induced and in a Genetically Modified Intestinal Cancer Mouse Model. Cancers, 2019, 11, 1214.	1.7	32
32	Methylation analysis of Gasdermin E shows great promise as a biomarker for colorectal cancer. Cancer Medicine, 2019, 8, 2133-2145.	1.3	58
33	ClinGen expert clinical validity curation of 164 hearing loss geneâ€“disease pairs. Genetics in Medicine, 2019, 21, 2239-2247.	1.1	67
34	A systematic review of hearing and vestibular function in carriers of the Pro51Ser mutation in the COCH gene. European Archives of Oto-Rhino-Laryngology, 2019, 276, 1251-1262.	0.8	18
35	Insufficient evidence for a role of SERPINF1 in otosclerosis. Molecular Genetics and Genomics, 2019, 294, 1001-1006.	1.0	11
36	The Gasdermin E gene Potential as a Pan-Cancer Biomarker, While Discriminating between Different Tumor Types. Cancers, 2019, 11, 1810.	1.7	24

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37	Variants affecting diverse domains of MEPE are associated with two distinct bone disorders, a craniofacial bone defect and otosclerosis. Genetics in Medicine, 2019, 21, 1199-1208.	1.1	17
38	Resistance to targeted treatment of gastroenteropancreatic neuroendocrine tumors. Endocrine-Related Cancer, 2019, 26, R109-R130.	1.6	24
39	Bi-allelic inactivating variants in the COCH gene cause autosomal recessive prelingual hearing impairment. European Journal of Human Genetics, 2018, 26, 587-591.	1.4	22
40	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.	1.0	39
41	Large-scale analysis of DFNA5 methylation reveals its potential as biomarker for breast cancer. Clinical Epigenetics, 2018, 10, 51.	1.8	86
42	GLI2 promoter hypermethylation in saliva of children with a respiratory allergy. Clinical Epigenetics, 2018, 10, 50.	1.8	19
43	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.	1.0	41
44	A new perspective on the genetics of keratoconus: why have we not been more successful?. Ophthalmic Genetics, 2018, 39, 158-174.	0.5	33
45	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.	2.0	45
46	The prognostic value of KRAS, NRAS, BRAF and DNA mismatch repair (MMR) status in left- and right-sided metastatic colorectal cancer (mCRC): A Belgian population-based study. Annals of Oncology, 2018, 29, viii196.	0.6	0
47	Detection of mutations and copy number alterations in circulating DNA from pancreatic neuroendocrine tumor patients. Annals of Oncology, 2018, 29, viii477.	0.6	0
48	Cell-Free DNA From Metastatic Pancreatic Neuroendocrine Tumor Patients Contains Tumor-Specific Mutations and Copy Number Variations. Frontiers in Oncology, 2018, 8, 467.	1.3	25
49	Comparing survival in left-sided and right-sided colorectal carcinoma: A Belgian population-based study. Annals of Oncology, 2018, 29, v98.	0.6	1
50	Nano-targeted induction of dual ferroptotic mechanisms eradicates high-risk neuroblastoma. Journal of Clinical Investigation, 2018, 128, 3341-3355.	3.9	406
51	Molecular analysis of an asbestos-exposed Belgian family with a high prevalence of mesothelioma. Familial Cancer, 2018, 17, 569-576.	0.9	3
52	Tumor-specific genetic variants can be detected in circulating cell-free DNA of malignant pleural mesothelioma patients. Lung Cancer, 2018, 124, 19-22.	0.9	9
53	Cx26 partial loss causes accelerated presbycusis by redox imbalance and dysregulation of Nfr2 pathway. Redox Biology, 2018, 19, 301-317.	3.9	50
54	Role of Targeted Next Generation Sequencing in the Etiological Work-Up of Congenitally Deaf Children. Otology and Neurotology, 2018, 39, 732-738.	0.7	10

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55	Congenital hearing loss. Nature Reviews Disease Primers, 2017, 3, 16094.	18.1	328
56	Deep sequencing of the TP53 gene reveals a potential risk allele for nonâ€“small cell lung cancer and supports the negative prognostic value of TP53 variants. Tumor Biology, 2017, 39, 101042831769432.	0.8	22
57	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.	3.3	42
58	Interaction between prenatal pesticide exposure and a common polymorphism in the PON1 gene on DNA methylation in genes associated with cardio-metabolic disease riskâ€”an exploratoryÂstudy. Clinical Epigenetics, 2017, 9, 35.	1.8	29
59	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.	0.6	174
60	Molecular diagnostics for hereditary hearing loss in children. Expert Review of Molecular Diagnostics, 2017, 17, 751-760.	1.5	21
61	The FASâ€670 AA genotype is associated with high proviral load in peruvian HAM/TSP patients. Journal of Medical Virology, 2017, 89, 726-731.	2.5	7
62	pyAmpli: an amplicon-based variant filter pipeline for targeted resequencing data. BMC Bioinformatics, 2017, 18, 554.	1.2	7
63	A Pilot Genome-Wide Association Study Identifies Potential Metabolic Pathways Involved in Tinnitus. Frontiers in Neuroscience, 2017, 11, 71.	1.4	35
64	MDM2 SNP309 and SNP285 Act as Negative Prognostic Markers for Non-small Cell Lung Cancer Adenocarcinoma Patients. Journal of Cancer, 2017, 8, 2154-2162.	1.2	4
65	Unique autosomal recessive variant of palmoplantar keratoderma associated with hearing loss not caused by known mutations. Anais Brasileiros De Dermatologia, 2017, 92, 154-158.	0.5	1
66	Mutations in Splicing Factor Genes Are a Major Cause of Autosomal Dominant Retinitis Pigmentosa in Belgian Families. PLoS ONE, 2017, 12, e0170038.	1.1	47
67	DFNA5promoter methylation a marker for breast tumorigenesis. Oncotarget, 2017, 8, 31948-31958.	0.8	37
68	Large-scale copy number analysis reveals variations in genes not previously associated with malignant pleural mesothelioma. Oncotarget, 2017, 8, 113673-113686.	0.8	21
69	A novel missense mutation in the C2C domain of otoferlin causes profound hearing impairment in an Omani family with auditory neuropathy. Journal of King Abdulaziz University, Islamic Economics, 2016, 37, 1068-1075.	0.5	11
70	Whole-Genome Saliva and Blood DNA Methylation Profiling in Individuals with a Respiratory Allergy. PLoS ONE, 2016, 11, e0151109.	1.1	44
71	Large scale DFNA5 methylation and expression analysis in primary breast adenocarcinoma using data from the Cancer Genome Atlas. Annals of Oncology, 2016, 27, vi31.	0.6	0
72	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.	2.6	124

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73	DNA Diagnostics of Hereditary Hearing Loss: A Targeted Resequencing Approach Combined with a Mutation Classification System. Human Mutation, 2016, 37, 812-819.	1.1	76
74	Loss of function of Ywhah in mice induces deafness and cochlear outer hair cellâ€™s degeneration. Cell Death and Disease, 2016, 7, e2187-e2187.	2.7	4
75	Loss of function of Ywhah in mice induces deafness and cochlear outer hair cells' degeneration. Cell Death Discovery, 2016, 2, 16017.	2.0	8
76	Primary tumor sidedness impacts on prognosis and treatment outcome: results from three randomized studies of panitumumab plus chemotherapy versus chemotherapy or chemotherapy plus bevacizumab in 1st and 2nd line RAS/BRAF WT mCRC. Annals of Oncology, 2016, 27, vi27.	0.6	8
77	Withaferin A induces heme oxygenase (HO-1) expression in endothelial cells via activation of the Keap1/Nrf2 pathway. Biochemical Pharmacology, 2016, 109, 48-61.	2.0	55
78	The Genetic Landscape of Malignant Pleural Mesothelioma: Results from Massively Parallel Sequencing. Journal of Thoracic Oncology, 2016, 11, 1615-1626.	0.5	74
79	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.	2.9	69
80	Novel and recurrent CIB2 variants, associated with nonsyndromic deafness, do not affect calcium buffering and localization in hair cells. European Journal of Human Genetics, 2016, 24, 542-549.	1.4	28
81	A comprehensive catalogue of the coding and non-coding transcripts of the human inner ear. Hearing Research, 2016, 333, 266-274.	0.9	51
82	Role of DFNA5 in hearing loss and cancer – a comment on Rakusic et al. OncoTargets and Therapy, 2015, 8, 2613.	1.0	2
83	The deafness gene DFNA5 induces programmed cell death through mitochondria and MAPK-related pathways. Frontiers in Cellular Neuroscience, 2015, 9, 231.	1.8	47
84	A Frame-Shift Mutation in CAV1 Is Associated with a Severe Neonatal Progeroid and Lipodystrophy Syndrome. PLoS ONE, 2015, 10, e0131797.	1.1	46
85	Whole-exome characterization of pancreatic neuroendocrine tumor cell lines BON-1 and QGP-1. Journal of Molecular Endocrinology, 2015, 54, 137-147.	1.1	83
86	Genome-wide association analysis demonstrates the highly polygenic character of age-related hearing impairment. European Journal of Human Genetics, 2015, 23, 110-115.	1.4	84
87	Heimler Syndrome Is Caused by Hypomorphic Mutations in the Peroxisome-Biogenesis Genes PEX1 and PEX6. American Journal of Human Genetics, 2015, 97, 535-545.	2.6	103
88	Prognostic and Predictive Value of RAS Gene Mutations in Colorectal Cancer: Moving Beyond KRAS Exon 2. Drugs, 2015, 75, 1739-1756.	4.9	6
89	Next generation exome sequencing of pancreatic neuroendocrine tumor cell lines BON-1 and QGP-1 reveals different lineages. Cancer Genetics, 2015, 208, 523.	0.2	14
90	Potentiometric detection in UPLC as an easy alternative to determine cocaine in biological samples. Biomedical Chromatography, 2015, 29, 1124-1129.	0.8	8

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91	Abstract P4-01-14: Whole exome sequencing of circulating and disseminated tumour cells in patients with metastatic breast cancer. , 2015, , .		0
92	Establishment and characterization of cetuximab resistant head and neck squamous cell carcinoma cell lines: focus on the contribution of the AP-1 transcription factor. American Journal of Cancer Research, 2015, 5, 1921-38.	1.4	19
93	Pharmacological Levels of Withaferin A (Withania somnifera) Trigger Clinically Relevant Anticancer Effects Specific to Triple Negative Breast Cancer Cells. PLoS ONE, 2014, 9, e87850.	1.1	70
94	Anti-EGFR Resistance in Colorectal Cancer: Current Knowledge and Future Perspectives. Current Colorectal Cancer Reports, 2014, 10, 380-394.	1.0	1
95	Rare Variants in BMP2 and BMP4 Found in Otosclerosis Patients Reduce Smad Signaling. Otology and Neurotology, 2014, 35, 395-400.	0.7	10
96	Potentiometric sensors doped with biomolecules as a new approach to small molecule/biomolecule binding kinetics analysis. Biosensors and Bioelectronics, 2014, 54, 515-520.	5.3	13
97	A Dominant-NegativeGFI1BMutation in the Gray Platelet Syndrome. New England Journal of Medicine, 2014, 370, 245-253.	13.9	152
98	Broadening the phenotype of <scp>LRP2</scp> mutations: a new mutation in <scp>LRP2</scp> causes a predominantly ocular phenotype suggestive of Stickler syndrome. Clinical Genetics, 2014, 86, 282-286.	1.0	37
99	Concentration-Related Response Potentiometric Titrations To Study the Interaction of Small Molecules with Large Biomolecules. Analytical Chemistry, 2014, 86, 12243-12249.	3.2	11
100	Overcoming cetuximab resistance in HNSCC: The role of AURKB and DUSP proteins. Cancer Letters, 2014, 354, 365-377.	3.2	53
101	Genetic Association Analysis in a Clinically and Histologically Confirmed Otosclerosis Population Confirms Association With the TGFB1 Gene but Suggests an Association of the RELN Gene With a Clinically Indistinguishable Otosclerosis-Like Phenotype. Otology and Neurotology, 2014, 35, 1058-1064.	0.7	17
102	Focal Sclerosis of Semicircular Canals With Severe DFNA9 Hearing Impairment Caused by a P51S COCH-Mutation. Otology and Neurotology, 2014, 35, 1077-1086.	0.7	19
103	Ectopic MicroRNA-150-5p Transcription Sensitizes Glucocorticoid Therapy Response in MM1S Multiple Myeloma Cells but Fails to Overcome Hormone Therapy Resistance in MM1R Cells. PLoS ONE, 2014, 9, e113842.	1.1	38
104	Expression profiling of migrated and invaded breast cancer cells predicts early metastatic relapse and reveals KrÃ¼ppel-like factor 9 as a potential suppressor of invasive growth in breast cancer. Oncoscience, 2014, 1, 69-81.	0.9	24
105	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	0.8	22
106	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.	0.7	58
107	Genetic and clinical diagnosis in non-syndromic hearing loss. Hearing, Balance and Communication, 2013, 11, 138-145.	0.1	5
108	Animal models of organic heart valve disease. International Journal of Cardiology, 2013, 165, 398-409.	0.8	14

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109	Genome-wide analysis reveals a novel autosomal-recessive hearing loss locus DFNB80 on chromosome 2p16.1-p21. Journal of Human Genetics, 2013, 58, 98-101.	1.1	3
110	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.	0.7	61
111	Echocardiographic Integrated Backscatter for Assessing Reduction of Aortic Valve Calcifications by R-568 in a Rat Model of Chronic Kidney Disease. Ultrasound in Medicine and Biology, 2013, 39, 2075-2083.	0.7	4
112	Use of potentiometric detection in (ultra) high performance liquid chromatography and modelling with adsorption/desorption binding kinetics. Analytica Chimica Acta, 2013, 777, 25-31.	2.6	8
113	Familial Aggregation of Pure Tone Hearing Thresholds in an Aging European Population. Otology and Neurotology, 2013, 34, 838-844.	0.7	15
114	Abstract 5628: Overcoming cetuximab resistance in HNSCC: the role of AURKB and DUSP6.. , 2013, , .		0
115	A Dominant-Negative GFI1B Mutation in Gray Platelet Syndrome. Blood, 2013, 122, LBA-3-LBA-3.	0.6	1
116	The splicing mutant of the human tumor suppressor protein DFNA5 induces programmed cell death when expressed in the yeast Saccharomyces cerevisiae. Frontiers in Oncology, 2012, 2, 77.	1.3	35
117	DFNA5, a Gene Involved in Hearing Loss and Cancer: A Review. Annals of Otology, Rhinology and Laryngology, 2012, 121, 197-207.	0.6	58
118	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.	1.0	85
119	Use of Potentiometric Sensors To Study (Bio)molecular Interactions. Analytical Chemistry, 2012, 84, 4921-4927.	3.2	17
120	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. BMC Medical Genomics, 2012, 5, 17.	0.7	49
121	Analysis of inner ear potassium recycling genes as potential factors associated with tinnitus. International Journal of Occupational Medicine and Environmental Health, 2012, 25, 356-64.	0.6	24
122	A Mutation in CABP2 , Expressed in Cochlear Hair Cells, Causes Autosomal-Recessive Hearing Impairment. American Journal of Human Genetics, 2012, 91, 636-645.	2.6	96
123	Genome wide analysis in a family with sensorineural hearing loss, autism and mental retardation. Gene, 2012, 510, 102-106.	1.0	5
124	COL1A1 association and otosclerosis: A metaâ€analysis. American Journal of Medical Genetics, Part A, 2012, 158A, 1066-1070.	0.7	20
125	Occurrence of cardiovascular calcifications in normal, aging rats. Experimental Gerontology, 2012, 47, 614-619.	1.2	12
126	Possible implication of NFKB1A and NKG2D genes in susceptibility to HTLVâ€1â€associated myelopathy/tropical spastic paraparesis in Peruvian patients infected with HTLVâ€1. Journal of Medical Virology, 2012, 84, 319-326.	2.5	10

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127	Inherited mitochondrial variants are not a major cause of age-related hearing impairment in the European population. Mitochondrion, 2011, 11, 729-734.	1.6	13
128	Large scale mtDNA sequencing reveals sequence and functional conservation as major determinants of homoplasmic mtDNA variant distribution. Mitochondrion, 2011, 11, 964-972.	1.6	8
129	Apoptosis in acquired and genetic hearing impairment: The programmed death of the hair cell. Hearing Research, 2011, 281, 18-27.	0.9	128
130	Commentary on â€œOtosclerosis: Thirty-Year Follow-Up After Surgeryâ€• Annals of Otology, Rhinology and Laryngology, 2011, 120, 615-616.	0.6	0
131	A new locus for otosclerosis, OTSC10, maps to chromosome 1q41-44. Clinical Genetics, 2011, 79, 495-497.	1.0	20
132	DFNB93, a novel locus for autosomal recessive moderate-to-severe hearing impairment. Clinical Genetics, 2011, 79, 594-598.	1.0	24
133	Association of COL1A1 and TGFB1 Polymorphisms with Otosclerosis in a Tunisian Population. Annals of Human Genetics, 2011, 75, 598-604.	0.3	24
134	A genome-wide analysis of population structure in the Finnish Saami with implications for genetic association studies. European Journal of Human Genetics, 2011, 19, 347-352.	1.4	19
135	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.	1.4	99
136	Functional Null Mutations of MSRB3 Encoding Methionine Sulfoxide Reductase Are Associated with Human Deafness DFNB74. American Journal of Human Genetics, 2011, 88, 19-29.	2.6	107
137	Phenotype of the first otosclerosis family linked to OTSC10. Laryngoscope, 2011, 121, 838-845.	1.1	7
138	Two Iranian families with a novel mutation in GJB2 causing autosomal dominant nonsyndromic hearing loss. American Journal of Medical Genetics, Part A, 2011, 155, 1202-1211.	0.7	9
139	A 1â€‰bp deletion in the dual reading frame deafness gene LRTOMT causes a frameshift from the first into the second reading frame. American Journal of Medical Genetics, Part A, 2011, 155, 2021-2023.	0.7	9
140	DFNA8/12 caused by TECTA mutations is the most identified subtype of nonsyndromic autosomal dominant hearing loss. Human Mutation, 2011, 32, 825-834.	1.1	73
141	Autosomal Recessive Stickler Syndrome in Two Families Is Caused by Mutations in theCOL9A1Gene. , 2011, 52, 4774.		40
142	Genetic variants in the RELN gene are associated with otosclerosis in multiple European populations. Human Genetics, 2010, 127, 155-162.	1.8	28
143	Multiple enhancers located in a 1-Mb region upstream of POU3F4 promote expression during inner ear development and may be required for hearing. Human Genetics, 2010, 128, 411-419.	1.8	35
144	Evaluation of host genetic and viral factors as surrogate markers for HTLVâ€1â€associated myelopathy/tropical spastic paraparesis in Peruvian HTLVâ€1â€infected patients. Journal of Medical Virology, 2010, 82, 460-466.	2.5	16

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145	The etiology of otosclerosis: A combination of genes and environment. Laryngoscope, 2010, 120, 1195-1202.	1.1	75
146	Genetic variants in RELN are associated with otosclerosis in a nonâ€European population from Tunisia. Annals of Human Genetics, 2010, 74, 399-405.	0.3	18
147	A genome-wide association study for age-related hearing impairment in the Saami. European Journal of Human Genetics, 2010, 18, 685-693.	1.4	88
148	Involvement of T-cell receptor-Î² alterations in the development of otosclerosis linked to OTSC2. Genes and Immunity, 2010, 11, 246-253.	2.2	14
149	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.	1.0	75
150	Genotype-Phenotype Correlation for DFNA22: Characterization of Non-Syndromic, Autosomal Dominant, Progressive Sensorineural Hearing Loss due to <i>MYO6</i> Mutations. Audiology and Neuro-Otology, 2010, 15, 211-220.	0.6	16
151	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.	0.3	41
152	Heritability of audiometric shape parameters and familial aggregation of presbycusis in an elderly Flemish population. Hearing Research, 2010, 265, 1-10.	0.9	18
153	Role of killer cell immunoglobulin-like receptor gene content and human leukocyte antigenâ€“C group in susceptibility to human T-lymphotropic virus 1â€“associated myelopathy/tropical spastic paraparesis in Peru. Human Immunology, 2010, 71, 804-808.	1.2	4
154	Genome-wide SNP analysis reveals no gain in power for association studies of common variants in the Finnish Saami. European Journal of Human Genetics, 2010, 18, 569-574.	1.4	3
155	A large deletion in GPR98 causes type IIC Usher syndrome in male and female members of an Iranian family. Journal of Medical Genetics, 2009, 46, 272-276.	1.5	36
156	Amino acid 572 in TMC1: hot spot or critical functional residue for dominant mutations causing hearing impairment. Journal of Human Genetics, 2009, 54, 188-190.	1.1	15
157	Cyproheptadine prevents pergolide-induced valvulopathy in rats: an echocardiographic and histopathological study. American Journal of Physiology - Heart and Circulatory Physiology, 2009, 296, H1940-H1948.	1.5	32
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