Florence Demenais

List of Publications by Year in descending order

192 papers	12,383 citations	36271 51 h-index	28275 105 g-index
202 all docs	202 docs citations	202 times ranked	15163 citing authors

#	Article	IF	Citations
1	Genome-Wide Association Study of Fluorescent Oxidation Products Accounting for Tobacco Smoking Status in Adults from the French EGEA Study. Antioxidants, 2022, 11, 802.	2.2	3
2	Associations between specific IgE sensitization to 26 respiratory allergen molecules and HLA class II alleles in the EGEA cohort. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 2575-2586.	2.7	9
3	Identification of OCA2 as a novel locus for the coâ€morbidity of asthmaâ€plusâ€eczema. Clinical and Experimental Allergy, 2021, , .	1.4	3
4	PID1 is associated to a respiratory endotype related to occupational exposures to irritants. Free Radical Biology and Medicine, 2021, 172, 503-507.	1.3	3
5	Overlapping genetic architecture between Parkinson disease and melanoma. Acta Neuropathologica, 2020, 139, 347-364.	3.9	23
6	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	5.8	53
7	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
8	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	9.4	138
9	Genomeâ€wide interaction study of earlyâ€life smoking exposure on timeâ€toâ€asthma onset in childhood. Clinical and Experimental Allergy, 2019, 49, 1342-1351.	1.4	9
10	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. Journal of the American Academy of Dermatology, 2019, 81, 386-394.	0.6	17
11	Associations of pigmentary and naevus phenotype with melanoma risk in two populations with comparable ancestry but contrasting levels of ambient sun exposure. Journal of the European Academy of Dermatology and Venereology, 2019, 33, 1874-1885.	1.3	10
12	MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. The Lancet Child and Adolescent Health, 2019, 3, 332-342.	2.7	16
13	Interactive effect between ATPase-related genes and early-life tobacco smoke exposure on bronchial hyper-responsiveness detected in asthma-ascertained families. Thorax, 2019, 74, 254-260.	2.7	4
14	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
15	A novel role for ciliary function in atopy: ADGRV1 and DNAH5 interactions. Journal of Allergy and Clinical Immunology, 2018, 141, 1659-1667.e11.	1.5	9
16	The <scp>COL</scp>5A3 and <scp>MMP</scp>9 genes interact in eczema susceptibility. Clinical and Experimental Allergy, 2018, 48, 297-305.	1.4	9
17	Cell-typeâ€“specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	2.4	67
18	Integration of the human exposome with the human genome to advance medicine. Biochimie, 2018, 152, 155-158.	1.3	36

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19	Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure. Nature Communications, 2018, 9, 1684.	5.8	80
20	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. Journal of Investigative Dermatology, 2018, 138, 2617-2624.	0.3	52
21	Influence of gene-by-sex interaction on time-to-asthma onset: a large-scale genome-wide meta-analysis. , 2018, , .		1
22	Genome-wide interaction study of environmental tobacco smoke exposure on time-to-asthma onset in childhood. , 2018, , .		1
23	New susceptibility loci for cutaneous melanoma risk and progression revealed using a porcine model. Oncotarget, 2018, 9, 27682-27697.	0.8	11
24	Abstract 228: Association analysis across different populations identifies 26 new cutaneous melanoma risk loci. , 2018, , .		0
25	Abstract 234: Understanding melanoma susceptibility through GWAS of risk phenotypes. , 2018, , .		0
26	DNA methylation and serum total immunoglobulin E (IgE) levels: a methylome-wide association study in adults with asthma. , 2018, , .		0
27	SigMod: an exact and efficient method to identify a strongly interconnected disease-associated module in a gene network. Bioinformatics, 2017, 33, 1536-1544.	1.8	29
28	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
29	Network-assisted analysis of GWAS data identifies a functionally-relevant gene module for childhood-onset asthma. Scientific Reports, 2017, 7, 938.	1.6	14
30	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
31	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.3	18
32	Gain of power of the general regression model compared to Cochran-Armitage Trend tests: simulation study and application to bipolar disorder. BMC Genetics, 2017, 18, 24.	2.7	8
33	Melanoma Expression Genes Identified through Genome-Wide Association Study ofÂBreslow Tumor Thickness. Journal of Investigative Dermatology, 2017, 137, 253-257.	0.3	2
34	Vitamin D levels and susceptibility to asthma, elevated immunoglobulin E levels, and atopic dermatitis: A Mendelian randomization study. PLoS Medicine, 2017, 14, e1002294.	3.9	78
35	Adult onset asthma and interaction between genes and active tobacco smoking: The GABRIEL consortium. PLoS ONE, 2017, 12, e0172716.	1.1	25
36	Genes Interacting with Occupational Exposures to Low Molecular Weight Agents and Irritants on Adult-Onset Asthma in Three European Studies. Environmental Health Perspectives, 2017, 125, 207-214.	2.8	23

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37	DNA methylation and lung function: an epigenome-wide association study. , 2017, , .		0
38	Genes Involved in Interleukin-1 Receptor Type II Activities Are Associated With Asthmatic Phenotypes. Allergy, Asthma and Immunology Research, 2016, 8, 466.	1.1	5
39	DNA methylation within melatonin receptor 1A (MTNR1A) mediates paternally transmitted genetic variant effect on asthma plus rhinitis. Journal of Allergy and Clinical Immunology, 2016, 138, 748-753.	1.5	25
40	Rare variants analysis of cutaneous malignant melanoma genes in Parkinson's disease. Neurobiology of Aging, 2016, 48, 222.e1-222.e7.	1.5	19
41	A comprehensive genomeâ€wide analysis of melanoma Breslow thickness identifies interaction between CDC42 and SCIN genetic variants. International Journal of Cancer, 2016, 139, 2012-2020.	2.3	8
42	Identification of a new locus at 16q12 associated with time to asthma onset. Journal of Allergy and Clinical Immunology, 2016, 138, 1071-1080.	1.5	25
43	Interaction between the DNAH9 gene and early smoke exposure in bronchial hyperresponsiveness. European Respiratory Journal, 2016, 47, 1072-1081.	3.1	17
44	Unsupervised text mining for assessing and augmenting GWAS results. Journal of Biomedical Informatics, 2016, 60, 252-259.	2.5	15
45	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofAMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.3	13
46	Association of Forced Vital Capacity with the Developmental Gene NCOR2. PLoS ONE, 2016, 11, e0147388.	1.1	17
47	Influence of gene-by-early environmental tobacco smoke exposure interactions on time-to-asthma onset. , 2016, , .		0
48	Integrated pathway and epistasis analysis reveals interactive effect of genetic variants at <scp>TERF1</scp> and <scp>AFAP1L2</scp> loci on melanoma risk. International Journal of Cancer, 2015, 137, 1901-1909.	2.3	16
49	Meta-analysis identifies seven susceptibility loci involved in the atopic march. Nature Communications, 2015, 6, 8804.	5.8	148
50	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
51	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. International Journal of Cancer, 2015, 136, 1351-1360.	2.3	30
52	A common variant in <scp>RAB</scp>27A gene is associated with fractional exhaled nitric oxide levels in adults. Clinical and Experimental Allergy, 2015, 45, 797-806.	1.4	11
53	Human leukocyte antigen class II variants and adult-onset asthma: does occupational allergen exposure play a role?. European Respiratory Journal, 2014, 44, 1234-1242.	3.1	10
54	Association of Genetic Variants in CDK6 and XRCC1 with the Risk of Dysplastic Nevi in Melanoma-Prone Families. Journal of Investigative Dermatology, 2014, 134, 481-487.	0.3	10

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55	Genetic heterogeneity of asthma phenotypes identified by a clustering approach. European Respiratory Journal, 2014, 43, 439-452.	3.1	57
56	George Bonney (1947â€“2013) Remembered. Genetic Epidemiology, 2014, 38, 95-96.	0.6	0
57	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109
58	Fraction of exhaled nitric oxide values in childhood are associated with 17q11.2-q12 and 17q12-q21 variants. Journal of Allergy and Clinical Immunology, 2014, 134, 46-55.	1.5	33
59	A Common 16p11.2 Inversion Underlies the Joint Susceptibility to Asthma and Obesity. American Journal of Human Genetics, 2014, 94, 361-372.	2.6	66
60	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	9.4	283
61	<scp>KIT</scp> and melanoma predisposition in pigs: sequence variants and association analysis. Animal Genetics, 2014, 45, 445-448.	0.6	8
62	The nuclear factor I/A (NFIA) gene is associated with the asthma plus rhinitis phenotype. Journal of Allergy and Clinical Immunology, 2014, 134, 576-582.e1.	1.5	17
63	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. Journal of Allergy and Clinical Immunology, 2014, 133, 885-888.	1.5	47
64	Abstract 941: Exome sequencing identifiedPOT1, a telomere shelterin gene, as a major susceptibility gene for familial cutaneous malignant melanoma. , 2014, , .		0
65	Selection of genes for gene-environment interaction studies: a candidate pathway-based strategy using asthma as an example. Environmental Health, 2013, 12, 56.	1.7	11
66	Genital and anorectal mucosal melanoma is associated with cutaneous melanoma in patients and in families. British Journal of Dermatology, 2013, 169, 594-599.	1.4	15
67	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	9.4	111
68	Genomeâ€wide association study of body mass index in 23Â000 individuals with and without asthma. Clinical and Experimental Allergy, 2013, 43, 463-474.	1.4	68
69	Using eQTL weights to improve power for genome-wide association studies: a genetic study of childhood asthma. Frontiers in Genetics, 2013, 4, 103.	1.1	68
70	Gene-environment interactions in asthma and allergic diseases: Challenges and perspectives. Journal of Allergy and Clinical Immunology, 2012, 130, 1229-1240.	1.5	88
71	39 The Search for Rare Variants That Contribute to Cancer Susceptibility. European Journal of Cancer, 2012, 48, S9.	1.3	0
72	Comparative Power of Familyâ€Based Association Strategies to Detect Diseaseâ€Causing Variants Under Twoâ€Locus Models. Genetic Epidemiology, 2012, 36, 848-855.	0.6	4

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73	Transient receptor potential genes, smoking, occupational exposures and cough in adults. Respiratory Research, 2012, 13, 26.	1.4	84
74	Familial melanoma: Clinical factors associated with germline CDKN2A mutations according to the number of patients affected by melanoma in a family. Journal of the American Academy of Dermatology, 2012, 67, 1257-1264.e2.	0.6	26
75	Genome-wide association study of lung function decline in adults with and without asthma. Journal of Allergy and Clinical Immunology, 2012, 129, 1218-1228.	1.5	94
76	The ANO3/MUC15 locus is associated with eczema in families ascertained through asthma. Journal of Allergy and Clinical Immunology, 2012, 129, 1547-1553.e3.	1.5	18
77	Associations between Nitric Oxide Synthase Genes and Exhaled NO-Related Phenotypes according to Asthma Status. PLoS ONE, 2012, 7, e36672.	1.1	33
78	Different Genes Interact with Particulate Matter and Tobacco Smoke Exposure in Affecting Lung Function Decline in the General Population. PLoS ONE, 2012, 7, e40175.	1.1	40
79	Genome-wide association study identifies novel loci predisposing to cutaneous melanomaâ€. Human Molecular Genetics, 2011, 20, 5012-5023.	1.4	187
80	Mold allergen sensitization in adult asthma according to integrin Î²3 polymorphisms and Toll-like receptor 2/+596 genotype. Journal of Allergy and Clinical Immunology, 2011, 128, 185-191.e7.	1.5	15
81	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
82	A SUMOylation-defective MITF germline mutation predisposes to melanoma and renal carcinoma. Nature, 2011, 480, 94-98.	13.7	466
83	Pathway-Based Analysis of a Melanoma Genome-Wide Association Study: Analysis of Genes Related to Tumour-Immunosuppression. PLoS ONE, 2011, 6, e29451.	1.1	18
84	Variants In NOSA Gene, Total Nitrite-Nitrate Level In Exhaled Breath Condensate And Response To SPT Among Adults From The EGEA Study. , 2011, , .		0
85	Genetic and functional evaluation of MITF as a candidate gene for cutaneous melanoma predisposition in pigs. Mammalian Genome, 2011, 22, 602-612.	1.0	7
86	Identification of SPOCK2 As a Susceptibility Gene for Bronchopulmonary Dysplasia. American Journal of Respiratory and Critical Care Medicine, 2011, 184, 1164-1170.	2.5	110
87	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
88	Characteristics of the coexistence of melanoma and renal cell carcinoma. Cancer, 2010, 116, 5716-5724.	2.0	22
89	Meta-analysis of 20 genome-wide linkage studies evidenced new regions linked to asthma and atopy. European Journal of Human Genetics, 2010, 18, 700-706.	1.4	54
90	17q21 variants modify the association between early respiratory infections and asthma. European Respiratory Journal, 2010, 36, 57-64.	3.1	87

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91	Association of MC1R Variants and Host Phenotypes With Melanoma Risk in CDKN2A Mutation Carriers: A GenoMEL Study. Journal of the National Cancer Institute, 2010, 102, 1568-1583.	3.0	108
92	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. New England Journal of Medicine, 2010, 363, 1211-1221.	13.9	1,762
93	CD14 and Toll-like Receptor Gene Polymorphisms, Country Living, and Asthma in Adults. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 363-368.	2.5	114
94	Smoking Exposure, 17q21 Variants, and Early-Onset Asthma. New England Journal of Medicine, 2009, 360, 1255-1256.	13.9	3
95	Protective effect of copy number polymorphism of glutathione S-transferase T1 gene on melanoma risk in presence of CDKN2A mutations, MC1R variants and host-related phenotypes. Familial Cancer, 2009, 8, 371-377.	0.9	10
96	Sex-specific effect of IL9 polymorphisms on lung function and polysensitization. Genes and Immunity, 2009, 10, 559-565.	2.2	26
97	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	9.4	422
98	MC1R variant alleles and malignant melanoma risk in Israel. European Journal of Cancer, 2009, 45, 2015-2022.	1.3	11
99	Prise en charge des formes familiales de tumeurs rares : mÃ©lanomes familiaux et primitifs multiples. Oncologie, 2008, 10, 411-414.	0.2	0
100	Evidence for linkage of a new region (11p14) to eczema and allergic diseases. Human Genetics, 2008, 122, 605-614.	1.8	24
101	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	9.4	209
102	Effect of 17q21 Variants and Smoking Exposure in Early-Onset Asthma. New England Journal of Medicine, 2008, 359, 1985-1994.	13.9	351
103	Replication of Association between ADAM33 Polymorphisms and Psoriasis. PLoS ONE, 2008, 3, e2448.	1.1	12
104	Evidence for a Locus in 1p31 Region Specifically Linked to the Co-Morbidity of Asthma and Allergic Rhinitis in the EGEA Study. Human Heredity, 2007, 63, 162-167.	0.4	13
105	Scores of asthma and asthma severity reveal new regions of linkage in EGEA study families. European Respiratory Journal, 2007, 30, 253-259.	3.1	24
106	Cutaneous phenotype andMC1R variants as modifying factors for the development of melanoma inCDKN2A G101W mutation carriers from 4 countries. International Journal of Cancer, 2007, 121, 825-831.	2.3	45
107	Evidence for gene Ã— smoking exposure interactions in a genome-wide linkage screen of asthma and bronchial hyper-responsiveness in EGEA families. European Journal of Human Genetics, 2007, 15, 810-815.	1.4	35
108	Evidence for a pleiotropic QTL on chromosome 5q13 influencing both time to asthma onset and asthma score in French EGEA families. Human Genetics, 2007, 121, 711-719.	1.8	17

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109	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. Cancer Research, 2006, 66, 9818-9828.	0.4	373
110	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. Journal of Medical Genetics, 2006, 44, 99-106.	1.5	350
111	Genome screen in the French EGEA study: detection of linked regions shared or not shared by allergic rhinitis and asthma. Genes and Immunity, 2005, 6, 95-102.	2.2	31
112	Melanocortin-1 Receptor (MC1R) Gene Variants and Dysplastic Nevi Modify Penetrance of CDKN2A Mutations in French Melanoma-Prone Pedigrees. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2384-2390.	1.1	64
113	Comprehensive analysis of CDKN2A (p16INK4A/p14ARF) and CDKN2B genes in 53 melanoma index cases considered to be at heightened risk of melanoma. Journal of Medical Genetics, 2005, 43, 39-47.	1.5	50
114	GÃ©nÃ©tique de lâ€™asthme et de lâ€™atopie : Combien de gÃ¨nes identifiÃ©s ?. Bulletin De L'Academie Nationale De Medecine, 2005, 189, 1435-1448.	0.0	1
115	Influence of Genes, Nevi, and Sun Sensitivity on Melanoma Risk in a Family Sample Unselected by Family History and in Melanoma-Prone Families. Journal of the National Cancer Institute, 2004, 96, 785-795.	3.0	97
116	Post-genome respiratory epidemiology: a multidisciplinary challenge. European Respiratory Journal, 2004, 24, 471-480.	3.1	26
117	Clustering patterns of LOD scores for asthma-related phenotypes revealed by a genome-wide screen in 295 French EGEA families. Human Molecular Genetics, 2004, 13, 3103-3113.	1.4	36
118	Familial correlations and inter-relationships of four asthma-associated quantitative phenotypes in 320 French EGEA families ascertained through asthmatic probands. European Journal of Human Genetics, 2004, 12, 955-963.	1.4	11
119	Segregation Analysis of Prostate Cancer in France: Evidence for Autosomal Dominant Inheritance and Residual Brother-brother Dependence. Annals of Human Genetics, 2003, 67, 125-137.	0.3	36
120	Using an age-at-onset phenotype with interval censoring to compare methods of segregation and linkage analysis in a candidate region for elevated systolic blood pressure. BMC Genetics, 2003, 4, S84.	2.7	3
121	Indication of linkage and genetic heterogeneity for asthma and atopy on chromosomes 8p and 12q in 107 French EGEA families. European Journal of Human Genetics, 2003, 11, 590-596.	1.4	3
122	A meta-analysis of four European genome screens (GIFT Consortium) shows evidence for a novel region on chromosome 17p11.2-q22 linked to type 2 diabetes. Human Molecular Genetics, 2003, 12, 1865-1873.	1.4	68
123	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903.	3.0	435
124	Epidemiologic Study of the Genetics and Environment of Asthma, Bronchial Hyperresponsiveness, and Atopy. Chest, 2002, 121, 27S.	0.4	9
125	Genetic and environmental factors in cutaneous malignant melanoma. Biochimie, 2002, 84, 67-74.	1.3	47
126	Interactions between genetic and reproductive factors in breast cancer risk in a population-based sample of African-American families. Genetic Epidemiology, 2002, 22, 285-297.	0.6	7

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127	Regressive threshold model for familial analysis of complex diseases with variable age of onset. Genetic Epidemiology, 2002, 23, 375-397.	0.6	5
128	Detection of putative functional angiotensinogen (AGT) gene variants controlling plasma AGT levels by combined segregation-linkage analysis. European Journal of Human Genetics, 2002, 10, 715-723.	1.4	67
129	Association between germ cell tumours, large numbers of naevi, atypical naevi and melanoma. Melanoma Research, 2001, 11, 117-122.	0.6	9
130	Detection of Parent-of-Origin Effects for Atopy by Model-Free and Model-Based Linkage Analyses. Genetic Epidemiology, 2001, 21, S186-S191.	0.6	10
131	Sporadic multiple primary melanoma cases:CDKN2Agermline mutations with a founder effect. Genes Chromosomes and Cancer, 2001, 32, 195-202.	1.5	63
132	Indication of linkage and genetic heterogeneity of asthma according to age at onset on chromosome 7q in 107 French EGEA families. European Journal of Human Genetics, 2001, 9, 867-872.	1.4	12
133	Segregation analysis of IgE levels in 335 French families (EGEA) using different strategies to correct for the ascertainment through a correlated trait (asthma). , 2000, 18, 128-142.		11
134	Patterns of familial aggregation of three melanoma risk factors: great number of naevi, light phototype and high degree of sun exposure. International Journal of Epidemiology, 2000, 29, 408-415.	0.9	18
135	Genome Screen for Asthma and Related Phenotypes in the French EGEA Study. American Journal of Respiratory and Critical Care Medicine, 2000, 162, 1812-1818.	2.5	217
136	CoPE: a collaborative pedigree drawing environment. Bioinformatics, 1999, 15, 345-346.	1.8	28
137	Genetic epidemiology of host predisposition microfilaraemia in human loiasis. Tropical Medicine and International Health, 1999, 4, 565-574.	1.0	48
138	Indication of linkage of serum IgE levels to the interleukin-4 gene and exclusion of the contribution of the (-590 C to T) interleukin-4 promoter polymorphism to IgE variation. , 1999, 16, 84-94.		35
139	Segregation analysis of the specific response to allergens: A recessive major gene controls the specific IgE response to Timothy grass pollen. , 1999, 16, 305-315.		3
140	Sibâ€pair linkage analysis of alcohol dependence taking into account covariates and ageâ€ofâ€onset variability: Evaluation of the residual approach. Genetic Epidemiology, 1999, 17, S349-54.	0.6	3
141	Detection of quantitative trait loci associated with alcoholâ€dependence: Use of modelâ€free sibâ€pair method and combined segregationâ€linkage analysis based on regressive models. Genetic Epidemiology, 1999, 17, S145-50.	0.6	0
142	Predisposing Gene for Early-Onset Prostate Cancer, Localized on Chromosome 1q42.2-43. American Journal of Human Genetics, 1998, 62, 1416-1424.	2.6	327
143	Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France. The French Familial Melanoma Study Group [published erratum appears in Hum Mol Genet 1998 May;7(5):941]. Human Molecular Genetics, 1998, 7, 209-216.	1.4	345
144	A missense mutation in hepatocyte nuclear factor-4 alpha, resulting in a reduced transactivation activity, in human late-onset non-insulin-dependent diabetes mellitus.. Journal of Clinical Investigation, 1998, 101, 521-526.	3.9	110

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145	Genetic control of blood infection levels in human malaria: evidence for a complex genetic model.. American Journal of Tropical Medicine and Hygiene, 1998, 58, 480-488.	0.6	47
146	Epidemiological Study of the Genetics and Environment of Asthma, Bronchial Hyperresponsiveness, and Atopy. American Journal of Respiratory and Critical Care Medicine, 1997, 156, S123-S129.	2.5	126
147	A susceptibility locus for early-onset non-insulin dependent (type 2) diabetes mellitus maps to chromosome 20q, proximal to the phosphoenolpyruvate carboxykinase gene. Human Molecular Genetics, 1997, 6, 1401-1408.	1.4	155
148	Mapping NIDDM Susceptibility Loci in French Families: Studies With Markers in the Region of NIDDM1 on Chromosome 2q. Diabetes, 1997, 46, 1225-1226.	0.3	27
149	Genetic studies of the renin-angiotensin system in arterial hypertension associated with non-insulin-dependent diabetes mellitus. Journal of Hypertension, 1997, 15, 601-606.	0.3	20
150	Interactions between Genetic and Reproductive Factors in Breast Cancer Risk in a French Family Sample. American Journal of Human Genetics, 1997, 61, 678-690.	2.6	23
151	Empirical affected-sib-pair statistics: Two simulation strategies. Genetic Epidemiology, 1997, 14, 1073-1078.	0.6	0
152	Affected sib-pair tests for linkage: Type I errors with dependent sib-pairs. Genetic Epidemiology, 1997, 14, 1107-1111.	0.6	19
153	Genetic studies of the sulfonylurea receptor gene locus in NIDDM and in morbid obesity among French Caucasians. Diabetes, 1997, 46, 688-694.	0.3	29
154	Genetics of NIDDM in France: studies with 19 candidate genes in affected sib pairs. Diabetes, 1997, 46, 1062-1068.	0.3	21
155	MÃ©thodes statistiques pour identifier les gÃ¨nes dans les maladies multifactorielles. Annales De L'Institut Pasteur / ActualitÃ©s, 1996, 7, 3-12.	0.1	3
156	The Relationship of Body Mass Index to Reproductive Factors in Preâ€•and Postmenopausal Africanâ€American Women With and Without Breast Cancer. Obesity, 1996, 4, 451-456.	4.0	30
157	Genetic and epidemiological risk factors for a malignant melanoma-predisposing phenotype: The great number of nevi. , 1996, 13, 385-402.		12
158	Dissecting the loci controlling fetal haemoglobin production on chromosomes 11p and 6q by the regressive approach. Nature Genetics, 1996, 12, 58-64.	9.4	181
159	Indication for linkage of the human OB gene region with extreme obesity. Diabetes, 1996, 45, 687-690.	0.3	40
160	Detection of a recessive major gene for high IgE levels acting independently of specific response to allergens. Genetic Epidemiology, 1995, 12, 93-105.	0.6	52
161	Complex segregation analysis of familial diseases with variable age of onset: Comparison of different methods by a simulation study. Genetic Epidemiology, 1995, 12, 231-249.	0.6	14
162	How can maximum likelihood methods reveal candidate gene effects on a quantitative trait?. Genetic Epidemiology, 1995, 12, 789-794.	0.6	7

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163	A missense mutation in the glucagon receptor gene is associated with nonâ€“insulinâ€“dependent diabetes mellitus. Nature Genetics, 1995, 9, 299-304.	9.4	177
164	Comparison between familial and nonfamilial melanoma in France. Archives of Dermatology, 1995, 131, 1154-1159.	1.7	34
165	Linkage analyses of the MODY3 locus on chromosome 12q with late-onset NIDDM. Diabetes, 1995, 44, 1243-1247.	0.3	8
166	MÃ©thodes mathÃ©matiques pour l'Ã©tude des gÃ¨nes contrÃ´lant des caractÃ¨res quantitatifs. Genetics Selection Evolution, 1994, 26, 1.	1.2	0
167	Use of the regressive models in linkage analysis of quantitative traits. Genetic Epidemiology, 1993, 10, 587-592.	0.6	16
168	Genetic analysis of diabetes and insulitis in an interspecific cross of the nonobese diabetic mouse with Mus spretus.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 1877-1881.	3.3	55
169	Linkage analysis and molecular scanning of glucokinase gene in NIDDM families. Diabetes, 1993, 42, 1238-1245.	0.3	19
170	Regressive logistic models in linkage analysis of the cutaneous malignant melanoma-dysplastic nevus syndrome. Cytogenetic and Genome Research, 1992, 59, 191-193.	0.6	0
171	Numerical comparisons of two formulations of the logistic regressive models with the mixed model in segregation analysis of discrete traits. Genetic Epidemiology, 1992, 9, 419-435.	0.6	20
172	Search for faster methods of fitting the regressive models to quantitative traits. Genetic Epidemiology, 1990, 7, 319-334.	0.6	48
173	Familial susceptibility to breast cancer: A complex inheritance. International Journal of Cancer, 1989, 44, 415-418.	2.3	9
174	Robustness of the unified model to shared environmental effects in the analysis of dichotomous traits. Genetic Epidemiology, 1989, 6, 229-234.	0.6	12
175	Modeling the age-of-onset function in segregation analysis: A causal scheme for leprosy. Genetic Epidemiology, 1989, 6, 501-516.	0.6	5
176	Equivalence of the mixed and regressive models for genetic analysis. I. Continuous traits. Genetic Epidemiology, 1989, 6, 597-617.	0.6	72
177	Genetic analysis of human breast cancer: Implications for family study designs. Genetic Epidemiology, 1988, 5, 225-233.	0.6	14
178	Detection of linkage between a quantitative trait and a marker locus by the lod score method: sample size and sampling considerations. Annals of Human Genetics, 1988, 52, 237-246.	0.3	13
179	Susceptibility to human cutaneous leishmaniasis and HLA, Gm, Km markers. Tissue Antigens, 1987, 30, 63-67.	1.0	28
180	HLA in Familial Malignant Melanoma. Dermatology, 1986, 173, 109-115.	0.9	1

#	Article	IF	Citations
181	Studies on an isolated West Indies population: IV. Genetic study of hearing loss. Genetic Epidemiology, 1986, 3, 113-119.	0.6	3
182	Segregation analysis of the Jacobsen data. Genetic Epidemiology, 1986, 3, 49-54.	0.6	15
183	An epidemiological and genetic study of facial clefting in France. II Segregation analysis.. Journal of Medical Genetics, 1984, 21, 436-440.	1.5	23
184	A linkage study between HLA and cutaneous malignant melanoma or precursor lesions or both.. Journal of Medical Genetics, 1984, 21, 429-435.	1.5	16
185	A linkage study of HLA and maturity onset type diabetes of the young (MODY). Tissue Antigens, 1983, 21, 391-396.	1.0	3
186	Exclusion of a tight linkage between familial polyposis coli and HLA. Tissue Antigens, 1983, 22, 354-358.	1.0	5
187	Neural tube defects in france: Segregation analysis. American Journal of Medical Genetics Part A, 1982, 11, 287-298.	2.4	32
188	A five-generation family with sacral agenesis and spina bifida: Possible similarities with the mouse T-locus. American Journal of Medical Genetics Part A, 1982, 12, 465-487.	2.4	66
189	A General Transmission Probability Model for Pedigree Data. Human Heredity, 1981, 31, 93-99.	0.4	38
190	Diseases Having Two Classes of Severity: Estimation of the Proportions of Each Manifestation by Maximum Likelihood. Biometrics, 1980, 36, 447.	0.8	3
191	Congenital glaucoma: Genetic models. Human Genetics, 1979, 46, 305-317.	1.8	24
192	Consanguinity in Multifactorial Inheritance. Human Heredity, 1978, 28, 361-371.	0.4	13