Marie-HÃ©lÃ¨ne Dizier

List of Publications by Year
in descending order

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63	3,483	361413	138484
papers	citations	20 h-index	58 g-index

64	64	64	5514
all docs	docs citations	times ranked	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.	5.1	3
2	Identification of OCA2 as a novel locus for the coâ€morbidity of asthmaâ€plusâ€eczema. Clinical and Experimental Allergy, 2021, , .	2.9	3
3	PID1 is associated to a respiratory endotype related to occupational exposures to irritants. Free Radical Biology and Medicine, 2021, 172, 503-507.	2.9	3
4	General regression model: A â€œmodelâ€freeâ€•association test for quantitative traits allowing to test for the underlying genetic model. Annals of Human Genetics, 2020, 84, 280-290.	0.8	0
5	Genomeâ€wide interaction study of earlyâ€life smoking exposure on timeâ€toâ€asthma onset in childhood. Clinical and Experimental Allergy, 2019, 49, 1342-1351.	2.9	9
6	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.	5.6	4
7	A novel role for ciliary function in atopy: ADGRV1 and DNAH5 interactions. Journal of Allergy and Clinical Immunology, 2018, 141, 1659-1667.e11.	2.9	9
8	The <scp>COL</scp>5A3 and <scp>MMP</scp>9 genes interact in eczema susceptibility. Clinical and Experimental Allergy, 2018, 48, 297-305.	2.9	9
9	Genome-wide interaction study of environmental tobacco smoke exposure on time-to-asthma onset in childhood. , 2018, , .		1
10	Network-assisted analysis of GWAS data identifies a functionally-relevant gene module for childhood-onset asthma. Scientific Reports, 2017, 7, 938.	3.3	14
11	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
12	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.	6.0	23
13	Genes Involved in Interleukin-1 Receptor Type II Activities Are Associated With Asthmatic Phenotypes. Allergy, Asthma and Immunology Research, 2016, 8, 466.	2.9	5
14	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.	2.9	25
15	Identification of a new locus at 16q12 associated with time to asthma onset. Journal of Allergy and Clinical Immunology, 2016, 138, 1071-1080.	2.9	25
16	Interaction between the DNAH9 gene and early smoke exposure in bronchial hyperresponsiveness. European Respiratory Journal, 2016, 47, 1072-1081.	6.7	17
17	A New Correction for Multiple Testing in Geneâ€“Gene Interaction Studies. Annals of Human Genetics, 2015, 79, 380-384.	0.8	7
18	Meta-analysis identifies seven susceptibility loci involved in the atopic march. Nature Communications, 2015, 6, 8804.	12.8	148

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19	Genetics of emotional reactivity in bipolar disorders. Journal of Affective Disorders, 2015, 188, 101-106.	4.1	8
20	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.	2.9	11
21	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.	2.9	17
22	Comparative Power of Familyâ€Based Association Strategies to Detect Diseaseâ€Causing Variants Under Twoâ€Locus Models. Genetic Epidemiology, 2012, 36, 848-855.	1.3	4
23	The ANO3/MUC15 locus is associated with eczema in families ascertained through asthma. Journal of Allergy and Clinical Immunology, 2012, 129, 1547-1553.e3.	2.9	18
24	Associations between Nitric Oxide Synthase Genes and Exhaled NO-Related Phenotypes according to Asthma Status. PLoS ONE, 2012, 7, e36672.	2.5	33
25	Genetic heterogeneity according to age at onset in bipolar disorder: A combined positional cloning and candidate gene approach. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 653-659.	1.7	13
26	European collaborative study of earlyâ€onset bipolar disorder: Evidence for genetic heterogeneity on 2q14 according to age at onset. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1425-1433.	1.7	16
27	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.	2.8	54
28	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. New England Journal of Medicine, 2010, 363, 1211-1221.	27.0	1,762
29	Sex-specific effect of IL9 polymorphisms on lung function and polysensitization. Genes and Immunity, 2009, 10, 559-565.	4.1	26
30	Evidence for linkage of a new region (11p14) to eczema and allergic diseases. Human Genetics, 2008, 122, 605-614.	3.8	24
31	Effect of 17q21 Variants and Smoking Exposure in Early-Onset Asthma. New England Journal of Medicine, 2008, 359, 1985-1994.	27.0	351
32	Replication of Association between ADAM33 Polymorphisms and Psoriasis. PLoS ONE, 2008, 3, e2448.	2.5	12
33	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.	0.8	13
34	Scores of asthma and asthma severity reveal new regions of linkage in EGEA study families. European Respiratory Journal, 2007, 30, 253-259.	6.7	24
35	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.	2.8	35
36	Confirmation of Psoriasis Susceptibility Loci on Chromosome 6p21 and 20p13 in French Families. Journal of Investigative Dermatology, 2007, 127, 1403-1409.	0.7	20

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37	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.	3.8	17
38	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.	4.1	31
39	Impact of the diagnosis definition on linkage detection. BMC Genetics, 2005, 6, S140.	2.7	1
40	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.	2.9	36
41	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.	2.8	11
42	Testing linkage and Gene Ã— Environment interaction: Comparison of different affected sib-pair methods. Genetic Epidemiology, 2003, 25, 73-79.	1.3	9
43	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.	2.8	3
44	Familial Resemblance of Asthma Severity in the EGEA* Study. American Journal of Respiratory and Critical Care Medicine, 2002, 165, 185-189.	5.6	35
45	Epidemiologic Study of the Genetics and Environment of Asthma, Bronchial Hyperresponsiveness, and Atopy. Chest, 2002, 121, 27S.	0.8	9
46	Triangle Test Statistic in Discordant Sib Pairs: Test of Genetic Heterogeneity of Asthma and Atopy in CSGA Families. Genetic Epidemiology, 2001, 21, S192-7.	1.3	1
47	Homogeneity of Asthma Genome Scan Results. Genetic Epidemiology, 2001, 21, S44-8.	1.3	1
48	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.	2.8	12
49	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
50	The triangle test statistic (TTS): a test of genetic homogeneity using departure from the triangle constraints in IBD distribution among affected sibâ€pairs. Annals of Human Genetics, 2000, 64, 433-442.	0.8	19
51	Genome Screen for Asthma and Related Phenotypes in the French EGEA Study. American Journal of Respiratory and Critical Care Medicine, 2000, 162, 1812-1818.	5.6	217
52	Segregation analysis of IgE levels in 335 French families (EGEA) using different strategies to correct for the ascertainment through a correlated trait (asthma). Genetic Epidemiology, 2000, 18, 128.	1.3	0
53	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. Genetic Epidemiology, 1999, 16, 84-94.	1.3	35
54	Departure from the triangle constraints in discordant sib pairs: A test for genetic heterogeneity. Genetic Epidemiology, 1999, 17, S685-S689.	1.3	3

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55	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.	5.6	126
56	Detection of a recessive major gene for high IgE levels acting independently of specific response to allergens. Genetic Epidemiology, 1995, 12, 93-105.	1.3	52
57	Modeling the role of two susceptibility loci by the MASC method. Genetic Epidemiology, 1995, 12, 589-593.	1.3	1
58	EGEA (Epidemiological study on the Genetics and Environment of Asthma, bronchial) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (hype	2.9	44
59	GÃ©nÃ©tique de l'asthme. Medecine/Sciences, 1991, 7, 1041.	0.2	0
60	Twoâ€diseaseâ€locus model: segregation analysis using information on two markers in nuclear families. Application to IDDM *. Tissue Antigens, 1990, 36, 1-7.	1.0	4
61	Segregation analysis of two genetic markers in IDDM families under two-locus models. Genetic Epidemiology, 1989, 6, 71-75.	1.3	6
62	A Gm Haplotype Study in Relation with HLA-DR in 155 Insulin-Dependent Diabetic Patients and Their Affected and Non Affected Siblings. Experimental and Clinical Endocrinology and Diabetes, 1987, 89, 325-332.	1.2	7
63	Two-disease locus model: Sib pair method using information on both HLA and Gm. Genetic Epidemiology, 1986, 3, 343-356.	1.3	20