Dan L Nicolae

List of Publications by Year
in descending order

156 papers	40,258 citations	18887 64 h-index	8878 150 g-index
172 all docs	172 docs citations	172 times ranked	57510 citing authors

#	Article	IF	Citations
1	Estimating and Accounting for Unobserved Covariates in High-Dimensional Correlated Data. Journal of the American Statistical Association, 2022, 117, 225-236.	1.8	5
2	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. Genome Medicine, 2022, 14, .	3.6	2
3	Longitudinal data reveal strong genetic and weak non-genetic components of ethnicity-dependent blood DNA methylation levels. Epigenetics, 2021, 16, 662-676.	1.3	18
4	Chromosome 17q12-21 Variants Are Associated with Multiple Wheezing Phenotypes in Childhood. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 864-870.	2.5	24
5	Multi-omics colocalization with genome-wide association studies reveals a context-specific genetic mechanism at a childhood onset asthma risk locus. Genome Medicine, 2021, 13, 157.	3.6	21
6	Epigenetic landscape links upper airway microbiota in infancy with allergic rhinitis at 6 years of age. Journal of Allergy and Clinical Immunology, 2020, 146, 1358-1366.	1.5	31
7	Altered transcriptional and chromatin responses to rhinovirus in bronchial epithelial cells from adults with asthma. Communications Biology, 2020, 3, 678.	2.0	13
8	Expression quantitative trait locus fine mapping of the 17q12â€“21 asthma locus in African American children: a genetic association and gene expression study. Lancet Respiratory Medicine,the, 2020, 8, 482-492.	5.2	47
9	Association of HLA-DRB1âˆ—09:01 with tIgE levels among African-ancestry individuals with asthma. Journal of Allergy and Clinical Immunology, 2020, 146, 147-155.	1.5	14
10	Estimation and inference in metabolomics with nonrandom missing data and latent factors. Annals of Applied Statistics, 2020, 14, 789-808.	0.5	4
11	Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. Lancet Respiratory Medicine,the, 2019, 7, 509-522.	5.2	238
12	Parent-of-origin effects on quantitative phenotypes in a large Hutterite pedigree. Communications Biology, 2019, 2, 28.	2.0	20
13	Integrating predicted transcriptome from multiple tissues improves association detection. PLoS Genetics, 2019, 15, e1007889.	1.5	239
14	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	5.8	71
15	Accounting for unobserved covariates with varying degrees of estimability in high-dimensional biological data. Biometrika, 2019, 106, 823-840.	1.3	22
16	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	9.4	276
17	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. Journal of Allergy and Clinical Immunology, 2019, 143, 957-969.	1.5	33
18	Role of local CpG DNA methylation in mediating the 17q21 asthma susceptibility gasdermin B (GSDMB)/ORMDL sphingolipid biosynthesis regulator 3 (ORMDL3) expression quantitative trait locus. Journal of Allergy and Clinical Immunology, 2018, 141, 2282-2286.e6.	1.5	20

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19	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
20	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
21	A decade of research on the 17q12-21 asthma locus: Piecing together the puzzle. Journal of Allergy and Clinical Immunology, 2018, 142, 749-764.e3.	1.5	143
22	Gene Coexpression Networks in Whole Blood Implicate Multiple Interrelated Molecular Pathways in Obesity in People with Asthma. Obesity, 2018, 26, 1938-1948.	1.5	11
23	Parent of origin gene expression in a founder population identifies two new candidate imprinted genes at known imprinted regions. PLoS ONE, 2018, 13, e0203906.	1.1	9
24	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	9.4	389
25	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	9.4	106
26	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
27	Host genetic variation in mucosal immunity pathways influences the upper airway microbiome. Microbiome, 2017, 5, 16.	4.9	61
28	Gene Expression Profiling in Blood Provides Reproducible Molecular Insights into Asthma Control. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 179-188.	2.5	49
29	Rare non-coding variants are associated with plasma lipid traits in a founder population. Scientific Reports, 2017, 7, 16415.	1.6	31
30	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423.	1.5	143
31	DNA methylation in lung cells is associated with asthma endotypes and genetic risk. JCI Insight, 2016, 1, e90151.	2.3	133
32	A Unified Set-Based Test with Adaptive Filtering for Geneâ€“Environment Interaction Analyses. Biometrics, 2016, 72, 629-638.	0.8	14
33	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	2.6	51
34	Genetic associations with viral respiratory illnesses and asthma control inÂchildren. Clinical and Experimental Allergy, 2016, 46, 112-124.	1.4	39
35	Association Tests for Rare Variants. Annual Review of Genomics and Human Genetics, 2016, 17, 117-130.	2.5	56
36	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. Nature Communications, 2016, 7, 12522.	5.8	136

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37	Genome-Wide Methylation Study Identifies an IL-13â€“induced Epigenetic Signature in Asthmatic Airways. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 376-385.	2.5	90
38	Estimating Variance Components in Functional Linear Models With Applications to Genetic Heritability. Journal of the American Statistical Association, 2016, 111, 407-422.	1.8	12
39	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. Journal of Allergy and Clinical Immunology, 2015, 135, 1502-1510.	1.5	52
40	PRIMAL: Fast and Accurate Pedigree-based Imputation from Sequence Data in a Founder Population. PLoS Computational Biology, 2015, 11, e1004139.	1.5	36
41	Stress and Bronchodilator Response in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 47-56.	2.5	99
42	Genome-wide association study of recalcitrant atopic dermatitis in Korean children. Journal of Allergy and Clinical Immunology, 2015, 136, 678-684.e4.	1.5	45
43	Noninvasive Analysis of the Sputum Transcriptome Discriminates Clinical Phenotypes of Asthma. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 1116-1125.	2.5	86
44	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
45	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
46	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	9.4	1,473
47	Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. Nature Communications, 2015, 6, 5965.	5.8	66
48	Prenatal Tobacco Smoke Exposure Is Associated with Childhood DNA CpG Methylation. PLoS ONE, 2014, 9, e99716.	1.1	105
49	GWAS to Sequencing: Divergence in Study Design and Analysis. Genes, 2014, 5, 460-476.	1.0	14
50	Genome-wide interaction studies reveal sex-specific asthma risk alleles. Human Molecular Genetics, 2014, 23, 5251-5259.	1.4	70
51	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	3.3	152
52	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies PFKM as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	1.1	77
53	Ethnicity-specific pharmacogenetics: the case of warfarin in African Americans. Pharmacogenomics Journal, 2014, 14, 223-228.	0.9	59
54	Genome-wide association study of lung function phenotypes in a founder population. Journal of Allergy and Clinical Immunology, 2014, 133, 248-255.e10.	1.5	50

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55	A genome-wide survey of CD4+ lymphocyte regulatory genetic variants identifies novel asthma genes. Journal of Allergy and Clinical Immunology, 2014, 134, 1153-1162.	1.5	46
56	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. BMC Medical Genomics, 2014, 7, 48.	0.7	63
57	A functional data analysis approach for genetic association studies. Annals of Applied Statistics, 2014, 8, .	0.5	30
58	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	13.5	209
59	Maternal asthma and microRNA regulation of soluble HLA-G in the airway. Journal of Allergy and Clinical Immunology, 2013, 131, 1496-1503.e4.	1.5	44
60	Genetic variants associated with idiopathic pulmonary fibrosis susceptibility and mortality: a genome-wide association study. Lancet Respiratory Medicine,the, 2013, 1, 309-317.	5.2	486
61	A meta-analysis of genome-wide association studies for serum total IgE in diverse study populations. Journal of Allergy and Clinical Immunology, 2013, 131, 1176-1184.	1.5	58
62	Rhinovirus Wheezing Illness and Genetic Risk of Childhood-Onset Asthma. New England Journal of Medicine, 2013, 368, 1398-1407.	13.9	449
63	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
64	Marbled Inflation From Population Structure in Geneâ€Based Association Studies With Rare Variants. Genetic Epidemiology, 2013, 37, 286-292.	0.6	34
65	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
66	On Quantifying Dependence: A Framework for Developing Interpretable Measures. Statistical Science, 2013, 28, .	1.6	21
67	Integration of Mouse and Human Genome-Wide Association Data Identifies KCNIP4 as an Asthma Gene. PLoS ONE, 2013, 8, e56179.	1.1	28
68	Increased Protein-Coding Mutations in the Mitochondrial Genome of African American Women With Preeclampsia. Reproductive Sciences, 2012, 19, 1343-1351.	1.1	12
69	Estimating the proportion of true null hypotheses under dependence. Statistica Sinica, 2012, , .	0.2	0
70	Genome-wide ancestry association testing identifies a common European variant on 6q14.1 as a risk factor for asthma in African American subjects. Journal of Allergy and Clinical Immunology, 2012, 130, 622-629.e9.	1.5	31
71	Genome-wide association studies of asthma indicate opposite immunopathogenesis direction from autoimmune diseases. Journal of Allergy and Clinical Immunology, 2012, 130, 861-868.e7.	1.5	130
72	Further replication studies of the EVE Consortium meta-analysis identifies 2 asthma risk loci in European Americans. Journal of Allergy and Clinical Immunology, 2012, 130, 1294-1301.	1.5	30

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73	Response to Knoppers etÂal.. American Journal of Human Genetics, 2012, 91, 579.	2.6	0
74	An Exponential Combination Procedure for Set-Based Association Tests in Sequencing Studies. American Journal of Human Genetics, 2012, 91, 977-986.	2.6	34
75	Expression Quantitative Trait Locus (eQTL) Mapping In Diverse Populations And Cell Types Identifies Numerous Asthma-Associated Regulatory Variants. , 2012, , .		2
76	Replication Analysis for Severe Diabetic Retinopathy. , 2012, 53, 2377.		42
77	Accurate Imputation of Rare and Common Variants in a Founder Population From a Small Number of Sequenced Individuals. Genetic Epidemiology, 2012, 36, 312-319.	0.6	19
78	Resequencing Candidate Genes Implicates Rare Variants in Asthma Susceptibility. American Journal of Human Genetics, 2012, 90, 273-281.	2.6	65
79	On Sharing Quantitative Trait GWAS Results in an Era of Multiple-omics Data and the Limits of Genomic Privacy. American Journal of Human Genetics, 2012, 90, 591-598.	2.6	87
80	Exome sequencing reveals a novel mutation for autosomal recessive non-syndromic mental retardation in the TECR gene on chromosome 19p13. Human Molecular Genetics, 2011, 20, 1285-1289.	1.4	94
81	Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. Nature Genetics, 2011, 43, 887-892.	9.4	736
82	Recombination rates in admixed individuals identified by ancestry-based inference. Nature Genetics, 2011, 43, 847-853.	9.4	111
83	Asthma Bridge: The Asthma Biorepository For Integrative Genomic Exploration. , 2011, , .		4
84	You've Gotta Be Lucky: Coverage and the Elusive Gene-Gene Interaction. Annals of Human Genetics, 2011, 75, 105-111.	0.3	7
85	The Missing Association: Sequencing-Based Discovery of Novel SNPs in VKORC1 and CYP2C9 That Affect Warfarin Dose in African Americans. Clinical Pharmacology and Therapeutics, 2011, 89, 408-415.	2.3	100
86	Finding Disease Variants in Mendelian Disorders By Using Sequence Data: Methods and Applications. American Journal of Human Genetics, 2011, 89, 701-712.	2.6	50
87	Genome-wide association and meta-analysis in populations from Starr County, Texas, and Mexico City identify type 2 diabetes susceptibility loci and enrichment for expression quantitative trait loci in top signals. Diabetologia, 2011, 54, 2047-2055.	2.9	106
88	Genome-wide meta-analysis for severe diabetic retinopathy. Human Molecular Genetics, 2011, 20, 2472-2481.	1.4	141
89	A Study of CNVs As Trait-Associated Polymorphisms and As Expression Quantitative Trait Loci. PLoS Genetics, 2011, 7, e1001292.	1.5	50
90	Gene, region and pathway level analyses in wholeâ€genome studies. Genetic Epidemiology, 2010, 34, 222-231.	0.6	46

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91	Spoiling the Whole Bunch: Quality Control Aimed at Preserving the Integrity of High-Throughput Genotyping. American Journal of Human Genetics, 2010, 87, 123-128.	2.6	48
92	Shades of gray: a comparison of linkage disequilibrium between Hutterites and Europeans. Genetic Epidemiology, 2010, 34, 133-139.	0.6	10
93	Estimating the mixing proportion in a semiparametric mixture model. Computational Statistics and Data Analysis, 2010, 54, 2276-2283.	0.7	6
94	Trait-Associated SNPs Are More Likely to Be eQTLs: Annotation to Enhance Discovery from GWAS. PLoS Genetics, 2010, 6, e1000888.	1.5	1,161
95	A Genome-Wide Association Study Identifies a Novel Major Locus for Glycemic Control in Type 1 Diabetes, as Measured by Both A1C and Glucose. Diabetes, 2010, 59, 539-549.	0.3	103
96	SCAN: SNP and copy number annotation. Bioinformatics, 2010, 26, 259-262.	1.8	214
97	An Evolutionary Framework for Association Testing in Resequencing Studies. PLoS Genetics, 2010, 6, e1001202.	1.5	46
98	The pattern of somatic hypermutation of Ig genes is altered when p53 is inactivated. Molecular Immunology, 2010, 47, 2611-2618.	1.0	8
99	Sequence variations at the human leukocyte antigenâ€“linked olfactory receptor cluster do not influence female preferences for male odors. Human Immunology, 2010, 71, 100-103.	1.2	10
100	Somatic hypermutation: Processivity of the cytosine deaminase AID and error-free repair of the resulting uracils. Cell Cycle, 2009, 8, 3097-3101.	1.3	28
101	(Too) Great Expectations. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 1078-1079.	2.5	6
102	Genome-wide association study of plasma lipoprotein(a) levels identifies multiple genes on chromosome 6q. Journal of Lipid Research, 2009, 50, 798-806.	2.0	86
103	Ethnic Differences and Functional Analysis of MET Mutations in Lung Cancer. Clinical Cancer Research, 2009, 15, 5714-5723.	3.2	174
104	Restricted parameter space models for testing geneâ€gene interaction. Genetic Epidemiology, 2009, 33, 386-393.	0.6	15
105	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	9.4	459
106	A sequential clustering algorithm with applications to gene expression data. Journal of the Korean Statistical Society, 2009, 38, 175-184.	0.3	5
107	Patient Self-Report of Prior Laser Treatment Reliably Indicates Presence of Severe Diabetic Retinopathy. American Journal of Ophthalmology, 2009, 147, 501-504.	1.7	17
108	A common cortactin gene variation confers differential susceptibility to severe asthma. Genetic Epidemiology, 2008, 32, 757-766.	0.6	18

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109	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature Genetics, 2008, 40, 955-962.	9.4	2,422
110	Allele-Specific Targeting of microRNAs to HLA-G and Risk of Asthma. American Journal of Human Genetics, 2008, 82, 251.	2.6	3
111	On Single-Array Genotype Calling Algorithms. , 2008, , .		0
112	Effect of Variation inCHI3L1on Serum YKL-40 Level, Risk of Asthma, and Lung Function. New England Journal of Medicine, 2008, 358, 1682-1691.	13.9	445
113	A Signature of Evolutionary Constraint on a Subset of Ectopically Expressed Olfactory Receptor Genes. Molecular Biology and Evolution, 2008, 26, 491-494.	3.5	59
114	Association studies for untyped markers with TUNA. Bioinformatics, 2008, 24, 435-437.	1.8	13
115	Quantifying the Fraction of Missing Information for Hypothesis Testing in Statistical and Genetic Studies. Statistical Science, 2008, 23, .	1.6	5
116	Rejoinder: Quantifying the Fraction of Missing Information for Hypothesis Testing in Statistical and Genetic Studies. Statistical Science, 2008, 23, .	1.6	0
117	Invited Keynote Talk: Set-Level Analyses for Genome-Wide Association Data. Lecture Notes in Computer Science, 2008, , 1-1.	1.0	1
118	FURTHER EXPLORATIONS OF LIKELIHOOD THEORY FOR MONTE CARLO INTEGRATION. , 2007, , 563-592.		3
119	Allele-Specific Targeting of microRNAs to HLA-G and Risk of Asthma. American Journal of Human Genetics, 2007, 81, 829-834.	2.6	344
120	Characterizing the expression of the human olfactory receptor gene family using a novel DNA microarray. Genome Biology, 2007, 8, R86.	13.9	148
121	Integrin Î²3 genotype influences asthma and allergy phenotypes in the first 6 years of life. Journal of Allergy and Clinical Immunology, 2007, 119, 1423-1429.	1.5	26
122	Smoking and inflammatory bowel disease. Inflammatory Bowel Diseases, 2007, 13, 573-579.	0.9	40
123	Genome-wide association study identifies new susceptibility loci for Crohn disease and implicates autophagy in disease pathogenesis. Nature Genetics, 2007, 39, 596-604.	9.4	1,633
124	A Genome-Wide Association Study Identifies IL23R as an Inflammatory Bowel Disease Gene. Science, 2006, 314, 1461-1463.	6.0	2,739
125	Quantifying the amount of missing information in genetic association studies. Genetic Epidemiology, 2006, 30, 703-717.	0.6	19
126	Testing Untyped Alleles (TUNA)â€”applications to genome-wide association studies. Genetic Epidemiology, 2006, 30, 718-727.	0.6	112

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127	Coverage and Characteristics of the Affymetrix GeneChip Human Mapping 100K SNP Set. PLoS Genetics, 2006, 2, e67.	1.5	38
128	GEL: a novel genotype calling algorithm using empirical likelihood. Bioinformatics, 2006, 22, 1942-1947.	1.8	17
129	Somatic Hypermutation and Class Switch Recombination in Msh6â^'/â^'Ungâ^'/â^' Double-Knockout Mice. Journal of Immunology, 2006, 177, 5386-5392.	0.4	113
130	Phenotype-Stratified Genetic Linkage Study Demonstrates that IBD2 Is an Extensive Ulcerative Colitis Locus. American Journal of Gastroenterology, 2006, 101, 572-580.	0.2	32
131	Dominant-negative TLR5 polymorphism reduces adaptive immune response to flagellin and negatively associates with Crohn's disease. American Journal of Physiology - Renal Physiology, 2006, 290, G1157-G1163.	1.6	175
132	The very 5â€² end and the constant region of Ig genes are spared from somatic mutation because AID does not access these regions. Journal of Experimental Medicine, 2005, 202, 1443-1454.	4.2	55
133	Fine Mapping and Positional Candidate Studies Identify HLA-G as an Asthma Susceptibility Gene on Chromosome 6p21. American Journal of Human Genetics, 2005, 76, 349-357.	2.6	238
134	Gene-Environment Interaction Effects on the Development of Immune Responses in the 1st Year of Life. American Journal of Human Genetics, 2005, 76, 696-704.	2.6	104
135	Measuring the Relative Information in Allele-Sharing Linkage Studies. Biometrics, 2004, 60, 368-375.	0.8	12
136	A Genome Scan in 260 Inflammatory Bowel Disease-Affected Relative Pairs. Inflammatory Bowel Diseases, 2004, 10, 15-22.	0.9	28
137	A Genome Scan in 260 Inflammatory Bowel Disease-Affected Relative Pairs. Inflammatory Bowel Diseases, 2004, 10, 513-520.	0.9	55
138	Regulation of IL-8 and IL-1Â expression in Crohn's disease associated NOD2/CARD15 mutations. Human Molecular Genetics, 2004, 13, 1715-1725.	1.4	243
139	Genetic variation in immunoregulatory pathways and atopic phenotypes in infancy. Journal of Allergy and Clinical Immunology, 2004, 113, 511-518.	1.5	95
140	Effects of dog ownership and genotype on immune development and atopy in infancyâ˜†. Journal of Allergy and Clinical Immunology, 2004, 113, 307-314.	1.5	202
141	Microarray analysis of changes in bone cell gene expression early after cadmium gavage in mice. Toxicology and Applied Pharmacology, 2003, 191, 272-293.	1.3	60
142	Evidence for gene-environment interactions in a linkage study of asthma and smoking exposure. Journal of Allergy and Clinical Immunology, 2003, 111, 840-846.	1.5	146
143	Ulcerative colitis and ex-smoking: The later the diagnosis, the greater the burden. Gastroenterology, 2003, 124, A207.	0.6	0
144	Association studies for asthma and atopic diseases: a comprehensive review of the literature. Respiratory Research, 2003, 4, 14.	1.4	189

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145	Crohn's disease-associated NOD2 variants share a signaling defect in response to lipopolysaccharide and peptidoglycan. Gastroenterology, 2003, 124, 140-146.	0.6	382
146	MDR1 Ala893 Polymorphism Is Associated with Inflammatory Bowel Disease. American Journal of Human Genetics, 2003, 73, 1282-1292.	2.6	213
147	Effects of Sequence and Structure on the Hypermutability of Immunoglobulin Genes. Immunity, 2002, 16, 123-134.	6.6	76
148	Rapid divergence in expression between duplicate genes inferred from microarray data. Trends in Genetics, 2002, 18, 609-613.	2.9	286
149	MERLIN...and the Geneticist's Stone?. Nature Genetics, 2002, 30, 3-4.	9.4	13
150	A genome-wide scan for preeclampsia in the Netherlands. European Journal of Human Genetics, 2001, 9, 758-764.	1.4	140
151	A frameshift mutation in NOD2 associated with susceptibility to Crohn's disease. Nature, 2001, 411, 603-606.	13.7	4,589
152	On a Randomization Procedure. American Journal of Human Genetics, 2000, 67, 1352-1355.	2.6	4
153	A Genome-Wide Scan Reveals a Maternal Susceptibility Locus for Pre-Eclampsia on Chromosome 2p13. Human Molecular Genetics, 1999, 8, 1799-1805.	1.4	196
154	Loci on chromosomes 2 (NIDDM1) and 15 interact to increase susceptibility to diabetes in Mexican Americans. Nature Genetics, 1999, 21, 213-215.	9.4	374
155	[Multipoint Linkage Analysis Using Affected Relative Pairs and Partially Informative Markers]: Discussion. Biometrics, 1998, 54, 1271.	0.8	5
156	Identification of novel susceptibility loci for inflammatory bowel disease on chromosomes 1p, 3q, and 4q: Evidence for epistasis between 1p and IBD1. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 7502-7507.	3.3	366