Stefan Schreiber

List of Publications by Year
in descending order

140 papers	50,317 citations	7672 79 h-index	11608 140 g-index
147 all docs	147 docs citations	147 times ranked	68310 citing authors

#	Article	IF	Citations
1	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. Human Molecular Genetics, 2021, 30, 356-369.	1.4	19
2	TYK2 inhibition and its potential in the treatment of chronic inflammatory immune diseases. JDDG - Journal of the German Society of Dermatology, 2021, 19, 1409-1420.	0.4	9
3	Case-only analysis of geneâ€“gene interactions in inflammatory bowel disease. Scandinavian Journal of Gastroenterology, 2020, 55, 897-906.	0.6	2
4	Risk for development of inflammatory bowel disease under inhibition of interleukin 17: A systematic review and meta-analysis. PLoS ONE, 2020, 15, e0233781.	1.1	32
5	Identifying Crohnâ€™s disease signal from variome analysis. Genome Medicine, 2019, 11, 59.	3.6	21
6	Metabolic Functions of Gut Microbes Associate With Efficacy ofÂTumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. Gastroenterology, 2019, 157, 1279-1292.e11.	0.6	180
7	Missense variants in NOX1 and p22phox in a case of very-early-onset inflammatory bowel disease are functionally linked to NOD2. Journal of Physical Education and Sports Management, 2019, 5, a002428.	0.5	13
8	Ulcerative Colitis: Shifting Sands. Drugs in R and D, 2019, 19, 227-234.	1.1	13
9	Incidence rates of inflammatory bowel disease in patients with psoriasis, psoriatic arthritis and ankylosing spondylitis treated with secukinumab: a retrospective analysis of pooled data from 21 clinical trials. Annals of the Rheumatic Diseases, 2019, 78, 473-479.	0.5	143
10	Small bowel capsule endoscopy in ulcerative colitis: the capcolitis study: a prospective observational study. European Journal of Gastroenterology and Hepatology, 2019, 31, 766-772.	0.8	2
11	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. Gut, 2018, 67, 1517-1524.	6.1	42
12	ATG16L1 orchestrates interleukin-22 signaling in the intestinal epithelium via cGASâ€“STING. Journal of Experimental Medicine, 2018, 215, 2868-2886.	4.2	122
13	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
14	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	1.5	66
15	Uncoupling of mucosal gene regulation, mRNA splicing and adherent microbiota signatures in inflammatory bowel disease. Gut, 2017, 66, 2087-2097.	6.1	81
16	Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. Scientific Reports, 2017, 7, 45652.	1.6	48
17	Genetic interplay between human longevity and metabolic pathways â€” a largeâ€scale <scp>eQTL</scp> study. Aging Cell, 2017, 16, 716-725.	3.0	14
18	A haplotype block downstream of plasminogen is associated with chronic and aggressive periodontitis. Journal of Clinical Periodontology, 2017, 44, 962-970.	2.3	16

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19	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. Nature Genetics, 2017, 49, 269-273.	9.4	230
20	Genome-wide rare copy number variation screening in ulcerative colitis identifies potential susceptibility loci. BMC Medical Genetics, 2016, 17, 26.	2.1	14
21	Haplotype synthesis analysis reveals functional variants underlying known genome-wide associated susceptibility loci. Bioinformatics, 2016, 32, 2136-2142.	1.8	2
22	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
23	Pooled Resequencing of 122 Ulcerative Colitis Genes in a Large Dutch Cohort Suggests Population-Specific Associations of Rare Variants in MUC2. PLoS ONE, 2016, 11, e0159609.	1.1	21
24	Identification of Immune-Relevant Factors Conferring Sarcoidosis Genetic Risk. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 727-736.	2.5	94
25	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. American Journal of Human Genetics, 2015, 96, 104-120.	2.6	163
26	Psoriasis and Cardiometabolic Traits: Modest Association but Distinct Genetic Architectures. Journal of Investigative Dermatology, 2015, 135, 1283-1293.	0.3	56
27	Genetic Evidence for PLASMINOGEN as a Shared Genetic Risk Factor of Coronary Artery Disease and Periodontitis. Circulation: Cardiovascular Genetics, 2015, 8, 159-167.	5.1	74
28	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
29	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
30	Genome-wide association study identifies multiple susceptibility loci for glioma. Nature Communications, 2015, 6, 8559.	5.8	112
31	XIAP variants in male Crohn's disease. Gut, 2015, 64, 66-76.	6.1	133
32	Early-onset Crohnâ€™s disease and autoimmunity associated with a variant in CTLA-4. Gut, 2015, 64, 1889-1897.	6.1	106
33	Sparse Modeling Reveals miRNA Signatures for Diagnostics of Inflammatory Bowel Disease. PLoS ONE, 2015, 10, e0140155.	1.1	31
34	Refinement of the MHC Risk Map in a Scandinavian Primary Sclerosing Cholangitis Population. PLoS ONE, 2014, 9, e114486.	1.1	24
35	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. European Heart Journal, 2014, 35, 1069-1077.	1.0	137
36	Genetics of Sarcoidosis. Seminars in Respiratory and Critical Care Medicine, 2014, 35, 296-306.	0.8	49

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37	A large candidateâ€gene association study suggests genetic variants at <scp>IRF</scp>5 and <scp>PRDM</scp>1 to be associated with aggressive periodontitis. Journal of Clinical Periodontology, 2014, 41, 1122-1131.	2.3	24
38	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
39	Whole genome and exome sequencing of monozygotic twins discordant for Crohnâ€™s disease. BMC Genomics, 2014, 15, 564.	1.2	39
40	Mitochondrial DNA Variants in Obesity. PLoS ONE, 2014, 9, e94882.	1.1	26
41	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
42	Dysfunctional nitric oxide signalling increases risk of myocardial infarction. Nature, 2013, 504, 432-436.	13.7	230
43	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347.	0.6	149
44	Epigenetics of Inflammatory Bowel Disease. , 2013, , 171-187.		0
45	The large non-coding RNA ANRIL, which is associated with atherosclerosis, periodontitis and several forms of cancer, regulates ADIPOR1, VAMP3 and C11ORF10. Human Molecular Genetics, 2013, 22, 4516-4527.	1.4	183
46	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
47	Paneth cells as a site of origin for intestinal inflammation. Nature, 2013, 503, 272-276.	13.7	605
48	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
49	Genetic factors conferring an increased susceptibility to develop Crohn's disease also influence disease phenotype: results from the IBDchip European Project. Gut, 2013, 62, 1556-1565.	6.1	221
50	Genome-wide association analysis in Primary sclerosing cholangitis and ulcerative colitis identifies risk loci atGPR35andTCF4. Hepatology, 2013, 58, 1074-1083.	3.6	150
51	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
52	High-density genotyping study identifies four new susceptibility loci for atopic dermatitis. Nature Genetics, 2013, 45, 808-812.	9.4	167
53	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	9.4	339
54	NOD2 Mutations Affect Muramyl Dipeptide Stimulation of Human B Lymphocytes and Interact with Other IBD-Associated Genes. Digestive Diseases and Sciences, 2013, 58, 2599-2607.	1.1	12

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55	Genome-wide association analysis reveals 12q13.3â€“q14.1 as new risk locus for sarcoidosis. European Respiratory Journal, 2013, 41, 888-900.	3.1	43
56	Deep Resequencing of GWAS Loci Identifies Rare Variants in CARD9, IL23R and RNF186 That Are Associated with Ulcerative Colitis. PLoS Genetics, 2013, 9, e1003723.	1.5	185
57	Replication Study of Ulcerative Colitis Risk Loci in a Lithuanianâ€“Latvian Caseâ€“Control Sample. Inflammatory Bowel Diseases, 2013, 19, 2349-2355.	0.9	10
58	Common obesity risk alleles in childhood attentionâ€deficit/hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 295-305.	1.1	77
59	Validation of reported genetic risk factors for periodontitis in a largeâ€scale replication study. Journal of Clinical Periodontology, 2013, 40, 563-572.	2.3	74
60	Genetic and functional identification of the likely causative variant for cholesterol gallstone disease at theABCG5/8lithogenic locus. Hepatology, 2013, 57, 2407-2417.	3.6	74
61	A functional methylome map of ulcerative colitis. Genome Research, 2012, 22, 2130-2137.	2.4	116
62	A Novel Sarcoidosis Risk Locus for Europeans on Chromosome 11q13.1. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 877-885.	2.5	51
63	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
64	Accurate variant detection across non-amplified and whole genome amplified DNA using targeted next generation sequencing. BMC Genomics, 2012, 13, 500.	1.2	23
65	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
66	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
67	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	9.4	848
68	Risk factors in German twins with inflammatory bowel disease: Results of a questionnaire-based survey. Journal of Crohn's and Colitis, 2012, 6, 29-42.	0.6	33
69	Improving mapping and SNP-calling performance in multiplexed targeted next-generation sequencing. BMC Genomics, 2012, 13, 417.	1.2	7
70	Limited Evidence for Parent-of-Origin Effects in Inflammatory Bowel Disease Associated Loci. PLoS ONE, 2012, 7, e45287.	1.1	10
71	A Genome-Wide Association Study for Coronary Artery Disease Identifies a Novel Susceptibility Locus in the Major Histocompatibility Complex. Circulation: Cardiovascular Genetics, 2012, 5, 217-225.	5.1	125
72	No association between NOD2 variants and Parkinson's disease. Movement Disorders, 2012, 27, 1191-1192.	2.2	10

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73	Combined Analysis of Genome-wide Association Studies for Crohn Disease and Psoriasis Identifies Seven Shared Susceptibility Loci. American Journal of Human Genetics, 2012, 90, 636-647.	2.6	290
74	Genome-Wide Meta-Analysis of Psoriatic Arthritis Identifies Susceptibility Locus at REL. Journal of Investigative Dermatology, 2012, 132, 1133-1140.	0.3	99
75	A case-only study of gene-environment interaction between genetic susceptibility variants in NOD2 and cigarette smoking in Crohn's disease aetiology. BMC Medical Genetics, 2012, 13, 14.	2.1	22
76	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
77	Colonic mucosa-associated microbiota is influenced by an interaction of Crohn disease and FUT2 (Secretor) genotype. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19030-19035.	3.3	304
78	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
79	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
80	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
81	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
82	The complex interplay of NOD-like receptors and the autophagy machinery in the pathophysiology of Crohn disease. European Journal of Cell Biology, 2011, 90, 593-602.	1.6	32
83	Genome-wide association study identifies a new locus for coronary artery disease on chromosome 10p11.23. European Heart Journal, 2011, 32, 158-168.	1.0	124
84	Genomeâ€wide association study in German patients with attention deficit/hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 888-897.	1.1	76
85	Rare Copy Number Variation Discovery and Cross-Disorder Comparisons Identify Risk Genes for ADHD. Science Translational Medicine, 2011, 3, 95ra75.	5.8	304
86	Genetic Association of Nonsynonymous Variants of the IL23R with Familial and Sporadic Inflammatory Bowel Disease in Women. Digestive Diseases and Sciences, 2010, 55, 739-746.	1.1	19
87	Investigation of genetic susceptibility factors for human longevity â€“ A targeted nonsynonymous SNP study. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 694, 13-19.	0.4	16
88	Role of GRM4 in idiopathic generalized epilepsies analysed by genetic association and sequence analysis. Epilepsy Research, 2010, 89, 319-326.	0.8	19
89	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
90	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). Nature Genetics, 2010, 42, 292-294.	9.4	177

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91	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
92	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. Nature Genetics, 2010, 42, 991-995.	9.4	331
93	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	9.4	2,284
94	Mutational Characterization of the Bile Acid Receptor TGR5 in Primary Sclerosing Cholangitis. PLoS ONE, 2010, 5, e12403.	1.1	106
95	Recurrent microdeletions at 15q11.2 and 16p13.11 predispose to idiopathic generalized epilepsies. Brain, 2010, 133, 23-32.	3.7	406
96	Genome-Wide Copy Number Variation in Epilepsy: Novel Susceptibility Loci in Idiopathic Generalized and Focal Epilepsies. PLoS Genetics, 2010, 6, e1000962.	1.5	414
97	Disruption at the PTCHD1 Locus on Xp22.11 in Autism Spectrum Disorder and Intellectual Disability. Science Translational Medicine, 2010, 2, 49ra68.	5.8	178
98	A Genome-Wide Linkage Analysis in 181 German Sarcoidosis Families Using Clustered Biallelic Markers. Chest, 2010, 138, 151-157.	0.4	20
99	OCTN1 variant L503F is associated with familial and sporadic inflammatory bowel disease. Journal of Crohn's and Colitis, 2010, 4, 132-138.	0.6	20
100	NOD2,IL23RandATG16L1polymorphisms in Lithuanian patients with inflammatory bowel disease. World Journal of Gastroenterology, 2010, 16, 359.	1.4	23
101	G Protein-Coupled Receptor 43 Is Essential for Neutrophil Recruitment during Intestinal Inflammation. Journal of Immunology, 2009, 183, 7514-7522.	0.4	308
102	A functional EXO1 promoter variant is associated with prolonged life expectancy in centenarians. Mechanisms of Ageing and Development, 2009, 130, 691-699.	2.2	43
103	Investigation of the colorectal cancer susceptibility region on chromosome 8q24.21 in a large German caseâ€control sample. International Journal of Cancer, 2009, 124, 75-80.	2.3	44
104	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
105	Genome-wide scan reveals association of psoriasis with IL-23 and NF-Î²B pathways. Nature Genetics, 2009, 41, 199-204.	9.4	1,229
106	Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. Nature Genetics, 2009, 41, 283-285.	9.4	427
107	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nature Genetics, 2009, 41, 1182-1190.	9.4	481
108	Genome-wide association study reveals genetic risk underlying Parkinson's disease. Nature Genetics, 2009, 41, 1308-1312.	9.4	1,745

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109	Towards a molecular risk mapâ€"Recent advances on the etiology of inflammatory bowel disease. Seminars in Immunology, 2009, 21, 334-345.	2.7	70
110	A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. Human Molecular Genetics, 2009, 18, 3516-3524.	1.4	76
111	Confirmation of Multiple Crohn's Disease Susceptibility Loci in a Large Dutchâ€"Belgian Cohort. American Journal of Gastroenterology, 2009, 104, 630-638.	0.2	111
112	Genetic Risk Profiling and Prediction of Disease Course in Crohn's Disease Patients. Clinical Gastroenterology and Hepatology, 2009, 7, 972-980.e2.	2.4	138
113	Confirmation of Multiple CrohnÊ¼s Disease Susceptibility Loci in a Large Dutch-Belgian Cohort. American Journal of Gastroenterology, 2009, 104, 630-638.	0.2	23
114	Epidemiology of inflammatory bowel disease in a German twin cohort: Results of a nationwide study. Inflammatory Bowel Diseases, 2008, 14, 968-976.	0.9	137
115	Structural Variation of Chromosomes in Autism Spectrum Disorder. American Journal of Human Genetics, 2008, 82, 477-488.	2.6	1,641
116	Replication of signals from recent studies of Crohn's disease identifies previously unknown disease loci for ulcerative colitis. Nature Genetics, 2008, 40, 713-715.	9.4	333
117	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. Nature Genetics, 2008, 40, 1319-1323.	9.4	534
118	Genome-Wide Association Analysis in Sarcoidosis and Crohn's Disease Unravels a Common Susceptibility Locus on 10p12.2. Gastroenterology, 2008, 135, 1207-1215.	0.6	85
119	XBP1 Links ER Stress to Intestinal Inflammation and Confers Genetic Risk for Human Inflammatory Bowel Disease. Cell, 2008, 134, 743-756.	13.5	1,225
120	Genetics of Sarcoidosis. Clinics in Chest Medicine, 2008, 29, 391-414.	0.8	80
121	Expression signatures, barriers and beyond: the role of oxidative stress in murine colitis and human inflammatory bowel disease revisited. European Journal of Gastroenterology and Hepatology, 2008, 20, 496-499.	0.8	4
122	Lifelong Reduction of LDL-Cholesterol Related to a Common Variant in the LDL-Receptor Gene Decreases the Risk of Coronary Artery Diseaseâ€"A Mendelian Randomisation Study. PLoS ONE, 2008, 3, e2986.	1.1	137
123	Genome-wide association study for Crohn's disease in the Quebec Founder Population identifies multiple validated disease loci. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14747-14752.	3.3	197
124	A Nonsynonymous SNP in ATG16L1 Predisposes to Ileal Crohnâ€™s Disease and Is Independent of CARD15 and IBD5. Gastroenterology, 2007, 132, 1665-1671.	0.6	268
125	Diagnostics of Inflammatory Bowel Disease. Gastroenterology, 2007, 133, 1670-1689.	0.6	333
126	Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. PLoS ONE, 2007, 2, e691.	1.1	123

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127	Association analyses of GIP and GIPR polymorphisms with traits of the metabolic syndrome. Molecular Nutrition and Food Research, 2007, 51, 1046-1052.	1.5	37
128	A genome-wide association scan of nonsynonymous SNPs identifies a susceptibility variant for Crohn disease in ATG16L1. Nature Genetics, 2007, 39, 207-211.	9.4	1,712
129	Investigation of the Lith6 candidate genes APOBEC1 and PPARG in human gallstone disease. Liver International, 2007, 27, 910-919.	1.9	6
130	PopGen â€“ BevÃ¶lkerungsbasierte Rekrutierung von Patienten und Kontrollen fÃ¼r die Untersuchung komplexer Genotyp-PhÃnotyp-Beziehungen (PopGen â€“ Population-based Recruitment of Patients and) Tj ETQq0 0 0 rgBT /Overlock 10 0.6 0 2007, 49, 374-380.		
131	PopGen: Population-Based Recruitment of Patients and Controls for the Analysis of Complex Genotype-Phenotype Relationships. Public Health Genomics, 2006, 9, 55-61.	0.6	265
132	GENOMIZER: an integrated analysis system for genome-wide association data. Human Mutation, 2006, 27, 583-588.	1.1	24
133	InSNP: A tool for automated detection and visualization of SNPs and InDels. Human Mutation, 2005, 26, 11-19.	1.1	40
134	Genetic variation in DLG5 is associated with inflammatory bowel disease. Nature Genetics, 2004, 36, 476-480.	9.4	443
135	Stratification by CARD15 variant genotype in a genome-wide search for inflammatory bowel disease susceptibility loci. Human Genetics, 2003, 113, 514-521.	1.8	15
136	Haplotype structure and association to Crohn's disease of CARD15 mutations in two ethnically divergent populations. European Journal of Human Genetics, 2003, 11, 6-16.	1.4	216
137	Evidence for a NOD2-independent susceptibility locus for inflammatory bowel disease on chromosome 16p. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 321-326.	3.3	106
138	Association between insertion mutation in NOD2 gene and Crohn's disease in German and British populations. Lancet, The, 2001, 357, 1925-1928.	6.3	1,071
139	An integrated system for high throughput TaqManTM based SNP genotyping. Bioinformatics, 2001, 17, 654-655.	1.8	98
140	A Genomewide Analysis Provides Evidence for Novel Linkages in Inflammatory Bowel Disease in a Large European Cohort. American Journal of Human Genetics, 1999, 64, 808-816.	2.6	349