John A Todd

List of Publications by Citations

308 papers	38,950 citations	93 h-index	194 g-index
328 ext. papers	43,669 ext. citations	14.2 avg, IF	6.75 L-index

#	Paper	IF	Citations
308	HLA-DQ beta gene contributes to susceptibility and resistance to insulin-dependent diabetes mellitus. *Nature*, **1987**, 329, 599-604	50.4	1860
307	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. *Nature*, **2003**, 423, 506-11	50.4	1774
306	Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. *Nature Genetics*, **2009**, 41, 703-7	36.3	1298
305	A genome-wide search for human type 1 diabetes susceptibility genes. *Nature*, **1994**, 371, 130-6	50.4	1175
304	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. *Nature Genetics*, **2007**, 39, 857-64	36.3	1159
303	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
302	Haplotype tagging for the identification of common disease genes. *Nature Genetics*, **2001**, 29, 233-7	36.3	1014
301	Genome-wide association studies: theoretical and practical concerns. *Nature Reviews Genetics*, **2005**, 6, 109-18	30.1	881
300	Rare variants of IFIH1, a gene implicated in antiviral responses, protect against type 1 diabetes. *Science*, **2009**, 324, 387-9	33.3	772
299	Insulin expression in human thymus is modulated by INS VNTR alleles at the IDDM2 locus. *Nature Genetics*, **1997**, 15, 289-92	36.3	671
298	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
297	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nature Genetics*, **2006**, 38, 1166-72	36.3	618
296	Genetic analysis of autoimmune disease. *Cell*, **1996**, 85, 311-8	56.2	610
295	The CTLA-4 gene region of chromosome 2q33 is linked to, and associated with, type 1 diabetes. Belgian Diabetes Registry. *Human Molecular Genetics*, **1996**, 5, 1075-80	5.6	560
294	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19	56.2	556
293	Shared and distinct genetic variants in type 1 diabetes and celiac disease. *New England Journal of Medicine*, **2008**, 359, 2767-77	59.2	546
292	A genome-wide association study of nonsynonymous SNPs identifies a type 1 diabetes locus in the interferon-induced helicase (IFIH1) region. *Nature Genetics*, **2006**, 38, 617-9	36.3	544

291	Genomic atlas of the human plasma proteome. *Nature*, **2018**, 558, 73-79	50.4	529
290	HLA DR-DQ haplotypes and genotypes and type 1 diabetes risk: analysis of the type 1 diabetes genetics consortium families. *Diabetes*, **2008**, 57, 1084-92	0.9	522
289	Genetic analysis of autoimmune type 1 diabetes mellitus in mice. *Nature*, **1991**, 351, 542-7	50.4	466
288	Population structure, differential bias and genomic control in a large-scale, case-control association study. *Nature Genetics*, **2005**, 37, 1243-6	36.3	458
287	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. *Nature*, **2007**, 450, 887-92	50.4	421
286	Towards construction of a high resolution map of the mouse genome using PCR-analysed microsatellites. *Nucleic Acids Research*, **1990**, 18, 4123-30	20.1	415
285	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. *Nature Genetics*, **2015**, 47, 381-6	36.3	414
284	Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genetics*, **2011**, 7, e1002254	6	413
283	Replication of an association between the lymphoid tyrosine phosphatase locus (LYP/PTPN22) with type 1 diabetes, and evidence for its role as a general autoimmunity locus. *Diabetes*, **2004**, 53, 3020-3	0.9	401
282	Meta-analysis of genome-wide association study data identifies additional type 1 diabetes risk loci. *Nature Genetics*, **2008**, 40, 1399-401	36.3	400
281	Etiology of type 1 diabetes. *Immunity*, **2010**, 32, 457-67	32.3	378
280	Detecting disease associations due to linkage disequilibrium using haplotype tags: a class of tests and the determinants of statistical power. *Human Heredity*, **2003**, 56, 18-31	1.1	367
279	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
278	Large-scale genetic fine mapping and genotype-phenotype associations implicate polymorphism in the IL2RA region in type 1 diabetes. *Nature Genetics*, **2007**, 39, 1074-82	36.3	326
277	Towards fully automated genome-wide polymorphism screening. *Nature Genetics*, **1995**, 9, 341-2	36.3	320
276	Interleukin-2 gene variation impairs regulatory T cell function and causes autoimmunity. *Nature Genetics*, **2007**, 39, 329-37	36.3	306
275	A search for type 1 diabetes susceptibility genes in families from the United Kingdom. *Nature Genetics*, **1998**, 19, 297-300	36.3	287
274	Localization of a type 1 diabetes locus in the IL2RA/CD25 region by use of tag single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2005**, 76, 773-9	11	286

273	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. *Nature Communications*, **2015**, 6, 7000	17.4	268
272	Linkage and association of insulin gene VNTR regulatory polymorphism with polycystic ovary syndrome. *Lancet, The*, **1997**, 349, 986-90	40	254
271	Variation analysis and gene annotation of eight MHC haplotypes: the MHC Haplotype Project. *Immunogenetics*, **2008**, 60, 1-18	3.2	246
270	Association of the INS VNTR with size at birth. ALSPAC Study Team. Avon Longitudinal Study of Pregnancy and Childhood. *Nature Genetics*, **1998**, 19, 98-100	36.3	239
269	The imprinted DLK1-MEG3 gene region on chromosome 14q32.2 alters susceptibility to type 1 diabetes. *Nature Genetics*, **2010**, 42, 68-71	36.3	238
268	Complete MHC haplotype sequencing for common disease gene mapping. *Genome Research*, **2004**, 14, 1176-87	9.7	235
267	Human type 1 diabetes and the insulin gene: principles of mapping polygenes. *Annual Review of Genetics*, **1996**, 30, 343-70	14.5	234
266	Seven regions of the genome show evidence of linkage to type 1 diabetes in a consensus analysis of 767 multiplex families. *American Journal of Human Genetics*, **2001**, 69, 820-30	11	225
265	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. *Nature*, **2010**, 467, 460-4	50.4	224
264	Cell-specific protein phenotypes for the autoimmune locus IL2RA using a genotype-selectable human bioresource. *Nature Genetics*, **2009**, 41, 1011-5	36.3	224
263	Genetic control of autoimmunity in type 1 diabetes. *Trends in Immunology*, **1990**, 11, 122-9		224
262	Inherited variation in vitamin D genes is associated with predisposition to autoimmune disease type 1 diabetes. *Diabetes*, **2011**, 60, 1624-31	0.9	222
261	Genetics of type 1 diabetes: what's next?. *Diabetes*, **2010**, 59, 1561-71	0.9	218
260	Overexpression of the Cytokine BAFF and Autoimmunity Risk. *New England Journal of Medicine*, **2017**, 376, 1615-1626	59.2	198
259	Parameters for reliable results in genetic association studies in common disease. *Nature Genetics*, **2002**, 30, 149-50	36.3	198
258	Genome-wide association analysis of autoantibody positivity in type 1 diabetes cases. *PLoS Genetics* , **2011**, 7, e1002216	6	195
257	Type 1 diabetes: evidence for susceptibility loci from four genome-wide linkage scans in 1,435 multiplex families. *Diabetes*, **2005**, 54, 2995-3001	0.9	195
256	Cloning of a novel member of the low-density lipoprotein receptor family. *Gene*, **1998**, 216, 103-11	3.8	193

255	A type I interferon transcriptional signature precedes autoimmunity in children genetically at risk for type 1 diabetes. *Diabetes*, **2014**, 63, 2538-50	0.9	188
254	IL2RA genetic heterogeneity in multiple sclerosis and type 1 diabetes susceptibility and soluble interleukin-2 receptor production. *PLoS Genetics*, **2009**, 5, e1000322	6	183
253	Remapping the insulin gene/IDDM2 locus in type 1 diabetes. *Diabetes*, **2004**, 53, 1884-9	0.9	180
252	Genetic protection from the inflammatory disease type 1 diabetes in humans and animal models. *Immunity*, **2001**, 15, 387-95	32.3	173
251	Functional IL6R 358Ala allele impairs classical IL-6 receptor signaling and influences risk of diverse inflammatory diseases. *PLoS Genetics*, **2013**, 9, e1003444	6	170
250	Isolation and characterization of LRP6, a novel member of the low density lipoprotein receptor gene family. *Biochemical and Biophysical Research Communications*, **1998**, 248, 879-88	3.4	169
249	Type 1 diabetes in mice is linked to the interleukin-1 receptor and Lsh/Ity/Bcg genes on chromosome 1. *Nature*, **1991**, 353, 262-5	50.4	165
248	Metagenomics and personalized medicine. *Cell*, **2011**, 147, 44-56	56.2	164
247	The genetically isolated populations of Finland and sardinia may not be a panacea for linkage disequilibrium mapping of common disease genes. *Nature Genetics*, **2000**, 25, 320-3	36.3	164
246	Insulin VNTR allele-specific effect in type 1 diabetes depends on identity of untransmitted paternal allele. The IMDIAB Group. *Nature Genetics*, **1997**, 17, 350-2	36.3	163
245	Association of the vitamin D metabolism gene CYP27B1 with type 1 diabetes. *Diabetes*, **2007**, 56, 2616-21	0.9	163
244	The predisposition to type 1 diabetes linked to the human leukocyte antigen complex includes at least one non-class II gene. *American Journal of Human Genetics*, **1999**, 64, 793-800	11	163
243	Absolute risk of childhood-onset type 1 diabetes defined by human leukocyte antigen class II genotype: a population-based study in the United Kingdom. *Journal of Clinical Endocrinology and Metabolism*, **2004**, 89, 4037-43	5.6	162
242	Comparative high-resolution analysis of linkage disequilibrium and tag single nucleotide polymorphisms between populations in the vitamin D receptor gene. *Human Molecular Genetics*, **2004**, 13, 1633-9	5.6	161
241	Statistical false positive or true disease pathway?. *Nature Genetics*, **2006**, 38, 731-3	36.3	158
240	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. *Nature*, **2013**, 498, 232-5	50.4	156
239	Evaluation of single nucleotide polymorphism typing with invader on PCR amplicons and its automation. *Genome Research*, **2000**, 10, 330-43	9.7	155
238	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. *Nature Genetics*, **2015**, 47, 898-905	36.3	154

237	Additional microsatellite markers for mouse genome mapping. *Mammalian Genome*, **1991**, 1, 273-82	3.2	153
236	Genome-wide analysis of allelic expression imbalance in human primary cells by high-throughput transcriptome resequencing. *Human Molecular Genetics*, **2010**, 19, 122-34	5.6	152
235	Type 1 diabetes-associated IL2RA variation lowers IL-2 signaling and contributes to diminished CD4+CD25+ regulatory T cell function. *Journal of Immunology*, **2012**, 188, 4644-53	5.3	147
234	Panning for gold: genome-wide scanning for linkage in type 1 diabetes. *Human Molecular Genetics*, **1996**, 5 Spec No, 1443-8	5.6	145
233	Blood and islet phenotypes indicate immunological heterogeneity in type 1 diabetes. *Diabetes*, **2014**, 63, 3835-45	0.9	144
232	The NOD Idd9 genetic interval influences the pathogenicity of insulitis and contains molecular variants of Cd30, Tnfr2, and Cd137. *Immunity*, **2000**, 13, 107-15	32.3	143
231	Genetic analysis of completely sequenced disease-associated MHC haplotypes identifies shuffling of segments in recent human history. *PLoS Genetics*, **2006**, 2, e9	6	140
230	A correlation between the relative predisposition of MHC class II alleles to type 1 diabetes and the structure of their proteins. *Human Molecular Genetics*, **2001**, 10, 2025-37	5.6	140
229	IDDM2-VNTR-encoded susceptibility to type 1 diabetes: dominant protection and parental transmission of alleles of the insulin gene-linked minisatellite locus. *Journal of Autoimmunity*, **1996**, 9, 415-21	15.5	137
228	The insulin gene VNTR, type 2 diabetes and birth weight. *Nature Genetics*, **1999**, 21, 262-3	36.3	131
227	The generation of a library of PCR-analyzed microsatellite variants for genetic mapping of the mouse genome. *Genomics*, **1991**, 10, 874-81	4.3	130
226	Regression mapping of association between the human leukocyte antigen region and Graves disease. *American Journal of Human Genetics*, **2005**, 76, 157-63	11	121
225	Seven newly identified loci for autoimmune thyroid disease. *Human Molecular Genetics*, **2012**, 21, 5202-85.6		120
224	Type 1 diabetes genes and pathways shared by humans and NOD mice. *Journal of Autoimmunity*, **2005**, 25 Suppl, 29-33	15.5	118
223	Congenic mapping of the type 1 diabetes locus, Idd3, to a 780-kb region of mouse chromosome 3: identification of a candidate segment of ancestral DNA by haplotype mapping. *Genome Research*, **2000**, 10, 446-53	9.7	112
222	SARS-CoV-2 within-host diversity and transmission. *Science*, **2021**, 372,	33.3	110
221	A male-female bias in type 1 diabetes and linkage to chromosome Xp in MHC HLA-DR3-positive patients. *Nature Genetics*, **1998**, 19, 301-2	36.3	107
220	Unbiased application of the transmission/disequilibrium test to multilocus haplotypes. *American Journal of Human Genetics*, **2000**, 66, 2009-12	11	102

219	The Type 1 Diabetes Genetics Consortium. *Annals of the New York Academy of Sciences*, **2006**, 1079, 1-8	6.5	98
218	Statistical colocalization of genetic risk variants for related autoimmune diseases in the context of common controls. *Nature Genetics*, **2015**, 47, 839-46	36.3	97
217	Integration of disease association and eQTL data using a Bayesian colocalisation approach highlights six candidate causal genes in immune-mediated diseases. *Human Molecular Genetics*, **2015**, 24, 3305-13	5.6	94
216	Fine mapping, gene content, comparative sequencing, and expression analyses support Ctla4 and Nramp1 as candidates for Idd5.1 and Idd5.2 in the nonobese diabetic mouse. *Journal of Immunology* , **2004**, 173, 164-73	5.3	94
215	FUT2 nonsecretor status links type 1 diabetes susceptibility and resistance to infection. *Diabetes*, **2011**, 60, 3081-4	0.9	92
214	Genetic analysis of adult-onset autoimmune diabetes. *Diabetes*, **2011**, 60, 2645-53	0.9	92
213	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. *Human Molecular Genetics*, **2012**, 21, 322-33	5.6	91
212	Association of the interleukin-2 receptor alpha (IL-2Ralpha)/CD25 gene region with Graves' disease using a multilocus test and tag SNPs. *Clinical Endocrinology*, **2007**, 66, 508-12	3.4	91
211	Major factors influencing linkage disequilibrium by analysis of different chromosome regions in distinct populations: demography, chromosome recombination frequency and selection. *Human Molecular Genetics*, **2000**, 9, 2947-57	5.6	89
210	From genome to aetiology in a multifactorial disease, type 1 diabetes. *BioEssays*, **1999**, 21, 164-74	4.1	89
209	IL-21 production by CD4+ effector T cells and frequency of circulating follicular helper T cells are increased in type 1 diabetes patients. *Diabetologia*, **2015**, 58, 781-90	10.3	86
208	A human type 1 diabetes susceptibility locus maps to chromosome 21q22.3. *Diabetes*, **2008**, 57, 2858-61	0.9	85
207	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. *Nature Genetics*, **2018**, 50, 1366-1374	36.3	82
206	A molecular basis for genetic susceptibility to insulin-dependent diabetes mellitus. *Trends in Genetics*, **1988**, 4, 129-34	8.5	80
205	Genetic control of autoimmunity: protection from diabetes, but spontaneous autoimmune biliary disease in a nonobese diabetic congenic strain. *Journal of Immunology*, **2004**, 173, 2315-23	5.3	79
204	Multifactorial inheritance in type 1 diabetes. *Trends in Genetics*, **1995**, 11, 499-504	8.5	79
203	Genome-wide scan for linkage to type 1 diabetes in 2,496 multiplex families from the Type 1 Diabetes Genetics Consortium. *Diabetes*, **2009**, 58, 1018-22	0.9	78
202	Regulatory T Cell Responses in Participants with Type 1 Diabetes after a Single Dose of Interleukin-2: A Non-Randomised, Open Label, Adaptive Dose-Finding Trial. *PLoS Medicine*, **2016**, 13, e1002139	11.6	76

201	Prevalence of abnormal lipid profiles and the relationship with the development of microalbuminuria in adolescents with type 1 diabetes. *Diabetes Care*, **2009**, 32, 658-63	14.6	74
200	Proteome-wide analysis of disease-associated SNPs that show allele-specific transcription factor binding. *PLoS Genetics*, **2012**, 8, e1002982	6	74
199	A novel and major association of HLA-C in Graves' disease that eclipses the classical HLA-DRB1 effect. *Human Molecular Genetics*, **2007**, 16, 2149-53	5.6	72
198	Statistical colocalization of monocyte gene expression and genetic risk variants for type 1 diabetes. *Human Molecular Genetics*, **2012**, 21, 2815-24	5.6	71
197	PTPN22 Trp620 explains the association of chromosome 1p13 with type 1 diabetes and shows a statistical interaction with HLA class II genotypes. *Diabetes*, **2008**, 57, 1730-7	0.9	69
196	Mononucleotide repeats are an abundant source of length variants in mouse genomic DNA. *Mammalian Genome*, **1991**, 1, 206-10	3.2	67
195	Reduced expression of IFIH1 is protective for type 1 diabetes. *PLoS ONE*, **2010**, 5, e12646	3.7	66
194	Analysis of the vitamin D receptor gene sequence variants in type 1 diabetes. *Diabetes*, **2004**, 53, 2709-12	0.9	65
193	Common polymorphism in H19 associated with birthweight and cord blood IGF-II levels in humans. *BMC Genetics*, **2005**, 6, 22	2.6	65
192	Experimental aspects of copy number variant assays at CCL3L1. *Nature Medicine*, **2009**, 15, 1115-7	50.5	63
191	Differential glycosylation of interleukin 2, the molecular basis for the NOD Idd3 type 1 diabetes gene?. *Cytokine*, **2000**, 12, 477-82	4	62
190	T1DBase: update 2011, organization and presentation of large-scale data sets for type 1 diabetes research. *Nucleic Acids Research*, **2011**, 39, D997-1001	20.1	61
189	Statistical independence of the colocalized association signals for type 1 diabetes and RPS26 gene expression on chromosome 12q13. *Biostatistics*, **2009**, 10, 327-34	3.7	60
188	Transmission ratio distortion at the INS-IGF2 VNTR. *Nature Genetics*, **1999**, 22, 324-5	36.3	60
187	A method to address differential bias in genotyping in large-scale association studies. *PLoS Genetics* , **2007**, 3, e74	6	59
186	Association of IL13 with total IgE: evidence against an inverse association of atopy and diabetes. *Journal of Allergy and Clinical Immunology*, **2006**, 117, 1306-13	11.5	57
185	T1DBase: integration and presentation of complex data for type 1 diabetes research. *Nucleic Acids Research*, **2007**, 35, D742-6	20.1	56
184	Maternal-fetal interactions and birth order influence insulin variable number of tandem repeats allele class associations with head size at birth and childhood weight gain. *Diabetes*, **2004**, 53, 1128-33	0.9	56

183	Assessing the validity of the association between the SUMO4 M55V variant and risk of type 1 diabetes. *Nature Genetics*, **2005**, 37, 110-1; author reply 112-3	36.3	56
182	The impact of proinflammatory cytokines on the □cell regulatory landscape provides insights into the genetics of type 1 diabetes. *Nature Genetics*, **2019**, 51, 1588-1595	36.3	55
181	Analysis of association of the TIRAP (MAL) S180L variant and tuberculosis in three populations. *Nature Genetics*, **2008**, 40, 261-2; author reply 262-3	36.3	55
180	Haplotype structure, LD blocks, and uneven recombination within the LRP5 gene. *Genome Research*, **2003**, 13, 845-55	9.7	54
179	Statistical modeling of interlocus interactions in a complex disease: rejection of the multiplicative model of epistasis in type 1 diabetes. *Genetics*, **2001**, 158, 357-67	4	54
178	Gene-gene interactions in the NOD mouse model of type 1 diabetes. *Advances in Immunology*, **2008**, 100, 151-75	5.6	53
177	Childhood adiposity and risk of type 1 diabetes: A Mendelian randomization study. *PLoS Medicine*, **2017**, 14, e1002362	11.6	53
176	Fine mapping of the diabetes-susceptibility locus, IDDM4, on chromosome 11q13. *American Journal of Human Genetics*, **1998**, 63, 547-56	11	51
175	Expression of the type I diabetes-associated gene LRP5 in macrophages, vitamin A system cells, and the Islets of Langerhans suggests multiple potential roles in diabetes. *Journal of Histochemistry and Cytochemistry*, **2000**, 48, 1357-68	3.4	51
174	Ten years of genetics and genomics: what have we achieved and where are we heading?. *Nature Reviews Genetics*, **2010**, 11, 723-33	30.1	50
173	Genetic and functional association of the immune signaling molecule 4-1BB (CD137/TNFRSF9) with type 1 diabetes. *Journal of Autoimmunity*, **2005**, 25, 13-20	15.5	50
172	Analysis of the CD3 gene region and type 1 diabetes: application of fluorescence-based technology to linkage disequilibrium mapping. *Human Molecular Genetics*, **1995**, 4, 197-202	5.6	50
171	Evidence of gene-gene interaction and age-at-diagnosis effects in type 1 diabetes. *Diabetes*, **2012**, 61, 3012-7	0.9	49
170	Association of human endogenous retrovirus K-18 polymorphisms with type 1 diabetes. *Diabetes*, **2004**, 53, 852-4	0.9	49
169	Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. *Nucleic Acids Research*, **2021**, 49, D1311-D1320	20.1	49
168	Evidence that HLA class I and II associations with type 1 diabetes, autoantibodies to GAD and autoantibodies to IA-2, are distinct. *Diabetes*, **2011**, 60, 2635-44	0.9	48
167	Extreme clonality in lymphoblastoid cell lines with implications for allele specific expression analyses. *PLoS ONE*, **2008**, 3, e2966	3.7	48
166	A long-lived IL-2 mutein that selectively activates and expands regulatory T cells as a therapy for autoimmune disease. *Journal of Autoimmunity*, **2018**, 95, 1-14	15.5	48

165	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity. *Journal of Autoimmunity*, **2017**, 84, 75-86	15.5	46
164	Interactions between Idd5.1/Ctla4 and other type 1 diabetes genes. *Journal of Immunology*, **2007**, 179, 8341-9	5.3	46
163	No association between variation of the FOXP3 gene and common type 1 diabetes in the Sardinian population. *Diabetes*, **2004**, 53, 1911-4	0.9	46
162	The inter-regional distribution of HLA class II haplotypes indicates the suitability of the Sardinian population for case-control association studies in complex diseases. *Human Molecular Genetics*, **2000**, 9, 2959-65	5.6	46
161	Genetics of autoimmune disease. *Current Opinion in Immunology*, **1995**, 7, 786-92	7.8	45
160	The IL23R A/Gln381 allele promotes IL-23 unresponsiveness in human memory T-helper 17 cells and impairs Th17 responses in psoriasis patients. *Journal of Investigative Dermatology*, **2013**, 133, 2381-2389	4.3	44
159	A method for gene-based pathway analysis using genomewide association study summary statistics reveals nine new type 1 diabetes associations. *Genetic Epidemiology*, **2014**, 38, 661-70	2.6	43
158	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. *PLoS Genetics*, **2015**, 11, e1005272	6	42
157	Analysis of polymorphisms in 16 genes in type 1 diabetes that have been associated with other immune-mediated diseases. *BMC Medical Genetics*, **2006**, 7, 20	2.1	42
156	Beta-Cell Fragility As a Common Underlying Risk Factor in Type 1 and Type 2 Diabetes. *Trends in Molecular Medicine*, **2017**, 23, 181-194	11.5	42
155	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. *Genome Biology*, **2017**, 18, 165	18.3	41
154	Contrasting genetic association of IL2RA with SLE and ANCA-associated vasculitis. *BMC Medical Genetics*, **2009**, 10, 22	2.1	41
153	An allele of IKZF1 (Ikaros) conferring susceptibility to childhood acute lymphoblastic leukemia protects against type 1 diabetes. *Diabetes*, **2011**, 60, 1041-4	0.9	41
152	T1DBase, a community web-based resource for type 1 diabetes research. *Nucleic Acids Research*, **2005**, 33, D544-9	20.1	41
151	The derivation of highly germline-competent embryonic stem cells containing NOD-derived genome. *Diabetes*, **2003**, 52, 205-8	0.9	40
150	Approaches and advances in the genetic causes of autoimmune disease and their implications. *Nature Immunology*, **2018**, 19, 674-684	19.1	39
149	Tests for genetic interactions in type 1 diabetes: linkage and stratification analyses of 4,422 affected sib-pairs. *Diabetes*, **2011**, 60, 1030-40	0.9	39
148	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. *Nature Genetics*, **2011**, 44, 3-5	36.3	39

147	Saturation multipoint linkage mapping of chromosome 6q in type 1 diabetes. *Human Molecular Genetics*, **1996**, 5, 1071-4	5.6	39
146	Linkage and association mapping of the LRP5 locus on chromosome 11q13 in type 1 diabetes. *Human Genetics*, **2003**, 113, 99-105	6.3	38
145	Molecular genetics of diabetes mellitus. *Baillieres Clinical Endocrinology and Metabolism*, **1995**, 9, 631-56		38
144	Association of insulin gene VNTR polymorphism with polycystic ovary syndrome. *Lancet, The*, **1997**, 349, 1771-1772	40	37
143	The candidate genes TAF5L, TCF7, PDCD1, IL6 and ICAM1 cannot be excluded from having effects in type 1 diabetes. *BMC Medical Genetics*, **2007**, 8, 71	2.1	37
142	No evidence of association or interaction between the IL4RA, IL4, and IL13 genes in type 1 diabetes. *American Journal of Human Genetics*, **2005**, 76, 517-21	11	37
141	Association of intercellular adhesion molecule-1 gene with type 1 diabetes. *Lancet, The*, **2003**, 362, 1723-4	40	37
140	Next generation sequencing reveals the association of DRB3*02:02 with type 1 diabetes. *Diabetes*, **2013**, 62, 2618-22	0.9	35
139	Genetic association analyses of atopic illness and proinflammatory cytokine genes with type 1 diabetes. *Diabetes/Metabolism Research and Reviews*, **2011**, 27, 838-43	7.5	35
138	Genome bioinformatic analysis of nonsynonymous SNPs. *BMC Bioinformatics*, **2007**, 8, 301	3.6	35
137	Resequencing and association analysis of the SP110 gene in adult pulmonary tuberculosis. *Human Genetics*, **2007**, 121, 155-60	6.3	35
136	Natural Variation in Interleukin-2 Sensitivity Influences Regulatory T-Cell Frequency and Function in Individuals With Long-standing Type 1 Diabetes. *Diabetes*, **2015**, 64, 3891-902	0.9	34
135	Postthymic expansion in human CD4 naive T cells defined by expression of functional high-affinity IL-2 receptors. *Journal of Immunology*, **2013**, 190, 2554-66	5.3	34
134	Analysis of the type 2 diabetes-associated single nucleotide polymorphisms in the genes IRS1, KCNJ11, and PPARG2 in type 1 diabetes. *Diabetes*, **2004**, 53, 870-3	0.9	34
133	Divergence between genetic determinants of IGF2 transcription levels in leukocytes and of IDDM2-encoded susceptibility to type 1 diabetes. *Journal of Clinical Endocrinology and Metabolism*, **1998**, 83, 2933-9	5.6	34
132	Mutation of the glucagon receptor gene and diabetes mellitus in the UK: association or founder effect?. *Human Molecular Genetics*, **1995**, 4, 1609-12	5.6	33
131	A practical approach to identification of susceptibility genes for IDDM. *Diabetes*, **1992**, 41, 1029-34	0.9	33
130	La carte des microsatellites est arrivé! [The map of microsatellites has arrived!]. *Human Molecular Genetics*, **1992**, 1, 663-6	5.6	32

129	Oral insulin therapy for primary prevention of type 1 diabetes in infants with high genetic risk: the GPPAD-POInT (global platform for the prevention of autoimmune diabetes primary oral insulin trial) study protocol. *BMJ Open*, **2019**, 9, e028578	3	31
128	The sequence and gene characterization of a 400-kb candidate region for IDDM4 on chromosome 11q13. *Genomics*, **2001**, 72, 231-42	4.3	31
127	Differential expression of penicillin-binding protein structural genes duringBacillus subtilissporulation. *FEMS Microbiology Letters*, **1983**, 18, 197-202	2.9	31
126	Sequencing-based genotyping and association analysis of the MICA and MICB genes in type 1 diabetes. *Diabetes*, **2008**, 57, 1753-6	0.9	29
125	Investigating the utility of combining phi29 whole genome amplification and highly multiplexed single nucleotide polymorphism BeadArray genotyping. *BMC Biotechnology*, **2004**, 4, 15	3.5	29
124	Analysis of polymorphisms of the interleukin-18 gene in type 1 diabetes and Hardy-Weinberg equilibrium testing. *Diabetes*, **2006**, 55, 559-62	0.9	28
123	Fine-mapping, trans-ancestral and genomic analyses identify causal variants, cells, genes and drug targets for type 1 diabetes. *Nature Genetics*, **2021**, 53, 962-971	36.3	28
122	Genetic Variants Predisposing Most Strongly to Type 1 Diabetes Diagnosed Under Age 7 Years Lie Near Candidate Genes That Function in the Immune System and in Pancreatic Cells. *Diabetes Care* , **2020**, 43, 169-177	14.6	28
121	Rationale and study design of the Adaptive study of IL-2 dose on regulatory T cells in type 1 diabetes (DILT1D): a non-randomised, open label, adaptive dose finding trial. *BMJ Open*, **2014**, 4, e005559	3	26
120	Nonobese diabetic congenic strain analysis of autoimmune diabetes reveals genetic complexity of the Idd18 locus and identifies Vav3 as a candidate gene. *Journal of Immunology*, **2010**, 184, 5075-84	5.3	26
119	Neonatal and adult recent thymic emigrants produce IL-8 and express complement receptors CR1 and CR2. *JCI Insight*, **2017**, 2,	9.9	26
118	Identification of Cd101 as a susceptibility gene for Novosphingobium aromaticivorans-induced liver autoimmunity. *Journal of Immunology*, **2011**, 187, 337-49	5.3	25
117	Framework YAC contig anchored into a 3.2-Mb high-resolution physical map in proximal 11q13. *Genomics*, **1997**, 40, 13-23	4.3	25
116	Haplotype tag single nucleotide polymorphism analysis of the human orthologues of the rat type 1 diabetes genes Ian4 (Lyp/Iddm1) and Cblb. *Diabetes*, **2004**, 53, 505-9	0.9	25
115	Identification of a structurally distinct CD101 molecule encoded in the 950-kb Idd10 region of NOD mice. *Diabetes*, **2003**, 52, 1551-6	0.9	25
114	The usefulness of different density SNP maps for disease association studies of common variants. *Human Molecular Genetics*, **2003**, 12, 3145-9	5.6	25
113	HLA antigens and insulin-dependent diabetes. *Nature*, **1988**, 333, 710	50.4	25
112	Discovery of CD80 and CD86 as recent activation markers on regulatory T cells by protein-RNA single-cell analysis. *Genome Medicine*, **2020**, 12, 55	14.4	24

111	No evidence for a major effect of two common polymorphisms of the catalase gene in type 1 diabetes susceptibility. *Diabetes/Metabolism Research and Reviews*, **2006**, 22, 356-60	7.5	24
110	Heterogeneity in the magnitude of the insulin gene effect on HLA risk in type 1 diabetes. *Diabetes*, **2004**, 53, 3286-91	0.9	24
109	Investigation of soluble and transmembrane CTLA-4 isoforms in serum and microvesicles. *Journal of Immunology*, **2014**, 193, 889-900	5.3	23
108	Evidence that Cd101 is an autoimmune diabetes gene in nonobese diabetic mice. *Journal of Immunology*, **2011**, 187, 325-36	5.3	22
107	An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. *Nature Genetics*, **2021**, 53, 1527-1533	36.3	22
106	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. *European Journal of Immunology*, **2015**, 45, 3200-3	6.1	21
105	Plasma concentrations of soluble IL-2 receptor α (CD25) are increased in type 1 diabetes and associated with reduced C-peptide levels in young patients. *Diabetologia*, **2014**, 57, 366-72	10.3	21
104	Commonality in the genetic control of Type 1 diabetes in humans and NOD mice: variants of genes in the IL-2 pathway are associated with autoimmune diabetes in both species. *Biochemical Society Transactions*, **2008**, 36, 312-5	5.1	21
103	The sporulation-specific penicillin-binding protein 5a from Bacillus subtilis is a DD-carboxypeptidase in vitro. *Biochemical Journal*, **1985**, 230, 825-8	3.8	21
102	Rebranding asymptomatic type 1 diabetes: the case for autoimmune beta cell disorder as a pathological and diagnostic entity. *Diabetologia*, **2017**, 60, 35-38	10.3	20
101	Sex-related bias and exclusion mapping of the nonrecombinant portion of chromosome Y in human type 1 diabetes in the isolated founder population of Sardinia. *Diabetes*, **2002**, 51, 3573-6	0.9	20
100	The chromosome 6q22.33 region is associated with age at diagnosis of type 1 diabetes and disease risk in those diagnosed under 5 ́years of age. *Diabetologia*, **2018**, 61, 147-157	10.3	19
99	Lack of association of the Ala(45)Thr polymorphism and other common variants of the NeuroD gene with type 1 diabetes. *Diabetes*, **2004**, 53, 1158-61	0.9	19
98	Association mapping of complex diseases in linked regions: estimation of genetic effects and feasibility of testing rare variants. *Genetic Epidemiology*, **2003**, 24, 36-43	2.6	19
97	Comparison of population- and family-based methods for genetic association analysis in the presence of interacting loci. *Genetic Epidemiology*, **2005**, 29, 51-67	2.6	19
96	Alteration in the penicillin-binding profile of Bacillus megaterium during sporulation. *Nature*, **1982**, 300, 640-3	50.4	19
95	Evidence of association with type 1 diabetes in the SLC11A1 gene region. *BMC Medical Genetics*, **2011**, 12, 59	2.1	18
94	Genetics of diabetes. Trans-racial gene mapping studies. *Baillieres Clinical Endocrinology and Metabolism*, **1991**, 5, 321-40		18

93	A method for identifying genetic heterogeneity within phenotypically defined disease subgroups. *Nature Genetics*, **2017**, 49, 310-316	36.3	17
92	Construction and analysis of tag single nucleotide polymorphism maps for six human-mouse orthologous candidate genes in type 1 diabetes. *BMC Genetics*, **2005**, 6, 9	2.6	17
91	Linkage analysis of 84 microsatellite markers in intra- and interspecific backcrosses. *Mammalian Genome*, **1992**, 3, 457-60	3.2	17
90	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity.. *Cell*, **2022**, 185, 916-938.e58	36.2	17
89	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. *Nature Genetics*, **2021**, 53, 1606-1615	36.3	17
88	Identification of infants with increased type 1 diabetes genetic risk for enrollment into Primary Prevention Trials-GPPAD-02 study design and first results. *Pediatric Diabetes*, **2019**, 20, 720-727	3.6	16
87	Protocol of the adaptive study of IL-2 dose frequency on regulatory T cells in type 1 diabetes (DILfrequency): a mechanistic, non-randomised, repeat dose, open-label, response-adaptive study. *BMJ Open*, **2015**, 5, e009799	3	16
86	A genome-wide assessment of the role of untagged copy number variants in type 1 diabetes. *PLoS Genetics*, **2014**, 10, e1004367	6	16
85	Molecular analysis of the MHC class II region in DR4, DR7, and DR9 haplotypes. *Immunogenetics*, **1991**, 34, 349-57	3.2	16
84	Human IL-6RTIGIT CD4CD127CD25 T cells display potent in vitro suppressive capacity and a distinct Th17 profile. *Clinical Immunology*, **2017**, 179, 25-39	9	15
83	The plasma biomarker soluble SIGLEC-1 is associated with the type I interferon transcriptional signature, ethnic background and renal disease in systemic lupus erythematosus. *Arthritis Research and Therapy*, **2018**, 20, 152	5.7	15
82	No evidence for association of OAS1 with type 1 diabetes in unaffected siblings or type 1 diabetic cases. *Diabetes*, **2006**, 55, 1525-8	0.9	15
81	Detection and frequency estimation of rare variants in pools of genomic DNA from large populations using mutational spectrometry. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **2005**, 570, 267-80	3.3	15
80	A comprehensive, statistically powered analysis of GAD2 in type 1 diabetes. *Diabetes*, **2002**, 51, 2866-70	0.9	15
79	Allele-specific methylation of type 1 diabetes susceptibility genes. *Journal of Autoimmunity*, **2018**, 89, 63-74	15.5	15
78	Development of an integrated genome informatics, data management and workflow infrastructure: a toolbox for the study of complex disease genetics. *Human Genomics*, **2004**, 1, 98-109	6.8	14
77	Mapping multiple linked quantitative trait loci in non-obese diabetic mice using a stepwise regression strategy. *Genetical Research*, **1998**, 71, 51-64	1.1	14
76	Chronic Immune Activation in Systemic Lupus Erythematosus and the Autoimmune PTPN22 Trp Risk Allele Drive the Expansion of FOXP3 Regulatory T Cells and PD-1 Expression. *Frontiers in Immunology*, **2019**, 10, 2606	8.4	14

75	Type 1 Diabetes Prevention: A Goal Dependent on Accepting a Diagnosis of an Asymptomatic Disease. *Diabetes*, **2016**, 65, 3233-3239	0.9	13
74	Capturing the systemic immune signature of a norovirus infection: an n-of-1 case study within a clinical trial. *Wellcome Open Research*, **2017**, 2, 28	4.8	13
73	CD70 expression determines the therapeutic efficacy of expanded human regulatory T cells. *Communications Biology*, **2020**, 3, 375	6.7	13
72	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. *BMC Genomics*, **2014**, 15, 274	4.5	12
71	NKG2D-RAE-1 receptor-ligand variation does not account for the NK cell defect in nonobese diabetic mice. *Journal of Immunology*, **2008**, 181, 7073-80	5.3	12
70	Mouse microsatellites from a flow-sorted 4:6 Robertsonian chromosome. *Mammalian Genome*, **1992**, 3, 620-4	3.2	12
69	Preventing type 1 diabetes in childhood. *Science*, **2021**, 373, 506-510	33.3	12
68	Detection and correction of artefacts in estimation of rare copy number variants and analysis of rare deletions in type 1 diabetes. *Human Molecular Genetics*, **2015**, 24, 1774-90	5.6	11
67	The PTPN22 locus and rheumatoid arthritis: no evidence for an effect on risk independent of Arg620Trp. *PLoS ONE*, **2010**, 5, e13544	3.7	11
66	D'oh! genes and environment cause Crohn's disease. *Cell*, **2010**, 141, 1114-6	56.2	11
65	Stem cells and a cure for type 1 diabetes?. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 15523-4	11.5	11
64	Encyclopedia of the mouse genome III. October 1993. Mouse chromosome 3. *Mammalian Genome*, **1993**, 4 Spec No, S47-57	3.2	11
63	The DILfrequency study is an adaptive trial to identify optimal IL-2 dosing in patients with type 1 diabetes. *JCI Insight*, **2018**, 3,	9.9	11
62	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. *Nature Communications*, **2021**, 12, 5861	17.4	11
61	Association analysis of myosin IXB and type 1 diabetes. *Human Immunology*, **2010**, 71, 598-601	2.3	10
60	Interaction analysis of the CBLB and CTLA4 genes in type 1 diabetes. *Journal of Leukocyte Biology*, **2007**, 81, 581-3	6.5	10
59	Consequences of natural perturbations in the human plasma proteome		10
58	Open Targets Genetics: An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci		10

57	Effective recruitment of participants to a phase I study using the internet and publicity releases through charities and patient organisations: analysis of the adaptive study of IL-2 dose on regulatory T cells in type 1 diabetes (DILT1D). *Trials*, **2015**, 16, 86	2.8	9
56	Fluorescence intensity normalisation: correcting for time effects in large-scale flow cytometric analysis. *Advances in Bioinformatics*, **2009**, 476106	5.5	9
55	Limitations of stratifying sib-pair data in common disease linkage studies: an example using chromosome 10p14-10q11 in type 1 diabetes. *American Journal of Medical Genetics Part A*, **2002**, 113, 158-66		9
54	Ptpn22 and Cd2 Variations Are Associated with Altered Protein Expression and Susceptibility to Type 1 Diabetes in Nonobese Diabetic Mice. *Journal of Immunology*, **2015**, 195, 4841-52	5.3	8
53	Evidence that UBASH3 is a causal gene for type 1 diabetes. *European Journal of Human Genetics*, **2018**, 26, 925-927	5.3	8
52	Discovery, linkage disequilibrium and association analyses of polymorphisms of the immune complement inhibitor, decay-accelerating factor gene (DAF/CD55) in type 1 diabetes. *BMC Genetics*, **2006**, 7, 22	2.6	8
51	Association analysis of the lymphocyte-specific protein tyrosine kinase (LCK) gene in type 1 diabetes. *Diabetes*, **2004**, 53, 2479-82	0.9	8
50	The murine type 1 diabetes loci, Idd1, Idd3, Idd5, Idd9, and Idd17/10/18, do not control thymic CD4-CD8-/TCRalphabeta+ deficiency in the nonobese diabetic mouse. *Mammalian Genome*, **2001**, 12, 175-6	3.2	8
49	Type 1 diabetes genome-wide association analysis with imputation identifies five new risk regions		8
48	An integrated platform to systematically identify causal variants and genes for polygenic human traits		8
47	Intolerable secretion and diabetes in tolerant transgenic mice, revisited. *Nature Genetics*, **2016**, 48, 476-7	36.3	8
46	First Domain Sequence Diversity of DR and DQ Subregion Alleles **1989**, 1027-1031		7
45	Constitutive antiviral immunity at the expense of autoimmunity. *Immunity*, **2014**, 40, 167-9	32.3	6
44	Mouse chromosome 3. *Mammalian Genome*, **1992**, 3 Spec No, S44-54	3.2	6
43	Capturing the systemic immune signature of a norovirus infection: an n-of-1 case study within a clinical trial. *Wellcome Open Research*,2, 28	4.8	6
42	From genome to aetiology in a multifactorial disease, type 1 diabetes **1999**, 21, 164		6
41	In-depth immunophenotyping data of IL-6R on the human peripheral regulatory T cell (Treg) compartment. *Data in Brief*, **2017**, 12, 676-691	1.2	5
40	Sequencing and association analysis of the type 1 diabetes-linked region on chromosome 10p12-q11. *BMC Genetics*, **2007**, 8, 24	2.6	5

39	No evidence for association of the TATA-box binding protein glutamine repeat sequence or the flanking chromosome 6q27 region with type 1 diabetes. *Biochemical and Biophysical Research Communications*, **2005**, 331, 435-41	3.4	5
38	Transmission-ratio distortion at Xp11.4-p21.1 in type 1 diabetes. *American Journal of Human Genetics*, **2000**, 66, 330-2	11	5
37	Reply to Insulin expression: is VNTR allele 698 really anomalous? *Nature Genetics*, **1995**, 10, 379-380	36.3	5
36	Analysis of overlapping genetic association in type 1 and type 2 diabetes. *Diabetologia*, **2021**, 64, 1342-1347	10.3	5
35	Using de novo assembly to identify structural variation of eight complex immune system gene regions. *PLoS Computational Biology*, **2021**, 17, e1009254	5	5
34	Extra-binomial variation approach for analysis of pooled DNA sequencing data. *Bioinformatics*, **2012**, 28, 2898-904	7.2	4
33	A multimarker regression-based test of linkage for affected sib-pairs at two linked loci. *Genetic Epidemiology*, **2006**, 30, 191-208	2.6	4
32	Polymorphism discovery and association analyses of the interferon genes in type 1 diabetes. *BMC Genetics*, **2006**, 7, 12	2.6	4
31	Fine-mapping identifies causal variants for RA and T1D in DNASE1L3, SIRPG, MEG3, TNFAIP3 and CD28/CTLA4 loci		4
30	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity		4
29	mutation alters immune system activation, inflammation, and risk of autoimmunity. *Multiple Sclerosis Journal*, **2021**, 27, 1332-1340	5	4
28	Validity of the family-based association test for copy number variant data in the case of non-linear intensity-genotype relationship. *Genetic Epidemiology*, **2012**, 36, 895-8	2.6	3
27	Diabetes mellitus. *Current Opinion in Genetics and Development*, **1992**, 2, 474-8	4.9	3
26	The interaction of nocardicin A with the penicillin-binding proteins of Bacillus megaterium KM. *FEBS Journal*, **1983**, 136, 545-51		3
25	Interleukin-2 Therapy of Autoimmunity in Diabetes (ITAD): a phase 2, multicentre, double-blind, randomized, placebo-controlled trial. *Wellcome Open Research*, **2020**, 5, 49	4.8	3
24	Supplementation with subspecies EVC001 for mitigation of type 1 diabetes autoimmunity: the GPPAD-SINT1A randomised controlled trial protocol. *BMJ Open*, **2021**, 11, e052449	3	3
23	Enhanced genetic analysis of type 1 diabetes by selecting variants on both effect size and significance, and by integration with autoimmune thyroid disease		3
22	Molecular Structure of Human Class II Antigens **1989**, 40-49		2

21	A rare IL2RA haplotype identifies SNP rs61839660 as causal for autoimmunity		2
20	Peripheral tolerance to insulin is encoded by mimicry in the microbiome		2
19	Dexi disruption depletes gut microbial metabolites and accelerates autoimmune diabetes		2
18	Prevention of type 1 diabetes: what next?. *Lancet, The*, **2008**, 372, 1710-1	40	1
17	Diabetes genes--mutatis mutandis. *Nature*, **1995**, 374, 601-2	50.4	1
16	A method to address differential bias in genotyping in large scale association studies. *PLoS Genetics* , **2005**, preprint, e74	6	1
15	A method for identifying genetic heterogeneity within phenotypically-defined disease subgroups		1
14	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity		1
13	Analysis of overlapping genetic association in type 1 and type 2 diabetes		1
12	Targeting regulatory T cells with Interleukin-2 treatment in type 1 diabetes: a response-adaptive, non-randomised, open-label trial of repeat doses of Aldesleukin (DILfrequency)		1
11	Recent thymic emigrants produce antimicrobial IL-8, express complement receptors and are precursors of a tissue-homing Th8 lineage of memory cells		1
10	Single-cell multi-omics analysis reveals IFN-driven alterations in T lymphocytes and natural killer cells in systemic lupus erythematosus.. *Wellcome Open Research*, **2021**, 6, 149	4.8	1
9	In vivo negative regulation of SARS-CoV-2 receptor, ACE2, by interferons and its genetic control. *Wellcome Open Research*,6, 47	4.8	0
8	Childhood body size directly increases type 1 diabetes risk based on a lifecourse Mendelian randomization approach.. *Nature Communications*, **2022**, 13, 2337	17.4	0
7	Individuals from multiplex insulin dependent diabetes mellitus families express higher levels of TCRBV2S1 than controls. *Biochemical Society Transactions*, **1997**, 25, 314S	5.1	
6	From genomics to aetiology in the multifactorial disease type-1 diabetes. *Biochemical Society Transactions*, **1999**, 27, A1-A1	5.1	
5	Linkage of chromosome 6 and type 1 diabetes. *DNA Sequence*, **1996**, 7, 25-6		
4	Mapping MHC Class II Genes and Disease-Susceptibility : Use of Polymerase Chain Reaction and Dot Hybridization for Human Leukocyte Antigen Allele Typing. *Methods in Molecular Biology*, **1993**, 15, 95-112	1.4	

3	Characterization of HLA-DR and HLA DQ Alleles Associated with Pemphigus Vulgaris **1989**, 426-428	
2	The HLA-DQB1 Gene Contributes to the Genetic Susceptibility to Insulin-Dependent Diabetes Mellitus **1989**, 402-403	
1	Single-cell multi-omics analysis reveals IFN-driven alterations in T lymphocytes and natural killer cells in systemic lupus erythematosus. *Wellcome Open Research*,6, 149	4.8