John A Todd

List of Publications by Year in Descending Order

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	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity.. *Cell*, **2022**, 185, 916-938.e58	36.2	17
307	Childhood body size directly increases type 1 diabetes risk based on a lifecourse Mendelian randomization approach.. *Nature Communications*, **2022**, 13, 2337	17.4	0
306	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. *Nature Genetics*, **2021**, 53, 1606-1615	36.3	17
305	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
304	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. *Nature Communications*, **2021**, 12, 5861	17.4	11
303	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
302	SARS-CoV-2 within-host diversity and transmission. *Science*, **2021**, 372,	33.3	110
301	Analysis of overlapping genetic association in type 1 and type 2 diabetes. *Diabetologia*, **2021**, 64, 1342-1347	10.3	5
300	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
299	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
298	Preventing type 1 diabetes in childhood. *Science*, **2021**, 373, 506-510	33.3	12
297	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
296	mutation alters immune system activation, inflammation, and risk of autoimmunity. *Multiple Sclerosis Journal*, **2021**, 27, 1332-1340	5	4
295	Using de novo assembly to identify structural variation of eight complex immune system gene regions. *PLoS Computational Biology*, **2021**, 17, e1009254	5	5
294	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
293	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
292	CD70 expression determines the therapeutic efficacy of expanded human regulatory T cells. *Communications Biology*, **2020**, 3, 375	6.7	13

291	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
290	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
289	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
288	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
287	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
286	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
285	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
284	Evidence that UBASH3 is a causal gene for type 1 diabetes. *European Journal of Human Genetics*, **2018**, 26, 925-927	5.3	8
283	Genomic atlas of the human plasma proteome. *Nature*, **2018**, 558, 73-79	50.4	529
282	Approaches and advances in the genetic causes of autoimmune disease and their implications. *Nature Immunology*, **2018**, 19, 674-684	19.1	39
281	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
280	Allele-specific methylation of type 1 diabetes susceptibility genes. *Journal of Autoimmunity*, **2018**, 89, 63-74	15.5	15
279	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
278	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
277	Overexpression of the Cytokine BAFF and Autoimmunity Risk. *New England Journal of Medicine*, **2017**, 376, 1615-1626	59.2	198
276	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
275	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
274	A method for identifying genetic heterogeneity within phenotypically defined disease subgroups. *Nature Genetics*, **2017**, 49, 310-316	36.3	17

273	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. *Genome Biology*, **2017**, 18, 165	18.3	41
272	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity. *Journal of Autoimmunity*, **2017**, 84, 75-86	15.5	46
271	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
270	Neonatal and adult recent thymic emigrants produce IL-8 and express complement receptors CR1 and CR2. *JCI Insight*, **2017**, 2,	9.9	26
269	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
268	Childhood adiposity and risk of type 1 diabetes: A Mendelian randomization study. *PLoS Medicine*, **2017**, 14, e1002362	11.6	53
267	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
266	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. *Cell*, **2016**, 167, 1369-1384.e19	56.2	556
265	Type 1 Diabetes Prevention: A Goal Dependent on Accepting a Diagnosis of an Asymptomatic Disease. *Diabetes*, **2016**, 65, 3233-3239	0.9	13
264	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
263	Intolerable secretion and diabetes in tolerant transgenic mice, revisited. *Nature Genetics*, **2016**, 48, 476-7	36.3	8
262	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
261	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
260	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. *Nature Communications*, **2015**, 6, 7000	17.4	268
259	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
258	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
257	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. *European Journal of Immunology*, **2015**, 45, 3200-3	6.1	21
256	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

255	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. *PLoS Genetics*, **2015**, 11, e1005272	6	42
254	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
253	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
252	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
251	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
250	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
249	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
248	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
247	Blood and islet phenotypes indicate immunological heterogeneity in type 1 diabetes. *Diabetes*, **2014**, 63, 3835-45	0.9	144
246	Constitutive antiviral immunity at the expense of autoimmunity. *Immunity*, **2014**, 40, 167-9	32.3	6
245	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
244	Investigation of soluble and transmembrane CTLA-4 isoforms in serum and microvesicles. *Journal of Immunology*, **2014**, 193, 889-900	5.3	23
243	A genome-wide assessment of the role of untagged copy number variants in type 1 diabetes. *PLoS Genetics*, **2014**, 10, e1004367	6	16
242	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
241	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
240	Next generation sequencing reveals the association of DRB3*02:02 with type 1 diabetes. *Diabetes*, **2013**, 62, 2618-22	0.9	35
239	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. *Nature*, **2013**, 498, 232-5	50.4	156
238	Functional IL6R 358Ala allele impairs classical IL-6 receptor signaling and influences risk of diverse inflammatory diseases. *PLoS Genetics*, **2013**, 9, e1003444	6	170

237	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
236	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
235	Seven newly identified loci for autoimmune thyroid disease. *Human Molecular Genetics*, **2012**, 21, 5202-8	5.6	120
234	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
233	Evidence of gene-gene interaction and age-at-diagnosis effects in type 1 diabetes. *Diabetes*, **2012**, 61, 3012-7	0.9	49
232	Proteome-wide analysis of disease-associated SNPs that show allele-specific transcription factor binding. *PLoS Genetics*, **2012**, 8, e1002982	6	74
231	Statistical colocalization of monocyte gene expression and genetic risk variants for type 1 diabetes. *Human Molecular Genetics*, **2012**, 21, 2815-24	5.6	71
230	Extra-binomial variation approach for analysis of pooled DNA sequencing data. *Bioinformatics*, **2012** , 28, 2898-904	7.2	4
229	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
228	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
227	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
226	Metagenomics and personalized medicine. *Cell*, **2011**, 147, 44-56	56.2	164
225	FUT2 nonsecretor status links type 1 diabetes susceptibility and resistance to infection. *Diabetes*, **2011**, 60, 3081-4	0.9	92
224	Evidence of association with type 1 diabetes in the SLC11A1 gene region. *BMC Medical Genetics*, **2011**, 12, 59	2.1	18
223	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
222	Genetic analysis of adult-onset autoimmune diabetes. *Diabetes*, **2011**, 60, 2645-53	0.9	92
221	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
220	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

219	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
218	Evidence that Cd101 is an autoimmune diabetes gene in nonobese diabetic mice. *Journal of Immunology*, **2011**, 187, 325-36	5.3	22
217	Inherited variation in vitamin D genes is associated with predisposition to autoimmune disease type 1 diabetes. *Diabetes*, **2011**, 60, 1624-31	0.9	222
216	Identification of Cd101 as a susceptibility gene for Novosphingobium aromaticivorans-induced liver autoimmunity. *Journal of Immunology*, **2011**, 187, 337-49	5.3	25
215	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
214	Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genetics*, **2011**, 7, e1002254	6	413
213	Genome-wide association analysis of autoantibody positivity in type 1 diabetes cases. *PLoS Genetics* , **2011**, 7, e1002216	6	195
212	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
211	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
210	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. *Nature*, **2010**, 467, 460-4	50.4	224
209	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
208	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
207	The PTPN22 locus and rheumatoid arthritis: no evidence for an effect on risk independent of Arg620Trp. *PLoS ONE*, **2010**, 5, e13544	3.7	11
206	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
205	Genetics of type 1 diabetes: what's next?. *Diabetes*, **2010**, 59, 1561-71	0.9	218
204	Association analysis of myosin IXB and type 1 diabetes. *Human Immunology*, **2010**, 71, 598-601	2.3	10
203	D'oh! genes and environment cause Crohn's disease. *Cell*, **2010**, 141, 1114-6	56.2	11
202	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

201	Etiology of type 1 diabetes. *Immunity*, **2010**, 32, 457-67	32.3	378
200	Reduced expression of IFIH1 is protective for type 1 diabetes. *PLoS ONE*, **2010**, 5, e12646	3.7	66
199	Fluorescence intensity normalisation: correcting for time effects in large-scale flow cytometric analysis. *Advances in Bioinformatics*, **2009**, 476106	5.5	9
198	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
197	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
196	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
195	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
194	IL2RA genetic heterogeneity in multiple sclerosis and type 1 diabetes susceptibility and soluble interleukin-2 receptor production. *PLoS Genetics*, **2009**, 5, e1000322	6	183
193	Contrasting genetic association of IL2RA with SLE and ANCA-associated vasculitis. *BMC Medical Genetics*, **2009**, 10, 22	2.1	41
192	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
191	Cell-specific protein phenotypes for the autoimmune locus IL2RA using a genotype-selectable human bioresource. *Nature Genetics*, **2009**, 41, 1011-5	36.3	224
190	Experimental aspects of copy number variant assays at CCL3L1. *Nature Medicine*, **2009**, 15, 1115-7	50.5	63
189	Rare variants of IFIH1, a gene implicated in antiviral responses, protect against type 1 diabetes. *Science*, **2009**, 324, 387-9	33.3	772
188	Meta-analysis of genome-wide association study data identifies additional type 1 diabetes risk loci. *Nature Genetics*, **2008**, 40, 1399-401	36.3	400
187	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
186	Gene-gene interactions in the NOD mouse model of type 1 diabetes. *Advances in Immunology*, **2008**, 100, 151-75	5.6	53
185	Shared and distinct genetic variants in type 1 diabetes and celiac disease. *New England Journal of Medicine*, **2008**, 359, 2767-77	59.2	546
184	Prevention of type 1 diabetes: what next?. *Lancet, The*, **2008**, 372, 1710-1	40	1

183	A human type 1 diabetes susceptibility locus maps to chromosome 21q22.3. *Diabetes*, **2008**, 57, 2858-61	0.9	85
182	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
181	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
180	Sequencing-based genotyping and association analysis of the MICA and MICB genes in type 1 diabetes. *Diabetes*, **2008**, 57, 1753-6	0.9	29
179	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
178	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
177	Variation analysis and gene annotation of eight MHC haplotypes: the MHC Haplotype Project. *Immunogenetics*, **2008**, 60, 1-18	3.2	246
176	Extreme clonality in lymphoblastoid cell lines with implications for allele specific expression analyses. *PLoS ONE*, **2008**, 3, e2966	3.7	48
175	Sequencing and association analysis of the type 1 diabetes-linked region on chromosome 10p12-q11. *BMC Genetics*, **2007**, 8, 24	2.6	5
174	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
173	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
172	Interleukin-2 gene variation impairs regulatory T cell function and causes autoimmunity. *Nature Genetics*, **2007**, 39, 329-37	36.3	306
171	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. *Nature Genetics*, **2007**, 39, 857-64	36.3	1159
170	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
169	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
168	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
167	Genome bioinformatic analysis of nonsynonymous SNPs. *BMC Bioinformatics*, **2007**, 8, 301	3.6	35
166	Resequencing and association analysis of the SP110 gene in adult pulmonary tuberculosis. *Human Genetics*, **2007**, 121, 155-60	6.3	35

165	Association of the vitamin D metabolism gene CYP27B1 with type 1 diabetes. *Diabetes*, **2007**, 56, 2616-21	10.9	163
164	A method to address differential bias in genotyping in large-scale association studies. *PLoS Genetics*, **2007**, 3, e74	6	59
163	T1DBase: integration and presentation of complex data for type 1 diabetes research. *Nucleic Acids Research*, **2007**, 35, D742-6	20.1	56
162	Interactions between Idd5.1/Ctla4 and other type 1 diabetes genes. *Journal of Immunology*, **2007**, 179, 8341-9	5.3	46
161	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
160	Interaction analysis of the CBLB and CTLA4 genes in type 1 diabetes. *Journal of Leukocyte Biology*, **2007**, 81, 581-3	6.5	10
159	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
158	A multimarker regression-based test of linkage for affected sib-pairs at two linked loci. *Genetic Epidemiology*, **2006**, 30, 191-208	2.6	4
157	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
156	Genetic analysis of completely sequenced disease-associated MHC haplotypes identifies shuffling of segments in recent human history. *PLoS Genetics*, **2006**, 2, e9	6	140
155	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
154	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
153	Polymorphism discovery and association analyses of the interferon genes in type 1 diabetes. *BMC Genetics*, **2006**, 7, 12	2.6	4
152	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
151	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
150	Statistical false positive or true disease pathway?. *Nature Genetics*, **2006**, 38, 731-3	36.3	158
149	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
148	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

147	The Type 1 Diabetes Genetics Consortium. *Annals of the New York Academy of Sciences*, **2006**, 1079, 1-8	6.5	98
146	Regression mapping of association between the human leukocyte antigen region and Graves disease. *American Journal of Human Genetics*, **2005**, 76, 157-63	11	121
145	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
144	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
143	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
142	Type 1 diabetes genes and pathways shared by humans and NOD mice. *Journal of Autoimmunity*, **2005**, 25 Suppl, 29-33	15.5	118
141	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
140	T1DBase, a community web-based resource for type 1 diabetes research. *Nucleic Acids Research*, **2005**, 33, D544-9	20.1	41
139	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
138	Population structure, differential bias and genomic control in a large-scale, case-control association study. *Nature Genetics*, **2005**, 37, 1243-6	36.3	458
137	Genome-wide association studies: theoretical and practical concerns. *Nature Reviews Genetics*, **2005** , 6, 109-18	30.1	881
136	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
135	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
134	Common polymorphism in H19 associated with birthweight and cord blood IGF-II levels in humans. *BMC Genetics*, **2005**, 6, 22	2.6	65
133	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
132	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
131	A method to address differential bias in genotyping in large scale association studies. *PLoS Genetics* , **2005**, preprint, e74	6	1
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16	A rare IL2RA haplotype identifies SNP rs61839660 as causal for autoimmunity		2
15	Type 1 diabetes genome-wide association analysis with imputation identifies five new risk regions		8
14	Consequences of natural perturbations in the human plasma proteome		10
13	Cells with Treg-specific FOXP3 demethylation but low CD25 are prevalent in autoimmunity		1
12	Fine-mapping identifies causal variants for RA and T1D in DNASE1L3, SIRPG, MEG3, TNFAIP3 and CD28/CTLA4 loci		4
11	Peripheral tolerance to insulin is encoded by mimicry in the microbiome		2
10	Analysis of overlapping genetic association in type 1 and type 2 diabetes		1
9	Open Targets Genetics: An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci		10
8	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
7	Dexi disruption depletes gut microbial metabolites and accelerates autoimmune diabetes		2
6	An integrated platform to systematically identify causal variants and genes for polygenic human traits		8
5	Recent thymic emigrants produce antimicrobial IL-8, express complement receptors and are precursors of a tissue-homing Th8 lineage of memory cells		1
4	In vivo negative regulation of SARS-CoV-2 receptor, ACE2, by interferons and its genetic control. *Wellcome Open Research*,6, 47	4.8	0

List of Publications

3	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity	4
2	Enhanced genetic analysis of type 1 diabetes by selecting variants on both effect size and significance, and by integration with autoimmune thyroid disease	3
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