David A Van Heel

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

11,384 96 91 52 h-index g-index citations papers 13,268 96 17.5 5.3 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
91	Integrating polygenic risk scores in the prediction of type 2 diabetes risk and subtypes in British Pakistanis and Bangladeshis: A population-based cohort study <i>PLoS Medicine</i> , 2022 , 19, e1003981	11.6	1
90	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
89	MC3R links nutritional state to childhood growth and the timing of puberty. <i>Nature</i> , 2021 , 599, 436-441	50.4	9
88	Fine-scale population structure and demographic history of British Pakistanis. <i>Nature Communications</i> , 2021 , 12, 7189	17.4	0
87	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020 , 581, 459-464	50.4	53
86	Characterising a healthy adult with a rare HAO1 knockout to support a therapeutic strategy for primary hyperoxaluria. <i>ELife</i> , 2020 , 9,	8.9	19
85	Cohort Profile: East London Genes & Health (ELGH), a community-based population genomics and health study in British Bangladeshi and British Pakistani people. <i>International Journal of Epidemiology</i> , 2020 , 49, 20-21i	7.8	19
84	A single nucleotide polymorphism genetic risk score to aid diagnosis of coeliac disease: a pilot study in clinical care. <i>Alimentary Pharmacology and Therapeutics</i> , 2020 , 52, 1165-1173	6.1	8
83	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020 , 182, 1198-1213.e14	56.2	88
82	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
81	Identification of rare sequence variation underlying heritable pulmonary arterial hypertension. Nature Communications, 2018, 9, 1416	17.4	182
80	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. <i>Nature Communications</i> , 2018 , 9, 711	17.4	35
79	Exome Sequencing and Rare Variant Analysis Reveals[Multiple Filaggrin Mutations in Bangladeshi[Families with Atopic Eczema and[Additional Risk Genes. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 2674-2677	4.3	19
78	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. <i>JAMA Oncology</i> , 2017 , 3, 636-651	13.4	236
77	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. <i>Nature Communications</i> , 2017 , 8, 303	17.4	52
76	DNAJC21 Mutations Link a Cancer-Prone Bone Marrow Failure Syndrome to Corruption in 60S Ribosome Subunit Maturation. <i>American Journal of Human Genetics</i> , 2016 , 99, 115-24	11	55
75	Health and population effects of rare gene knockouts in adult humans with related parents. <i>Science</i> , 2016 , 352, 474-7	33.3	185

(2010-2016)

74	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. <i>PLoS Medicine</i> , 2016 , 13, e1001976	11.6	100
73	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. <i>Nature Genetics</i> , 2015 , 47, 577-8	36.3	99
72	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. <i>Nature Genetics</i> , 2015 , 47, 1085-90	36.3	112
71	Exome sequencing of 75 individuals from multiply affected coeliac families and large scale resequencing follow up. <i>PLoS ONE</i> , 2015 , 10, e0116845	3.7	8
70	HLA-DQA1-HLA-DRB1 variants confer susceptibility to pancreatitis induced by thiopurine immunosuppressants. <i>Nature Genetics</i> , 2014 , 46, 1131-4	36.3	130
69	Diagnosis and management of adult coeliac disease: guidelines from the British Society of Gastroenterology. <i>Gut</i> , 2014 , 63, 1210-28	19.2	660
68	Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants. <i>Gut</i> , 2014 , 63, 415-22	19.2	92
67	Genetic insights into common pathways and complex relationships among immune-mediated diseases. <i>Nature Reviews Genetics</i> , 2013 , 14, 661-73	30.1	394
66	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. <i>Nature</i> , 2013 , 498, 232-5	50.4	156
65	Mutations in CSTA, encoding Cystatin A, underlie exfoliative ichthyosis and reveal a role for this protease inhibitor in cell-cell adhesion. <i>American Journal of Human Genetics</i> , 2011 , 89, 564-71	11	68
64	Inflammatory skin and bowel disease linked to ADAM17 deletion. <i>New England Journal of Medicine</i> , 2011 , 365, 1502-8	59.2	247
63	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. <i>Nature Genetics</i> , 2011 , 43, 1193-201	36.3	535
62	Comparative methylomics reveals gene-body H3K36me3 in Drosophila predicts DNA methylation and CpG landscapes in other invertebrates. <i>Genome Research</i> , 2011 , 21, 1841-50	9.7	44
61	Pervasive sharing of genetic effects in autoimmune disease. <i>PLoS Genetics</i> , 2011 , 7, e1002254	6	413
60	Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. <i>PLoS Genetics</i> , 2011 , 7, e1002197	6	261
59	A meta-analysis of genome-wide association scans identifies IL18RAP, PTPN2, TAGAP, and PUS10 as shared risk loci for Crohnß disease and celiac disease. <i>PLoS Genetics</i> , 2011 , 7, e1001283	6	142
58	Multiple common variants for celiac disease influencing immune gene expression. <i>Nature Genetics</i> , 2010 , 42, 295-302	36.3	727
57	Comprehensive, quantitative mapping of T cell epitopes in gluten in celiac disease. <i>Science Translational Medicine</i> , 2010 , 2, 41ra51	17.5	321

56	Evolutionary and functional analysis of celiac risk loci reveals SH2B3 as a protective factor against bacterial infection. <i>American Journal of Human Genetics</i> , 2010 , 86, 970-7	11	130
55	Common and different genetic background for rheumatoid arthritis and coeliac disease. <i>Human Molecular Genetics</i> , 2009 , 18, 4195-203	5.6	109
54	Recent advances in coeliac disease genetics. <i>Gut</i> , 2009 , 58, 473-6	19.2	19
53	Association study of the IL18RAP locus in three European populations with coeliac disease. <i>Human Molecular Genetics</i> , 2009 , 18, 1148-55	5.6	27
52	The genetics of chronic inflammatory diseases. Human Molecular Genetics, 2009, 18, R101-6	5.6	40
51	Replication of celiac disease UK genome-wide association study results in a US population. <i>Human Molecular Genetics</i> , 2009 , 18, 4219-25	5.6	60
50	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. <i>Nature Genetics</i> , 2009 , 41, 1182-90	36.3	433
49	Genetics and pathogenesis of coeliac disease. <i>Seminars in Immunology</i> , 2009 , 21, 346-54	10.7	40
48	Analysis of HLA and non-HLA alleles can identify individuals at high risk for celiac disease. <i>Gastroenterology</i> , 2009 , 137, 834-40, 840.e1-3	13.3	103
47	Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF-kappaB signalling. <i>Gut</i> , 2009 , 58, 1078-83	19.2	147
46	Association study of IL2/IL21 and FcgRIIa: significant association with the IL2/IL21 region in Scandinavian coeliac disease families. <i>Genes and Immunity</i> , 2008 , 9, 364-7	4.4	30
45	Newly identified genetic risk variants for celiac disease related to the immune response. <i>Nature Genetics</i> , 2008 , 40, 395-402	36.3	524
44	Translational mini-review series on the immunogenetics of gut disease: immunogenetics of coeliac disease. <i>Clinical and Experimental Immunology</i> , 2008 , 153, 162-73	6.2	38
43	Shared and distinct genetic variants in type 1 diabetes and celiac disease. <i>New England Journal of Medicine</i> , 2008 , 359, 2767-77	59.2	546
42	Genetic analysis of innate immunity in Crohnß disease and ulcerative colitis identifies two susceptibility loci harboring CARD9 and IL18RAP. <i>American Journal of Human Genetics</i> , 2008 , 82, 1202-7	10 ¹¹	196
41	Effective detection of human leukocyte antigen risk alleles in celiac disease using tag single nucleotide polymorphisms. <i>PLoS ONE</i> , 2008 , 3, e2270	3.7	113
40	Detection, imputation, and association analysis of small deletions and null alleles on oligonucleotide arrays. <i>American Journal of Human Genetics</i> , 2008 , 82, 1316-33	11	32
39	Associations with tight junction genes PARD3 and MAGI2 in Dutch patients point to a common barrier defect for coeliac disease and ulcerative colitis. <i>Gut</i> , 2008 , 57, 463-7	19.2	119

(2005-2007)

38	development of T-helper type 2-like lymphocytes - Possible implications for NOD2-associated Crohn ® disease. <i>Journal of Crohn</i> w and <i>Colitis</i> , 2007 , 1, 106-15	1.5	14
37	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. <i>Nature Genetics</i> , 2007 , 39, 827-9	36.3	518
36	Selective NOD1 agonists cause shock and organ injury/dysfunction in vivo. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2007 , 175, 595-603	10.2	49
35	A structural and immunological basis for the role of human leukocyte antigen DQ8 in celiac disease. <i>Immunity</i> , 2007 , 27, 23-34	32.3	128
34	Novel association in chromosome 4q27 region with rheumatoid arthritis and confirmation of type 1 diabetes point to a general risk locus for autoimmune diseases. <i>American Journal of Human Genetics</i> , 2007 , 81, 1284-8	11	171
33	Human pancreatic secretory trypsin inhibitor stabilizes intestinal mucosa against noxious agents. <i>American Journal of Pathology</i> , 2007 , 171, 1462-73	5.8	11
32	Modulation of dendritic cell phenotype and function in an in vitro model of the intestinal epithelium. <i>European Journal of Immunology</i> , 2006 , 36, 864-74	6.1	67
31	Normal responses to specific NOD1-activating peptidoglycan agonists in the presence of the NOD2 frameshift and other mutations in Crohnß disease. <i>European Journal of Immunology</i> , 2006 , 36, 1629-35	6.1	12
30	Interleukin 15: its role in intestinal inflammation. <i>Gut</i> , 2006 , 55, 444-5	19.2	29
29	Antagonists and non-toxic variants of the dominant wheat gliadin T cell epitope in coeliac disease. <i>Gut</i> , 2006 , 55, 485-91	19.2	49
28	Lack of association of MYO9B genetic variants with coeliac disease in a British cohort. <i>Gut</i> , 2006 , 55, 96	917922	49
27	Recent advances in coeliac disease. <i>Gut</i> , 2006 , 55, 1037-46	19.2	210
26	Detection of muramyl dipeptide-sensing pathway defects in patients with Crohn® disease. <i>Inflammatory Bowel Diseases</i> , 2006 , 12, 598-605	4.5	19
25	Calcium channel TRPV6 expression in human duodenum: different relationships to the vitamin D system and aging in men and women. <i>Journal of Bone and Mineral Research</i> , 2006 , 21, 1770-7	6.3	45
24	Muramyl dipeptide and toll-like receptor sensitivity in NOD2-associated Crohnß disease. <i>Lancet, The,</i> 2005 , 365, 1794-6	40	264
23	A common CTLA4 haplotype associated with coeliac disease. <i>European Journal of Human Genetics</i> , 2005 , 13, 440-4	5.3	65
22	Synergistic enhancement of Toll-like receptor responses by NOD1 activation. <i>European Journal of Immunology</i> , 2005 , 35, 2471-6	6.1	127
21	Genetics in coeliac disease. <i>Baillierew Best Practice and Research in Clinical Gastroenterology</i> , 2005 , 19, 323-39	2.5	78

20	Association between a complex insertion/deletion polymorphism in NOD1 (CARD4) and susceptibility to inflammatory bowel disease. <i>Human Molecular Genetics</i> , 2005 , 14, 1245-50	5.6	260
19	T cells in peripheral blood after gluten challenge in coeliac disease. <i>Gut</i> , 2005 , 54, 1217-23	19.2	101
18	Synergy between TLR9 and NOD2 innate immune responses is lost in genetic Crohnß disease. <i>Gut</i> , 2005 , 54, 1553-7	19.2	92
17	Inflammatory bowel disease susceptibility loci defined by genome scan meta-analysis of 1952 affected relative pairs. <i>Human Molecular Genetics</i> , 2004 , 13, 763-70	5.6	198
16	The IBD6 Crohn B disease locus demonstrates complex interactions with CARD15 and IBD5 disease-associated variants. <i>Human Molecular Genetics</i> , 2003 , 12, 2569-75	5.6	44
15	Further evidence of IBD5/CARD15 (NOD2) epistasis in the susceptibility to ulcerative colitis. <i>American Journal of Human Genetics</i> , 2003 , 73, 1465-6	11	53
14	Analysis of the IBD5 locus and potential gene-gene interactions in Crohn® disease. <i>Gut</i> , 2003 , 52, 541-6	19.2	85
13	Detecting the risks of osteoporotic fractures in coeliac disease. <i>Gut</i> , 2003 , 52, 1229-30	19.2	5
12	Association of TNF-alpha-857C with inflammatory bowel disease in the Australian population. <i>Scandinavian Journal of Gastroenterology</i> , 2003 , 38, 533-4	2.4	8
11	Inflammatory bowel disease is associated with a TNF polymorphism that affects an interaction between the OCT1 and NF(-kappa)B transcription factors. <i>Human Molecular Genetics</i> , 2002 , 11, 1281-9	5.6	214
10	Identification of novel polymorphisms in the beta7 integrin gene: family-based association studies in inflammatory bowel disease. <i>Genes and Immunity</i> , 2001 , 2, 455-60	4.4	16
9	NOD2 (CARD15), the first susceptibility gene for Crohn ß disease. <i>Gut</i> , 2001 , 49, 752-4	19.2	53
8	Crohn R disease: genetic susceptibility, bacteria, and innate immunity. <i>Lancet, The</i> , 2001 , 357, 1902-4	40	55
7	Colonoscopic appearances and diagnosis of intussusception due to large-bowel lipoma. <i>Endoscopy</i> , 1999 , 31, 508	3.4	3
6	A direct multi-generational estimate of the human mutation rate from autozygous segments seen in thousands of parentally related individuals		11
5	Fine-scale population structure and demographic history of British Pakistanis		1
4	Cohort Profile: East London Genes & Health (ELGH), a community based population genomics and health study of British-Bangladeshi and British-Pakistani people		6
3	Deep phenotyping of a healthy human HAO1 knockout informs therapeutic development for primary hyperoxaluria type 1		5

2 Evaluating potential drug targets through human loss-of-function genetic variation

12

Transferability of genetic loci and polygenic scores for cardiometabolic traits in British Pakistanis and Bangladeshis

3